

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:50 ; Search time 7690.41 Seconds
(without alignments)
2375.375 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGPLENQLSLLEKAI.....LSRQEGHASPPLPQPVSM 377

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO spool/US09736250/runat 07022005 154924 20406/app query.fasta_1.718
-DB=GenEmbl -QWMT=fastcap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=ptp -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250_QCGN 1 1 3890 @runat 07022005 154924 20406 -NCPJ=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	1962	100.0	1133	6	AR145734
2	1962	100.0	1260	6	AR087353
3	1962	100.0	1260	6	CQ812312
4	1962	100.0	1260	6	AR281918

5	1962	100.0	1260	6	AR380354
6	1962	100.0	1260	9	HDMCYI
7	1962	100.0	1384	9	AF135162
8	1962	100.0	1817	9	BC000420
9	1962	100.0	1889	6	CQ468129
10	1962	100.0	1889	9	BC004975
11	1962	99.5	1131	9	CR541783
12	1851	94.3	1535	10	AF005886
13	1841	94.3	2348	10	BC003290
14	1841	93.8	2755	6	CQ414515
15	1666.5	84.9	200850	2	AC101881
16	1666.5	84.9	202228	2	AC124646
17	1662	84.7	179333	2	AC117658
18	1325.5	67.6	1658	5	BC061670
19	1297.5	66.1	1553	5	BC075116
20	1176	59.9	690	6	CQ721727
21	1013	51.6	2339	5	BC068369
22	1011	51.5	2166	5	BC044400
23	891	45.4	601	11	BV167473
24	811	41.3	490	6	CQ685286
25	795	40.5	29867	9	AY207372
26	795	40.5	35191	9	AC111196
27	795	40.5	178916	2	AP002874
28	795	40.5	179443	2	AC079051
29	770.5	39.3	2146	6	CQ414223
30	763	38.9	804	6	BD079737
31	748	38.1	444	6	AX886044
32	748	38.1	444	6	BD025654
33	746.5	38.0	3597	5	BC081135
34	731	37.3	444	6	CQ671106
35	727	37.1	11793	10	AF228739S2
36	727	37.1	153811	10	AC134827
37	705	35.9	241543	2	AC099472
38	705	35.9	260517	2	AC111318
39	705	35.9	270068	2	AC113213
40	677	34.5	601	11	BV180201
41	650	33.1	818	5	BX930648
42	642	32.7	790	5	BX930233
43	638	32.5	389	6	CQ661908
44	625	31.9	369	6	CQ688465
45	621	31.7	516	6	CQ410974

ALIGNMENTS

RESULT 1	AR145734	AR145734	Sequence 2 from patent US 6218115.	1133 bp	DNA	linear	PAT 08-AUG-2001
LOCUS	AR145734	Sequence 2 from patent US 6218115.					
DEFINITION	AR145734	Sequence 2 from patent US 6218115.					
ACCESSION	AR145734	Sequence 2 from patent US 6218115.					
VERSION	AR145734.1	GI:15108923					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 1133)						
AUTHORS	Nakamura,T.						
TITLE	Human cyclin I and genes encoding same						
JOURNAL	Patent: US 6218115-A 2 17-APR-2001;						
FEATURES	Location/Qualifiers						
source	1..1133						
	/organism="unknown"						
	/mol_type="unassigned DNA"						

ORIGIN

Alignment Scores:							
Pred. No.:	1.22e-174	Length:	1133				
Score:	1962.00	Matches:	377				
Percent Similarity:	100.00%	Conservative:	0				
Best Local Similarity:	100.00%	Mismatches:	0				
Query Match:	100.00%	Indels:	0				
DB:	6	Gaps:	0				

```
US-09-736-250-1 (1-377) x AR145734 (1-1133)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGATGGAAAGTGAATGTGGAAATGCCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTTGGCTAGCAGTCTTTTGGATAGGTTTTCAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAATGTGGAAATGCCTTCAATCAGAAATGTT 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 360
Qy 121 GlyCysSerSerGluIleArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAATGGAGAAATTTATTCGGATAGGTTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGACACACCATTTGATTTCTTCATATTTTCCATGCCATGCAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCAATTCCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAACCTCTTCAGAAAGCACAGATGGATAGCTCCCATGTCATTCGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACCTTTTCACTCTGAGTCTTCCGCTTCCGCTCGAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCCTCAAGCACACCTGGTACCTGTGCAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCCTCTCTGTCAGGCGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGGCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAAATGGGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080
```

361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTCTGTGCATG 1131

RESULT 2
LOCUS AR087353 1260 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES Location/Qualifiers
1..1260
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR087353 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGATGGAAAGTGAATGTGGAAATGCCTTCAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTTGGCTAGCAGTCTTTTGGATAGGTTTTCAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAATGTGGAAATGCCTTCAATCAGAAATGTT 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 360
Qy 121 GlyCysSerSerGluIleArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAATGGAGAAATTTATTCGGATAGGTTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGACACACCATTTGATTTCTTCATATTTTCCATGCCATGCAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCAATTCCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAACCTCTTCAGAAAGCACAGATGGATAGCTCCCATGTCATTCGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACCTTTTCACTCTGAGTCTTCCGCTTCCGCTCGAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCCTCAAGCACACCTGGTACCTGTGCAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCCTCTCTGTCAGGCGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGGCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAAATGGGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080

Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGATCC 600
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATCTCTGATTGCTTTCT 660
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 661 CTTCAATTTGAATGCTTTCAAGAAACACAGATGATAGTCTCCCAAGTTGATCCATTGTCGG 720
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 721 GAGCTTGCGGCACATCACTTTCTACTCTGAGATCTTCCCTGCTCTGAAATCCGTTTAT 780
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 781 GTCTACCGTCCCTCAAGCACACCCCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300
 Db 841 CCCTCCTCTGCTCCAGGCCAGACTTCTCCAAGGACAAACAGCAAGCCAGAAAGTCCAGTC 900
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGACCTCT 960
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGCTTCTATGATGGATCAACGGCTC 1020
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1021 TATAATGAAGATAATGTCACGAAATGCGGTTCTGTGTGGCACTGATTTATCAAGA 1080
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1081 CAAGAGGACATGCTTCCCTTGTCACCTTTGCAGCCTGTTCTGTCTATG 1131

RESULT 3
 CQ812312
 LOCUS CQ812312 1260 bp DNA linear PAT 24-MAY-2004
 DEFINITION Sequence 64 from Patent WO2004038020.
 ACCESSION CQ812312
 VERSION CQ812312.1 GI:47601932
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 1 Wittig R., Poustka A., Mollenhauer, J. and Schadendorf, D.
 Target genes for the diagnosis and treatment of cancer
 Patent: WO 2004038020-A 64 06-MAY-2004;
 Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechtes (DE)

FEATURES
 source Location/Qualifiers
 1..1260
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="caxon:9606"
 misc_feature 1..1260
 /note="D50310"

ORIGIN
 Alignment Scores:
 Pred. No.: 1.4e-174 Length: 1260
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-736-250-1 (1-377) x CQ812312 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 1 ATGAAGTTTCAGGGCCTTTGGAAAACACAGAGATTGTCTTCTCTGTGGAAAAGCGCATC 60
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCGCTTCAAAATCAGAATGTT 120
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 121 TCTCATCCCGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATCAAC 180
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 181 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGTGATAGTGTTCAGTACCCTGA 240
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 241 AAGGCTCATCCAAATACTTGAAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 301 ACTGTTGAGGAGATGAGAGAAATTCAGTACTAAGGTATTGGCAGAGACAGATTTCTGT 360
 Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 361 GGATGTTCTCATCTGAAATTTTGAGAATGAGAGAAATTTCTGGATAAGTGAATGG 420
 Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 421 GATCTTCACACAGCACACCATTTGATTTCTCATATTTTCCATGTCATTCAGTGTGCA 480
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 481 ACTAGGCTCTAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGATCC 600
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATCTCTGATTGCTTTCT 660
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 661 CTTCAATTTGAATGCTTTCAAGAAACACAGATGATAGTCTCCCAAGTTGATCCATTGTCGG 720
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 721 GAGCTTGCGGCACATCACTTTCTACTCTGAGATCTTCCCTGCTCTGAAATCCGTTTAT 780
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 781 GTCTACCGTCCCTCAAGCACACCCCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300
 Db 841 CCCTCCTCTGCTCCAGGCCAGACTTCTCCAAGGACAAACAGCAAGCCAGAAAGTCCAGTC 900
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGACCTCT 960
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGCTTCTATGATGGATCAACGGCTC 1020
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1021 TATAATGAAGATAATGTCACGAAATGCGGTTCTGTGTGGCACTGATTTATCAAGA 1080

```
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCCTGTTCTGTGTCATG 1131

RESULT 4
AR281918
LOCUS AR281918 1260 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS unknown.
SOURCE unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang, M., Nandabalan, K. and Schulz, V.P.
TITLE HsReq*1 and hReq*2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
    Location/Qualifiers
        1..1260
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
  Pred. No.: 1.4e-174 Length: 1260
  Score: 1962.00 Matches: 377
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR281918 (1-1260)

Qy 1 MetLysPheProGlyProLeuGlnAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAACACAGAGATGCTTTCTTCTGTTGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGATGGAAGTGAATGTGGGAAATGCCTTCNAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTCAGTTGTATTGCAATCAGCTGTTTTCCTAGCTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluLysLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAATGAGAGAAATATTCTGGATGAATGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGGATTTTCTCATATTTTCCATGTCATTCGAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATAGGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCTCTGTATGGCTTGCACCACTCTGCAATTCAGAGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTTGGCCATGGTTAGTCTGGAATGGAAATCAATCTCTGATTGCTTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACAATTAAGCTTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTGCG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGACAAAGAGGTGTTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCCAGGCCAGACTTCTCCAAGACAAACAGCAGCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCTGTTCTGTGTCATG 1131

RESULT 5
AR380354
LOCUS AR380354 1260 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION AR380354.1 GI:40087988
KEYWORDS unknown.
ORGANISM unknown.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 899 19-AUG-2003;
FEATURES
    Location/Qualifiers
        1..1260
            /organism="unknown"
            /mol_type="genomic DNA"

ORIGIN
Alignment Scores:
  Pred. No.: 1.4e-174 Length: 1260
  Score: 1962.00 Matches: 377
  Percent Similarity: 100.00% Conservative: 0
  Best Local Similarity: 100.00% Mismatches: 0
  Query Match: 100.00% Indels: 0
  DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR380354 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAACACAGAGATGCTTTCTTCTGTTGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACAGAGATGGAAGTGAATGTGGGAAATGCCTTCNAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTCAGTTGTATTGCAATCAGCTGTTTTCCTAGCTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluLysLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAATGAGAGAAATATTCTGGATGAATGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATGGATTTTCTCATATTTTCCATGTCATTCGAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATAGGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCTCTGTATGGCTTGCACCACTCTGCAATTCAGAGATCC 600
```

Db 61 ACTAGGAGGACACAGATGGAAGTGAATGTGCGAAATGCCTTCAATCAAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAACTCAATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATATCTGAGTGTATTCCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGATTCAGTACTAAGGTATTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAATGAGAGATTAATCTGGATAAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTACACAGCCACACCACTTGGATTTCTTATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTCAAGTTGGCCAAATGAGCCCATCTCACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTGTGGAATGAGAACTCAATCTCGATTGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACATTTGACTGCTTCAGAAAGCAGATGATAGTCTCCAGTGTATCCATTTGCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrIleuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTTGGTGACCTGTGACAAAGGAGTGTTCAGATTTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTTCTCTGTCAGGCCAGACTTCTCCAGGACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCGAGTGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGAATGACCTTCTATGATGGAATCAAAAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAAGATATATGCTTCAGAAATATGGGTCTCTGTGTGGCAGTATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACTTTCAGCCTTGTTCGTGATG 1131

RESULT 6
HUMCYI

LOCUS HUMCYI 1260 bp mRNA linear PRI 10-FEB-1999
DEFINITION Human mRNA for cyclin I, complete cds.
ACCESSION D50310
VERSION D50310.1 GI:1183161
KEYWORDS cyclin I.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Nakamura,T., Sanokawa,R., Sasaki,Y.F., Ayusawa,D., Oishi,M. and Mori,N.
TITLE Cyclin I: a new cyclin encoded by a gene isolated from human brain
JOURNAL Exp. Cell Res. 221 (2), 534-542 (1995)
MEDLINE 96086776
PUBMED 7493655
REFERENCE 2 (bases 1 to 1260)
AUTHORS Nakamura,T.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1260)
AUTHORS Nakamura,T.
TITLE Direct Submission
JOURNAL Submitted (17-APR-1995) Takeshi Nakamura, Sumitomo Electric Industries, Biomedical R&D Department, 1, Taya-cho, Sakae-ku, Yokohama, Kanagawa 244, Japan (E-mail:tnakam@pele.sumiden.co.jp, Tel:045-853-7275, Fax:045-853-3528)
FEATURES
source
1..1260
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FC6"
/tissue_type="Brain"
1..1134
/codon_start=1
/product="cyclin I"
/protein_id="BAA0849.1"
/db_xref="GI:1183162"
/translation="MKFPGPLENQRSLFLEKAITREAOQMKVNRKMPNSQNVSPSQ RDEIPIVLAKLYQFNLYPETFALLASLLDRFLATVKAHPKYLSCIAISCFLLAAKT V EDERIPVLALARDSFCGSSSEILMERIILDKNLDLHTATPLDPLHFLHAIVS TRQLFSLPKLSPSHLAVLTQQLLHMACNQLQFRGSMALAMVLSLEKILPDW LSIUILLQKQMDSSQLIHRELVHHLSTLQSSPLNSVYVTRPLKHTLVTCDKGV FRIHPSPVGPFDISKNSKEVPVRGTAFFYHLLPAASGCKQTSKTKRKEEMVEDDFY DGIRLYNEDNVSENVSGVGTDLRSQEGHASPCLPQPVSVM"
CDS
Alignment Scores:
Pred. No.: 1.4e-174 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-1 (1-377) x HUMCYI (1-1260)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGAGCCCTTTGGAAACACAGAGATTGCTTCTTCTGTTGGAAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGCGAAATGCCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAACTCAATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240

```
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACCTTGAGTTGATTGCAATCAGCTGTTTCTTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGAGGAAGATGAGAAATTCAGTACTAAAGGTAATTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAAAGGAGAAATTTCTGGATAAGTTGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATGGAATTTCTTATATTTCCATGCAATTCAGAGTGCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCAACTTCTGCAATTCAGAGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCGCCATGTTAGTCTGGAATGGAATGAGAACTCAATCTGATTTGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCCCACTGATCCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTCTACTCTGAGTCTTCCCTGCTCTGAAATCCGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCAGGCGCCAGACTTCTCCAGGACACACAGCAAGAGTGCACGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGCCCTTTTACATCACTCCAGCTGCCAGTGGTGGCAACGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTTCAGAAATGCGGTCTGTGTGTCGACCTGATTTATCAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACTTTGAGCCCTGTTTCTGTCATG 1131

RESULT 7
AF135162 1384 bp mRNA linear PRI 17-MAR-2000
LOCUS Homo sapiens cyclin I (CYCL) mRNA, complete cds.
DEFINITION AF135162
ACCESSION AF135162
VERSION AF135162.1 GI:7259481
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1384)
AUTHORS Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and
```

```
Qiang, B.Q.
Isolating a new cDNA coding for human cyclin protein
Unpublished
2 (bases 1 to 1384)
Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and
Qiang, B.Q.
Direct Submission
Submitted (16-MAR-1999) Dept. of Biochemistry, Ins. of Basic Med.
Science, 5 Dong Dan 3 Tiao, Beijing 100005, P.R. China
Location/Qualifiers
1..1384
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1384
/gene="CYCL"
200..1333
/gene="CYCL"
/codon_start=1
/product="cyclin I"
/protein_id="AAP43786.1"
/db_xref="GI:7259482"
/translation="MRPGELENQRISFLEKAITREAQWKVNRKMPNQNVSPQ
RDEVIQWLAKLYQFNPETFALASSLLDRFLATVAKHPKYLISCIASFFFLAAKV
EEDRIPVLKVLARDSEFCGSSSEILMERIILDKLNDLHTATPDLFHFAIAYS
TRQLLFSLPKLSQHLAVTLKQLLHMCACNQLQPRGSMALAMVLSLEMEKLIPOW
LSLTIELLOKQMDSSQLIHRELVAHLSTLOSSLPNSVYVVRPLKHLVTCODKG
FRLHPSVPGPDFSKNSKEVPVRGTAAFYVHLPRASGCKQSTKRKEVEMEVDYF
DGIRLYNEDNVSENVSGVCTDLSRQEGHSPCPPLQPVSV"
ORIGIN
Alignment Scores:
Pred. No.: 1,57e-174 Length: 1384
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-736-250-1 (1-377) x AF135162 (1-1384)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 200 ATGAAGTTTCAGGCGCTTTGGAAACACAGAGATTGTCTTCTCTTTGGAAAGCGCAATC 259
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 260 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGCGAAATGCGCTTCAATCAGAAATGTT 319
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 320 TCTCCATCCACAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 379
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 380 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGCTCTTTTGGATAGGTTTTTACGCTACC 439
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 440 AAGGCTCATCCAAATACCTTGAGTTGATTGCAATCAGCTGTTTCTTAGCTGCCAAG 499
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 500 ACTGTGAGGAAGATGAGAAATTCAGTACTAAAGGTAATTGGCAAGACAGATTTCTGT 559
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 560 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATTTCTGGATAAGTTGAAATGG 619
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 620 GATCTTCACACAGCCACACCATGGAATTTCTTCAATTTTCCATGCAATTCAGAGTGCA 679
```

161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 680 ACTAGGCTCAGTTACTTTTCAGTTGCCCCAAATGAGCCCAATCTCAACATTTGGCAGTC 739
 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 740 CTTACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCC 799
 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
 800 ATGCTTGCTCTGGCCATGTTAGTCTGAAATGAGAACTCATCTCGATGTTGCTTCT 859
 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 860 CTTACAATGAACTGCTTTCAGAAAGCAGATGATAGTCCCACTGATCCATTTGTCGG 919
 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 920 GAGCTTGTGGCAGCATCACTTTCTACTCTGCACTCTCCCTGCTCTGAATTCGTTTAT 979
 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 980 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCACAAAGGAGTGTTCAGATTACAT 1039
 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 1040 CCCCCTCTGTGCCAGGCCAGACTTCTCCAAAGACACACAGCAGCAGGATGCCAGTC 1099
 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 1100 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCGAGTGGTGTCAGCAGACCTCT 1159
 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 1160 ACTAAACGCAAGTAGAGGAATGGAAGTGCATCTTATGATGCAATCAACAGCGCTC 1219
 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 1220 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGTGCACTGATTTATCAAGA 1279
 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 1280 CAAGAGGACATGCTTCCCTGTGCCACTTTGAGCGCTGTTCTGTGCAATG 1330

RESULT 8
 BC000420
 LOCUS
 DEFINITION Homo sapiens cyclin I, mRNA (cdna clone MGC:8665 IMAGE:2964432), complete cds.
 ACCESSION BC000420
 VERSION BC000420.2 GI:38197480
 KEYWORDS MGC.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1817)
 Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heide, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, D.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uesdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullen, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REMARK
 COMMENT

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Scherch, A., Schein, J.E., Jones, S.D., and Marra, M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16999-16903 (2002)
 12477932
 2 (bases 1 to 1817)
 Strausberg, R.
 Direct Submission
 Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 On Nov 6, 2003 this sequence version replaced gi:12653302.
 Contact: MGC help desk
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: http://www.nisc.nih.gov/
 Contact: nisc_mgc@hgrl.nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Teague, J., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 1 Row: 0 Column: 8
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17738314.

FEATURES
 Location/Qualifiers
 1..1817
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="MGC:8665 IMAGE:2964432"
 /tissue_type="Muscle, rhabdomyosarcoma"
 /clone_lib="NIH MGC 17"
 /lab_host="DH10B-R"
 /notes="Vector: pOTB7"
 1..1817
 /gene="CCNI"
 /notes="synonyms: CYC1, CYI"
 /db_xref="LocusID:10983"
 544..1677
 /gene="CCNI"
 /codon_start=1
 /product="cyclin I"
 /protein_id="AAH0420.1"
 /db_xref="GI:12653303"
 /db_xref="LocusID:10983"
 /translations="MKPGLPLENQRUSFLLEKAITREAOQMKVNRKMPNQNVPSQ RDEVIQMLAKYQFNLYPETFALSSLDRLFLATVKRHPKYLSCIAISCFFLAAVT EDERIPVLKVLARDFCGSSSEILMERIILDKNLDLITATPLDPLFLHFAIAVTS TRPQLFLPKLSPSOHLAVLTQKLHMACNOLLOPRGSMALAWYSLMEKLIPOW LSLTILLQKQANDSQLHLCRELVAHLSLTQSSLPNSVYVYPLKHTLTCTCDKGV FRUHPSPGPDFSKONSKREPEVPRGTAAFYHLLPRASGCKQSTKKRKEMEVDFFY DGIKRLYNEDNSVNSVSGTDLRSQEGHSGPCPLQPVSVM"

Alignment Scores:
 Pred. No.: 2,23e-174 Length: 1817
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0

ORIGIN

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x BC000420 (1-1817)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGAAGACACAGATGTCGAAAGTGAATGTGGGAAATGGCTTCTTCAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAACTTCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 723

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 784 AAGGCTCATCCAAAATATCTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843

Qy 101 ThrValGluGluAspGluValIleProValLeuLysValLeuAlaArgAsnSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 903

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAAATTAATCTGGATAAGTGAATTGG 963

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGCCACACACCAATGGAATTTCTCATATTTTCCATGTCATTCAGAGTGTCA 1023

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGGACCCATCTCAACATTTGGCAGTC 1083

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTTACCAGCAACTACTTCACTGTATGCGCTGCAACCAACTCTGCAATTCAGAGGATCC 1143

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAAACTCATTCCTGATGGCTTTCT 1203

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTTCAATGAACTGCTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTGTCGG 1263

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGTGGCACATCACCCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAAATTCGTTAT 1323

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTTCAAGCACACCCCTGGTGACCTGTGCAAAAGGAGTGTTCAGATTACAT 1383

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCTTCTCTGTCAGGCCAGACTTCTCCAGAGACACACAGCAAGCCAGAGTCCAGTC 1443

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCGAGTGGGTGCAAGCACACCTCT 1503

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 1504 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTC 1563
```

```
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATAATGAGATAATGCTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1623

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGGACATGCTTCCCTTGTCCACCTTTCAGCCTGTTTCTGTGTCATG 1674

RESULT 9
CQ468129 1889 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 10907 from Patent WO0192581.
DEFINITION
ACCESSION CQ468129
VERSION CQ468129.1 GI:41433748
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
MAMMALIA; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Algate, P.A., Harlocker, S.L. and Jones, R.
TITLE Compositions and methods for the therapy and diagnosis of
ovarian cancer
JOURNAL Patent: WO 0192581-A 10907 06-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
source 1..1889
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: 2,34e-174 Length: 1889
Pred. No.: 1962.00 Matches: 377
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-736-250-1 (1-377) x CQ468129 (1-1889)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 603

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGAAGACACAGATGTCGAAAGTGAATGTGGGAAATGGCTTCTTCAATCAGATGTT 663

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAAGTAACTTCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 723

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 783

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 784 AAGGCTCATCCAAAATATCTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843

Qy 101 ThrValGluGluAspGluValIleProValLeuLysValLeuAlaArgAsnSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 903

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAAATTAATCTGGATAAGTGAATTGG 963

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
```

Db 964 GATCTTCACAGCCACACCATGGATTCTTCATATTTTCCATGTCAGTGCA 1023

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180

Db 1024 ACTAGGCGCTAGTTACTTTTCAGTTGCGCAAAATGAGCCCATCTCAACATTTGGCAGTC 1083

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200

Db 1084 CTTACCAAGCAACTACTTCTACCTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220

Db 1144 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAACTCAATCTCGATGGCTTCT 1203

Qy 221 LeuThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArg 240

Db 1204 CTTCAATTTGAATGCTTTTCAGAAAGCAGATGATGATGATGATGATGATGATGATGATG 1263

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260

Db 1264 GAGCTTGTGGCACATCACTTCTACTCTGAGTCTTCCCTGCTGCTGCTGCTGCTGCTGCT 1323

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280

Db 1324 GTCTACCTGCTCCCTCAACACACCTGCTGACCTGTGACAAAGGAGTTCAGATTACAT 1383

Qy 281 ProSerSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300

Db 1384 CCTCTCTGTCCTCCAGGCGCAGACTTCTCCAAAGACACAGCAAGCCAGAAAGTGCAGTC 1443

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320

Db 1444 AGAGTACAGAGCGCTTTTACCATCATCTCCAGCTGCGAGTGGTGGTGGTGGTGGTGGTGGT 1503

Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLleLysArgLeu 340

Db 1504 ACTAAACCAAGTAGAGAAATGGAAGTGAATGATGATGATGATGATGATGATGATGATGATG 1563

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360

Db 1564 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGGTGGTGGTGGTGGTGGTGGT 1623

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377

Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCCTGTTCTGTGTCATG 1674

RESULT 10

BC004975

LOCUS BC004975 1889 bp mRNA linear PRI 29-JUN-2004

DEFINITION Homo sapiens cyclin I, mRNA (cdna clone MGC:3795 IMAGE:2957878), complete cds.

ACCESSION BC004975

VERSION BC004975.1 GI:13436391

KEYWORDS MGC.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 1889)

AUTHORS Mammalia; Eutheria; Primates; Carniaria; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Choirdata; Craniata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1889)

STRAUSBERG, R.L., FEINGOLD, E.A., GROUSE, L.H., DERGE, J.G., KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D., ALSCHUL, S.F., ZEEBORG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K., HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F., DATCHENKO, L., MARUSIN, K., FARMER, A.A., RUBIN, G.M., HONG, L., STAPLETON, M., SOARES, M.B., BONALDO, M.F., CASAVANT, T.L., SCHEETZ, T.E., BROWNSTEIN, M.J., USIDIN, T.B., TOSHIYUKI, S., CARNINCI, P., PRANGE, C., RAHA, S., LOQUELLANO, N.A., PETERS, G.J., AMBRONSON, R.J., BOSAK, S., MCEWAN, P.J., MCKERNAN, K.J., MALEK, J.A., GUNARATNE, P.H., RICHARDS, S., WORLEY, K.C., HALE, S., GARCIA, A.M., GAY, L.J., HULYK, S.W., VILLALON, D.K., MUZYNY, D.M., SODERGREN, E.J., LU, X., GIBBS, R.A., FANEY, J., HELTON, E., KETTEMAN, M., MADAN, A., RODRIGUES, S., SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A.C., SHEVCHENKO, Y.,

BOUFFARD, G.G., BLAKESLEY, R.W., TOUCHMAN, J.W., GREEN, E.D., DICKSON, M.C., RODRIGUEZ, A.C., GRIMWOOD, J., SCHMUZ, J., MYERS, R.M., BUTTERFIELD, Y.S., KRZYWINSKI, M.I., SKALSKA, U., SMALLUS, D.E., SCHNERCH, A., SCHEIN, J.E., JONES, S.J. and MARRA, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 1889)

STRAUSBERG, R.

Direct Submission

Submitted (21-MAR-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbe-r@mail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Rubin Laboratory

DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smalls, Jeff Stott, Miranda Tsai, George Yang, Jackie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAL Plate: 9 Row: b Column: 16.

Location/Qualifiers

1. 1889

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="MGC:3795 IMAGE:2957878"

/tissue_type="Kidney, renal cell adenocarcinoma"

/clone_lib="NIH MGC_14"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

1. 1889

/gene="CCNI"

/note="synonyms: CYC1, CYI"

/db_xref="LocusID:10983"

544. 1677

/gene="CCNI"

/codon_start=1

/product="cyclin I"

/protein_id="AAH04975.1"

/db_xref="GI:13436392"

/db_xref="LocusID:10983"

/translation="MKPPGLEPGLNQLFLLEKATTAQMKVNVKMPNSQNSVPSQ RDEVIOVLAKYQFNLYPETFALASSLDRLATVKAHPKLYSCIAISCFPLAAKTV EBERPVLKVLARDSCGSSSEILMERILIDKLNWDLHTATPLFLHFAIYVS TRQLGSLPKLSPSHLVATVITQLLHCHMACNQLLQPRGNLALVLENEKLIIPDW LSITIELLQAMDSQLIHRELVAHMLSTLQSSFLNSVYVYRPLKHTLVTCDDGV FLRLHPSVPGPDFSKNSKEPVPVGTAAFYHPLPAASGCKQTSTKRKRVEMEVDDEY DGIKRLYNEDNVSENVSGVCGTDLDRQEGHASPCCPLQPVSM"

ORIGIN

Alignment Scores:

Pred. No.: 2,34e-174 Length: 1889

Score: 1962.00 Matches: 377

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x BC004975 (1-1889)	
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20	
Db 544 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCCCTGGTTGGAAAAGGCAATC 603	
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40	
Db 604 ACTAGGGAAGCACAGATGCGAAAGTGAATGTGCGGAAAATGCCTTCAAATCAGATGTT 663	
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysLeuLysTrpGlnPheAsn 60	
Db 664 TCTCCATCCAGAGAGATGAAGTAAATTCATGTGGTGGCCAAACTCAAGTACCAATCAAC 723	
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80	
Db 724 CTTTACCAGAAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 783	
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100	
Db 784 AAGGCTCATCCAAAATACTTCAGTTGTATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 843	
Qy 101 ThrValGluLysAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120	
Db 844 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 903	
Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140	
Db 904 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATGAATGGAATGG 963	
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160	
Db 964 GATCTTCACACAGCCACACCATTTGATTTCTTATATTTTCCATGCAATTCAGTGTCA 1023	
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180	
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTGTCGCAAAATGAGCCCATCTCAACATTTGGCAGTC 1083	
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200	
Db 1084 CTTTACCAGCAACTACTTCACTGTATGGCTTGCACCAACTCTGCAATTCAGAGGATCC 1143	
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220	
Db 1144 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATCTCGATTGCTTCT 1203	
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240	
Db 1204 CTTACAAATTGAACCTGCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 1263	
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260	
Db 1264 GAGCTTGGGCACATCACTTCTACTCTGAGTCTTCCCTGCTTCCGCTTCAATCCGTTAT 1323	
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280	
Db 1324 GTCTACCTGCTCCCTCAAGCACACCTGCTGACCTGTGACAAAGAGTGTTCAGATTACAT 1383	
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300	
Db 1384 CCCTCTCTGTCGCCAGGCCAGACTTCTCCAAAGGACACAGCAAGCCAGAGTGCAGTC 1443	
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320	
Db 1444 AGAGTACAGAGCCCTTTTACCATCATCTCCAGCTGCGGTGGTGAACAGACCTCT 1503	
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340	
Db 1504 ACTAAACCAAGTAGAGAAATGGAAGTGGATGATCTTCTATGATGAATCAACGGCTC 1563	
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360	

Db 1564 TATAATGAAGATAATGTCTCAGAAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1623	
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377	
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGGCTGTTCTGTGTCATG 1674	

RESULT 11

CR541783

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CR541783

1131 bp mRNA linear PRI 29-JUN-2004

Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for

gene CCNI, cyclin I; complete cds, without stopcodon.

CR541783

GI:49456522

Full ORF shuttle clone, Gateway (TM), complete cds.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1131)

Halleck,A., Ebert,L., Mkundinya,M., Schick,M., Eisenstein,S.,

Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,

Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Cloning of human full open reading frames in Gateway (TM) system

entry vector (pDONR201)

2 (bases 1 to 1131)

Halleck,A., Ebert,L., Mkundinya,M., Schick,M., Eisenstein,S.,

Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,

Korn,B., Zuo,D., Hu,Y. and LaBaer,J.

Direct Substitution

Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer

Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,

Germany

RZPD: RZPD0834E0730D, ORFNo 3592

www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834E0730D RZPDLib;

Human Full ORF Clones Gateway (TM) - RZPD (kan-resist.) RZPD Lib No.

834

www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834

www.rzpd.de/products/orfclones/

Contact: Inge Arlart

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,

Heubnerweg 6, D-14059 Berlin, Germany

Tel: +49 30 32639 100

Fax: +49 30 32639 111

www.rzpd.de

This clone is available from RZPD;

Contact RZPD (customer.service@rzpd.de) for further information.

Clone name at Harvard Institute of Proteomics

(www.hip.harvard.edu): FLH131015.01L

This CDS clone is part of a collection of human full ORF clones

jointly established and verified by the Harvard Institute of

Proteomics (HIP) and RZPD.

This CDS has been cloned without stopcodon.

The CDS has been inserted into pDONR201 via a BP Clonase (TM)

reaction. Additional sequence has been added in front of the start

codon: att.AAGGCA GGC TCC ACC (ATG).

The last codon is followed by the 3' att site: GACCCAGCTTTCTT. .att

The clone is validated by full sequence check.

Compared to the reference sequence NM_006835 (GI:17738314) we found

AA exchange(s) at position (first base of changed triplet):

223 (arg->gly) 409 (lys->arg)

Clone distribution: http://www.rzpd.de/products/orfclones/.

Location/Qualifiers

1. .1131

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="RZPD0834E0730D"

/clone_lib="Human Full ORF Clones Gateway (TM) - RZPD"

/lab_hosts="DH5Alpha"

/note="vector: pDONR201, Site_1: attP1; Site_2: attP2"

1. .1131

/gene="CCNI"

source

gene

```

CDS
1. >1131
/gene="CCNI"
/codon_start=1
/protein_id="CAG46582.1"
/db_xref="GI:4945623"
/translation="MKPPGPLENORLSFLLEKAITRAQMKVNVKMPNSQNVSPSQ
RDEVIOIAKLKYQFNLYPETFALASSILDDGLATVKAHPKYLSCIALSCFPLAAKT
VEDERI PVLVKVLARDSFCGSSSEILRNERIILDRNLWDLHTATPLDPLHIFHAIVS
TRPQLLSPLKLSQSQUAVIUTKQLHCHMACNQLQFQSGMLALAMVSEMEKLIPOW
LSHTEIQKQADSSQIHLREIVAHHLSTLQSLPLNSVYVYRPLKHTLVLTCDKGV
FLHPSSVPGDPDFKDNKSPVVRGTAAFYHPLPAASGCKQTSTKRRVEMEDVDFY
DGIKRLYNEDNVSENVGSCVCTDLRSQBGHASPCPPLQPVSM"

ORIGIN
Alignment Scores:
Pred. No.: 1.06e-173 Length: 1131
Score: 1952.00 Matches: 375
Percent Similarity: 99.73% Conservative: 1
Best Local Similarity: 99.47% Mismatches: 1
Query Match: 99.49% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x CR541783 (1-1131)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 1 ACTAGGGAAGACAGATGTGGAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 1 TCTCCATCCAGAGAGATGAATTAATCAATGGCTGGCCAACTCAAGTCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 1 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATGGGTTTTTACGTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 1 AAGGCTCATCCAAATACTTGATGTGATTCGAATCAGCTGTTTTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 1 ACTGTTGAGGAAGATGAGAGAATCCACTACTAAGGTATTGGCAAGACAGATTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 1 GGATGTTCTCATCTGAAATTTGAGAATGGAGAGAAATTAATCTGGATAGGTTGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 1 GATCTTCACAGCCACACCATGATGATTTCTTCAATATTTCCATGCCATTCGAGTGCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1 ACTAGGCTCAGTACTTTTCACTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1 CTTACAGCAACTACTTCACTGTATGGCTTGCACCACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1 ATGCTTGTCTGGCCATGTTAGTCTGAAATGGAGAACTCATTTCTGATTTGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1 CTTACAAATTAAGTCTCTCAGNAACACAGATGGATAGTCTCCAGTTCATTCATTTGCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260

```

```

Db 721 GAGCTTGTGGCACATACCTTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGACACACCTCTGGTACCTGTGACAAAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCCAGAGCCCACTCTTCCAAAGACACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysValGlnThrSer 320
Db 901 AGGTACAGCAGCCTTTTACCATCTCCACTGCCAGTGGTGGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAATGTGGTCTCTGTGTGGCACTGATTTATCAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGGAGCATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTCTGTCATG 1131

RESULT 12
AF005886 1535 bp mRNA linear ROD 31-OCT-2000
LOCUS Mus musculus cyclin I mRNA, complete cds.
DEFINITION AF005886
ACCESSION AF005886.2 GI:6850163
VERSION
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 1535)
AUTHORS Jensen,M.R., Audolfsson,T., Factor,V.M. and Thorgeirsson,S.S.
TITLE In vivo expression and genomic organization of the mouse cyclin I
JOURNAL Gene (Cnii)
MEDLINE Gene 256 (1-2), 59-67 (2000)
PUBMED 20509992
REFERENCE 2 (bases 1 to 1535)
AUTHORS Audolfsson,T., Jensen,M.R. and Thorgeirsson,S.S.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1997) Laboratory of Experimental Carcinogenesis,
National Institutes of Health, 37 Convent Drive, Bethesda, MD
20982-4255, USA
REFERENCE 3 (bases 1 to 1535)
AUTHORS Audolfsson,T., Jensen,M.R. and Thorgeirsson,S.S.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2000) Laboratory of Experimental Carcinogenesis,
National Institutes of Health, 37 Convent Drive MSC4255, Building
37, room 3C28, Bethesda, Maryland 20892-4255, USA
REMARK sequence update by submitter
COMMENT On Feb 1, 2000 this sequence version replaced gi:4101686.
FEATURES
source
1. 1535
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
279..1412
/codon_start=1
/product="cyclin I"
/protein_id="AAD01253.2"
/db_xref="GI:6850164"
/translation="MKPPGPLENORLSLIERAISREAQMKVNVKPIPTNONVPSQ
RDEVIOIAKLKYQFNLYPETFALASSILDDGLATVKAHPKYLSCIALSCFPLAAKT
VEDEKIPVLKVLARDSFCGSSSEILRNERIILDRNLWDLHTATPLDPLHIFHAIVS
TRPQLLSPLKLSQSQUAVIUTKQLHCHMACNQLQFQSGMLALAMVSEMEKLIPOW

```


A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>
 Series: IRAK Plate: 9 Row: f Column: 22
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8393062.

FEATURES

source

1. .2348

/organism="Mus musculus"

/mol_type="mRNA"

/strain="FVB/N"

/db_xref="taxon:10090"

/clone="MGC:5636 IMAGE:3583418"

/tissue type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."

/clone.lib="NCI CGAP_Mam1"

/lab host="DH10B"

/note="Vector: pCMV-SPORT6"

1. .2348

/gene="Ccni"

/db_xref="LocusID:12453"

/db_xref="MGI:1341077"

160..1293

/gene="Ccni"

/codon_start=1

/product="cyclin I"

/protein_id="AAH03290.1"

/db_xref="GI:13096997"

/db_xref="LocusID:12453"

/db_xref="MGI:1341077"

/translation="MKFPGPLENQRLLSRLERASRAQMKVNVKPIPTNQVSPSQ
 DEVIOMLAKLYFNYPETFPALASLLDFLATVKAHPKYLNCIAISFPFLAAKT
 BEDSKIPLVLYLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHFHAIAS
 TRPLLPLKPLSPSHLAVLTQKLLHMCANQLLOPKGMLAMVSLMEKLIPOW
 LPLTELQKQMSQLIHCRELVAVHLSALPLANSVYVVRPLKHTLVTCDKGA
 FKLHPSSVGGDFKSDNSKPEVRGPAAPFLHPLFAAGCKQTSKAKRKBEMVEDDFY
 DGIKRLYNEDGNPENVSGVCGTDLRSQEGHASPCLPQPVSM"

ORIGIN

Alignment Scores:

Pred. No.: 8 35e-164 Length: 2348
 Score: 1851.00 Matches: 355
 Percent Similarity: 97.08% Conservative: 11
 Best Local Similarity: 94.16% Mismatches: 11
 Query Match: 94.34% Indels: 0
 DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x BC003290 (1-2348)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 160 ATGAAGTTTCAGGACCTTGGAAACCCAGAGATTGCTCTCTGTTGGAAGGCAATC 219
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 220 TCCAGGGAAGCCAGATGTGAAGGTGAATGTGCCGAAATACCTTACAAATCAGAATGTT 279
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
 Db 280 TCTCATCCAGAGAGATGAAGTAATTCAATGGTTGGCCAACTCAAAATACAGTTCAAC 339
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 340 CTCATCCAGAAACATTTGCTCTGCCAGCAGCTCTTTGGATAGGTTTTAGCTACAGTA 399
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 400 AAAGCCCATCAAAATATTGAATGTTATGCAATCAGCTGTTTTTTCTGCTGCTAAG 459
 Qy 101 ThrValGluGluAspGluArgIleProValLysValLeuAlaArgAspSerPheCys 120
 Db 460 ACTGTTGGGAAGATGAGAAATATCCAGTGTCAAGGATTATGGCAAGAGACAGATTCTGT 519

Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 520 GGAATGTTCTCATCTGAGATTTTGAAGATGGAGAGAAATATTCTGGAATAAATGAATGG 579
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 580 GATCTTCACACGGCTACACCATGGATTTCTTCACATTTTCCATGCAATGCGGTGCA 639
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 640 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTCAAAATGAGCCCATCTCAACATTTGGCAGTC 699
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
 Db 700 CTGACCAAGCAGCTGCTTCACTGTATGCGCTGCAACCAACTTTCGAGATTCAAAAGGTC 759
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 760 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATCTCTGATGCTTCCT 819
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 820 CTTACGATTGACTGCTTTCAGAAAGCACAGATGACAGCTCCCAAGTTGATCCACTGTGCG 879
 Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 880 GAGCTGGTGGCATATCACTTTCTGCTGTCAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 939
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 940 GTCTACCGTCCCTTCAAGCACACCTGTAACCTGTGACAAAGGAGCATTCAAAATTCAT 999
 Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1000 CCTCTCTGCTCAGGCCCGCAGATTTTCCAGGACCAACAGCAAGAGTGCACGTC 1059
 Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1060 CGAGGTCAGCAGCCTTCCACCTGCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1119
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 Db 1120 GCTAAACGGAAGTGGAGGAGATGGAGTGGATGACTTCTACGATGGATCAAGCGGCTC 1179
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1180 TATTAATGAGGACATGGTCTGACAATGTGGTTCTGTATGCTGCACTGATTTATCAAGG 1239
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1240 CAAGAGGCGCATGCTTCCCTGTCACCTTTGAGGCTGTTCTGTCATG 1290

RESULT 14
 LOCUS CQ414515 2755 bp DNA linear PAT 23-JAN-2004
 DEFINITION Sequence 21586 from Patent WO0170979.
 ACCESSION CQ414515
 VERSION CQ414515.1 GI:41322296
 KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS Lee, J. and Lillie, J.
 TITLE Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 JOURNAL Patent: WO 0170979-A 21586 27-SEP-2001;
 Millennium Pharmaceuticals, Inc. (US)
 FEATURES
 source Location/Qualifiers
 1. .2755 /organism="Homo sapiens"

/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 8.92e-163 Length: 2755
Score: 1841.00 Matches: 358
Percent Similarity: 94.96% Conservativity: 0
Best Local Similarity: 94.96% Mismatches: 1
Query Match: 93.83% Indels: 18
DB: 6 Gaps: 1

US-09-736-250-1 (1-377) x CQ414515 (1-2755)

QY 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
DB ATGAAGTTTCAGGCGCTTTGGAAACACAGAGATTGCTTTTCCTGTTGGAAAGCGCAATC 906
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
DB ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAATATGCTTCAATCAGATGTT 966
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
DB TCTCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 1026
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
DB CTTTACCAGAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTATAGCTACCGTA 1086
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
DB AAGGCTCATCT----- 1098
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
DB -----GAGGAAGATGAGAGATTCAGATCTAAAGGTATTGGCAAGAGACAGTTTCTGT 1152
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
DB GGATGTTCTCATCTGAATTTTGAGATGAGAGATTTATTCGGATAGTTGAATGG 1212
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB GATCTTCACACAGCACACCATTTGATTTTCTTCAATTTTCCATGCTTCAGTGCTCA 1272
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB ACTAGGCTCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 1332
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
DB CTTTACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 1392
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
DB ATGCTTGTCTTGGCCATGTTAGTCTGAAATGAGAAACTCAATCTCGATTGGCTTTCT 1452
QY 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
DB CTTTCAATTAAGTGTCTTCAAGAGCAGATGATAGTCTCCCAAGTTGATCCATTTGTCGG 1512
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
DB GAGCTTGTGGACATCATCTTCTACTCTGAGTCTTCCCTGGCTCTGAAATTCGTTAT 1572
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGGAGTTTCAGATTACAT 1632
QY 281 ProSerValProGlyProAspPheSerLysAsnSerLysProGluValProVal 300
DB CCCTCTCTGTGCCGCCAGAGCTTCTCAAGGACCAACAGCAAGCCAGAGTGCAGTC 1692

QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaHisSerGlyCysLysGlnThrSer 320
DB AGAGGTACAGCAGCCTTTTACCATCATCTCCAGTCCGAGTGGTCCAGACACCTCT 1752
QY 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
DB ATTAAGCGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACGGCTC 1812
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
DB TATAATGAAGATAATGCTCAGAAAATGTGGTCTGTGTGGCTGATTTATCAAGA 1872
QY 361 GluGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
DB CAAGAGGACATGCTTCCCTTGTCTACCTTTGAGCCTGTTTCTGTGTCATG 1923
RESULT 15
AC101881/c
LOCUS
DEFINITION Mus musculus chromosome 14 clone RP23-387F19 map 14, *** SEQUENCING
IN PROGRESS ***, 6 unordered pieces.
AC101881
ACCESSION AC101881.4 GI:42628095
VERSION HTG; HTGS PHASE1; HTGS FULLTOP; HTGS_ACTIVEFIN.
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
Direct Submission
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 200850)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
Anderson, S., Barna, N., Campione, A., Chang, J., Chazaro, B.,
Coe, P., Collinge, M., Collins, S., Collymore, A., Cook, A.,
Cooke, P., DeArillano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Gard, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K.,
Lamarez, R., Landers, T., Lebeck, J., Levine, R., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliou, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 200850)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Bouglavsky, L., Boukhgalter, B., Camarata, J., Chang, J., Choepe, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., DeArillano, K.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, X., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,

O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliou, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (19-FEB-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 19, 2004 this sequence version replaced gi:31442513.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L17690
 Center clone name: 387_F_19

*** NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

* 1 13662: contig of 13662 bp in length
* 13663 13762: gap of 100 bp
* 13763 111127: contig of 97365 bp in length
* 111128 111227: gap of 100 bp
* 111228 134282: contig of 23055 bp in length
* 134283 134382: gap of 100 bp
* 134383 157520: contig of 23138 bp in length
* 157521 157620: gap of 100 bp
* 157621 172448: contig of 14828 bp in length
* 172449 172548: gap of 100 bp
* 172549 200850: contig of 28302 bp in length.
```

FEATURES

```

source
1..200850
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="14"
/map="14"
/clones="RP23-387F19"
/clone_lib="RPCI-23 Female Mouse BAC"
```

ORIGIN

```

Alignment Scores:
Pred. No.: 5.32e-144 Length: 200850
Score: 1666.50 Matches: 332
Percent Similarity: 91.82% Conservative: 16
Best Local Similarity: 87.60% Mismatches: 21
Query Match: 84.94% Indels: 11
DB: 2 Gaps: 2
```

US-09-736-250-1 (1-377) x AC101881 (1-200850)

```

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLysAlaile 20
Db 155593 ATGAATTTTCAGGACCTTTGGAACACAGAGATGTTCTCTGTGGAAAGGGCAATC 155534
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 155533 TCCAGGGAAGCCAGATGCTGGAAGGTGAATGTGCGGAATAATACCTACAAATCAGATGTT 155474
Qy 41 SerProSerGlnArgAspGluValileGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
```

```

Db 155473 TCTCCATCCAGAGAGATGAAGTAATTAATCAATGGTTGGCCAACTCAATACCAGTTCAAC 155414
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 155413 CTCTATCCAGAAACATTTGCTCTATCAAGCAGCTCTTTGGATAGTTTGTAGCTACAGTA 155354
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCys----PhePheLeuAlaAla 99
Db 155353 AAAGCCCATCAAAATATTTGAATTTGTAATCGAATCAGCTGTTTTTTTTTCTGGCTGCT 155294
Qy 100 LysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe 119
Db 155293 AGACTGTTGAGGAGAGATGAGAAAATTCAGTGTCTAAGGTATTGGCAAGACAGCTTTC 155234
Qy 120 CysGlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsn 139
Db 155233 TGTGGATGTTCTCTCATCTGAGATTTTGAAGATGGAGAGAAATTTATCTGGATAAATTTGAAT 155174
Qy 140 TrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaVal 159
Db 155173 TGGGATCTTCACACGGCCACACCATTTGGATTTTCTTCACATTTTTCATGCTTCCGTG 155114
Qy 160 SerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAla 179
Db 155113 TCACTAGGCTCAGTTACTTTTCAGTTTCCCAATGAGCCCATCTCAACATTTGGCA 155054
Qy 180 ValLeuThrLysGln-LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgL 199
Db 155053 GTCTGACTAAGCAGCATGCTTCACGTATGGAGTCAACCAACTTCTGCAGTTCAAAGG 154994
Qy 199 YSerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLe 219
Db 154993 GTCCATGCTGGCTTGGCCATGTTAGTCTGGAAATGGAGAAATCTATCTCGATTGGCT 154934
Qy 219 uSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCy 239
Db 154933 TCCTTTAAGATTGAACCTGCTCAGGAGCAGACAGATGGGAGCTCCCGATTGATCCACTG 154874
Qy 239 sArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerVa 259
Db 154873 TCGGAGCTGGTGGCATATCACCGTTCTGCTCTGCACTCTGCCCTGCTCTAAATTCGT 154814
Qy 259 lTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLe 279
Db 154813 TTTTGTCTACCGTCCCTCAAGCACACCTGGTAACCTGTGACAAAGGAGCAGCTCAAAAT 154754
Qy 279 uHisProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValPr 299
Db 154753 ACATCCCTCTCTGTCTCAGGCCAGATTTCTCAAGGACAAACAGCAAGTCAAGTACC 154694
Qy 299 oValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnTh 319
Db 154693 AGTCCGAGGTTCCAGCAGCTTCCACCTGCATCTCCCGCAGCC----- 154651
Qy 319 rSerThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysAr 339
Db 154650 -----AAACCGAAAGTGAGGAGATGGAGTGGATGACTTCTCCGATGGATCAAGTG 154598
Qy 339 gLeuTyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSe 359
Db 154597 GCTCTATAATGAGGACAAATCTCTCTGAGAATGGGGTCTGTATGTGGCACTGATTATC 154538
Qy 359 rArgGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 154537 AAGGCAAGAGGGCAGTCTTC-CCCTGTCCACCTTTGCAGCCTGTTTCTGTCTATA 154484
```

Search completed: February 11, 2005, 05:55:25
 Job time : 7743.41 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:24 ; Search time 86.7775 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKFPGPLENQLSFLLEKAL.....LSRQGHASCPPLQPVSM 377

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	12	US-09-736-250-1
2	1309	66.7	254	9	US-09-796-149-4
3	326.5	16.6	344	15	US-10-170-385-321
4	271.5	13.8	249	9	US-09-796-149-3
5	234	11.9	238	14	US-10-218-542-2
6	218	11.1	88	14	US-10-029-386-30305
7	204	10.4	404	14	US-10-265-062-3
8	202	10.3	403	14	US-10-265-062-4
9	192	9.8	357	15	US-10-388-269-10
10	188.5	9.6	373	15	US-10-388-269-4
11	187.5	9.6	395	14	US-10-245-618-32
12	187.5	9.6	395	14	US-10-245-618-46
13	187.5	9.6	395	14	US-10-245-618-47

14	187.5	9.6	395	14	US-10-245-618-48	Sequence 48, Appl
15	187.5	9.6	410	14	US-10-245-618-31	Sequence 31, Appl
16	187.5	9.6	451	9	US-09-964-899-31	Sequence 31, Appl
17	177.5	9.0	289	13	US-10-024-066-2	Sequence 2, Appl
18	177.5	9.0	420	15	US-10-310-154-414	Sequence 414, App
19	177.5	9.0	424	10	US-09-496-444-2	Sequence 2, Appl
20	177	9.0	371	15	US-10-424-599-160823	Sequence 160823, A
21	177	9.0	394	15	US-10-425-114-48711	Sequence 48711, A
22	176.5	9.0	419	15	US-10-310-154-412	Sequence 412, App
23	176	9.0	471	15	US-10-369-493-21977	Sequence 21977, A
24	175.5	8.9	359	15	US-10-369-493-22561	Sequence 22561, A
25	175.5	8.9	424	15	US-10-310-154-418	Sequence 418, App
26	170.5	8.7	383	15	US-10-424-599-160824	Sequence 160824, A
27	170.5	8.7	427	15	US-10-425-114-38905	Sequence 38905, A
28	170	8.7	506	15	US-10-389-566-734	Sequence 734, App
29	170	8.7	532	15	US-10-389-566-1352	Sequence 1352, Ap
30	169.5	8.6	441	15	US-10-389-566-2182	Sequence 2182, Ap
31	169.5	8.6	469	15	US-10-424-599-238352	Sequence 238352, A
32	169	8.6	289	9	US-09-919-497-54	Sequence 54, Appl
33	169	8.6	289	13	US-10-024-066-4	Sequence 4, Appl
34	169	8.6	480	15	US-10-425-114-63937	Sequence 63937, A
35	169	8.6	508	15	US-10-310-154-415	Sequence 415, App
36	169	8.6	508	15	US-10-389-566-749	Sequence 749, App
37	169	8.6	508	15	US-10-389-566-2399	Sequence 2399, Ap
38	168.5	8.6	424	15	US-10-310-154-429	Sequence 429, App
39	168	8.6	276	15	US-10-369-493-22562	Sequence 22562, A
40	167.5	8.5	479	15	US-10-310-154-419	Sequence 419, App
41	167	8.5	84	9	US-09-864-761-46425	Sequence 46425, A
42	167	8.5	305	15	US-10-424-599-169546	Sequence 169546, A
43	167	8.5	450	15	US-10-389-566-745	Sequence 745, App
44	167	8.5	491	9	US-09-801-368-78	Sequence 78, Appl
45	167	8.5	491	15	US-10-369-493-22530	Sequence 22530, A

ALIGNMENTS

RESULT 1
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR FILING DATE: 2000-05-4,492
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 377
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-250-1

Query Match	100.0%	Score 1962;	DB 12;	Length 377;
Best Local Similarity	100.0%	Pred. No. 2e-184;		
Matches 377;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MKFPGLLENQLSFLLEKAITREAWKVNVRKPNQNVSPSORDEVIQHLAKLKQFN	60	
Db	1	MKFPGLLENQLSFLLEKAITREAWKVNVRKPNQNVSPSORDEVIQHLAKLKQFN	60	
Qy	61	LYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARSFC	120	
Db	61	LYPTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIPVLKVLARSFC	120	

QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQLLSPLKSPSOHLAV 180
QY 181 LTKQLLHMACNQLLOFRGSMALAMVLEMEKLIIPDWLSLTIELLOKAQWDSQLIHR 240
DB 181 LTKQLLHMACNQLLOFRGSMALAMVLEMEKLIIPDWLSLTIELLOKAQWDSQLIHR 240
QY 241 ELVAHHLSTLOSSPLNSVYVVRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
DB 241 ELVAHHLSTLOSSPLNSVYVVRPLKHTLVTCDKGVFRLHPSVPGPDFSKDNKPEVPV 300
QY 301 RGTAIFYHHLPAASCKGTSTKRKYEMEVDYDYGIKRLYNEDNVNVSVCVGTDLNR 360
DB 301 RGTAIFYHHLPAASCKGTSTKRKYEMEVDYDYGIKRLYNEDNVNVSVCVGTDLNR 360
QY 361 QEGHASPCCPPIQPVSVM 377
DB 361 QEGHASPCCPPIQPVSVM 377

RESULT 2

US-09-796-149-4
; Sequence 4, Application US/09796149
; Patent No. US20020035079A1
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149-4

Query Match 66.7%; Score 1309; DB 9; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7e-120; Indels 0; Gaps 0;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 VPSQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
DB 1 VPSQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60
QY 100 KTVEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIV 159
DB 61 KTVEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIV 120
QY 160 STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOFRGSMALAMVLEMEKLIIPDWL 219
DB 121 STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOFRGSMALAMVLEMEKLIIPDWL 180
QY 220 SLTIELLOKAQWDSQLIHCHRELVAHHLSTLQSSPLNSVYVVRPLKHTLVTCDKGVFRL 279
DB 181 SLTIELLOKAQWDSQLIHCHRELVAHHLSTLQSSPLNSVYVVRPLKHTLVTCDKGVFRL 240
QY 280 HPSSVPGPDFSKDN 293
DB 241 HPSSVPGPDFSKDN 254

RESULT 3

US-10-170-385-321
; Sequence 321, Application US/10170385
; Publication No. US2003020372A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Neil Raymond
; APPLICANT: Mundy, Christopher Robert
; APPLICANT: Kan, On

; APPLICANT: Harris, Robert Alan
; APPLICANT: White, Jonathan
; APPLICANT: Binley, Katie Mary
; APPLICANT: Rayner, William Nigel
; APPLICANT: Naylor, Stuart
; APPLICANT: Kingsman, Susan Mary
; APPLICANT: Krige, David
; TITLE OF INVENTION: ANALYSIS METHOD
; FILE REFERENCE: 532682000100
; CURRENT APPLICATION NUMBER: US/10/170,385
; CURRENT FILING DATE: 2002-06-12
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/05458
; PRIOR FILING DATE: 2001-12-10
; NUMBER OF SEQ ID NOS: 549
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-170-385-321

Query Match 16.6%; Score 326.5; DB 15; Length 344;
Best Local Similarity 36.4%; Pred. No. 3.1e-23;
Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;
QY 31 VRKMPSON-VSPQRDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
DB 41 IEATPENDNTICPLGRNAKVEDLRSLANFFGSCSTETFLAVNLIDRLALMKVQPKHLS 100
QY 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLD 149
DB 101 IGVCSPFLAARIVEEDCNIPSTHDVIRISOCKCTASDIKRMEXIISEKHLVELEATTALN 160
QY 150 FLHIFHAIIV---STRPQLLSPLKSPSOHLAVLTKQLLHMACNQLLOP---RGSMLA 203
DB 161 FLHLYHTIILCHTSERKEIL-SLDKLE-----AQLKACNCRLLIFSKAKPSVLA 207
QY 204 LAMVLEMEKLIIPDWLSLTIELLO-----KAQMDSSQLIHCHRELVAHHLSTQS 252
DB 208 LCLLNLEVEYL-----KSVELLEILLLVKHSKINDTEFFYRELVSCKLAIEYSS 257

RESULT 4

US-09-796-149-3
; Sequence 3, Application US/09796149
; Patent No. US20020035079A1
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149-3

Query Match 13.8%; Score 271.5; DB 9; Length 249;
Best Local Similarity 32.6%; Pred. No. 5e-18;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;
QY 45 RDEVIQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
DB 6 RDEFEVDLLSLTQTFPGPDTEFTFSLAVNLDRFLSKMKVQPKHLCVGLSCFYLAVKISIE 65
QY 105 DERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
DB 66 ERNVPLATDLIRISQYRFTVSDLRMEKIVLEKVCWKVATTAFQFLQLYSL----- 118

```

?
? OTHER INFORMATION: MAP TO CHR5.1
?
? OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.2
? OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
? OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.95
? OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
? OTHER INFORMATION: SWISSPROT HIT: Q922V9, EVALUE 2.00e-18
US-10-029-186-10305

```

```

Query Match      11.1%; Score 218; DB 14; Length 88;
Best Local Similarity 53.2%; Pred. NO. 2e-13;
Matches 42; Conservative 19; Mismatches 18; Indels 0; Gaps 0;

QY   154 FHAIVASTPQLFLSPKLSPSOHLAVLTQKLALHCACNOLQFRCSMLAMVSLMEK 213
      |||||:::||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db    9 FHAIWLSMHPVLELPLQRPNFSDHVASLRQLQHCWAGHQLLQFKGSTLALVIITLER 68

QY   214 LIPDWLSLTIELLQKAQMD 232
      |::|: : ::|||:|
Db    69 LMPGWCAPISDLJLKKAQVD 87

RESULT 7
US-10-265-062-3
; Sequence 3, Application US/10265062
; Publication No. US20030078370A1
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. US20030078370A1e1 Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
```

```

; CURRENT APPLICATION NUMBER: US/10/265,062
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/442,919
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 09/322,851
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/092,770
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
; US-10-265-062-3

Query Match 10.4%; Score 204; DB 14; Length 404;
Best Local Similarity 27.7%; Pred. No. 4.7e-11;
Matches 75; Conservative 54; Mismatches 96; Indels 46; Gaps 12;

```

```

99  P$PLPD--LSWGCK-----EYW-LNMUKESRYVHDKHFEVYLHSDLEFQMESILLDWL 149
Qy  AKUKYOFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFEFLAAKTVBDEIRIPVL 111
150 LEVCEVYTLHRETFYLAQDFDFRMLTQDKINKMMLQLIGITSFLTASKL--EIIYAPKL 207
Qy  KVLARDSFGCSSEIILMERIILDKLNDLHTATPLDFLHIHAI-AVSTRQLLSPLP 170
208 QEFAYYTDGACSEEDILRMBELIILKALKWBELCPVTIISWLNLFQVDALKDAPKVL--LP 265
Qy  KLSPSQHLAVLTKQLHMACNQLLQFRGSMILAMVSLMEKLIIPDWLSL-----TIEL 226
266 QY--SQETFIQIAQL-----DLCLALDSLEFQYRILTAALCHFTSIEV 310
Qy  QKAQ-WDSQLIHCRELVAHHLSTQSSPL 256
311 KKASGLEWDSISECDVMVPFVNWVKTSFV 341
Db

```

```
RESULT 8
US-10-265-062-4
; Sequence 4, Application US/10265062
; Publication No. US20030078370A1
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Baas, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/10/265,062
; PRIORITY FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/442,919
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 09/222,851
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/092,770
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 403
; TYPE: PRT
; ORGANISM: Mouse
US-10-265-062-4

Query Match      10.3%; Score 202; DB 14; Length 403;
Best Local Similarity 25.7%; Pred. No. 7.3e-11;
Matches 83; Conservative 54; Mismatches 126; Indels 60; Gaps 14;

QY 4 PPLENQLSFLLEKAITREAOQMKVNRK-----MPSNQVSPSORDEVIQWLA 53
DB 98 PSPLPD-----LSWACSQE--VMQNMLOKENVYVHDKHFQVLSHSDLEFQMRSLLDWLL 149
QY 54 KLKYQFNLYPETEALASSLLDRFLATV--AHPKYLSCLAIACFFLAAKTVEEDERIPVLK 112
DB 150 EVCEVYTHRETFYLAQDFRPMLTQDVNKMQLIGTISLFIASKL--EETVAPKLQ 207
QY 113 VLARDFSCGSSSEILMERIILDKLNWDLHTATPLDPLHIFHAI-AVSTRPQLLSLPK 171
DB 208 EFAYVTDGACSEVDILKMLNLKALKWELCPVTVISWNLFLQVDAVKDVKVL--LPQ 265
QY 172 LSPSOHLAVLTK--OALLHMACNQLLOFRGSMALAMVLSLEMEKLIIP----- 216
DB 266 Y--SOETFIQALDLCLALDAISLEFQYRILAAALCHFTSIEVVKKASGLEWDDISEC 323
QY 217 -DWL-----SLTIQLLOQAQMDSSQLIHCRELVVAHLSLTLQSSSLPLNSVYVYRP 264
DB 324 VDMVYFVSVVKVSPVKLTKFKIPMED-----RHNIQTHVYVALLNEVYVYVYRK 377
QY 265 LKHTLVTCDKGVFRLHPSVPGP 287
DB 378 GQQLSPVCNGGIM-TPPKSTKP 399

RESULT 9
US-10-388-269-10
; Sequence 10, Application US/10388269
; Publication No. US20030221221A1
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/10/388,269
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 10
; LENGTH: 357
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-10-388-269-10

Query Match      9.8%; Score 192; DB 15; Length 357;
Best Local Similarity 25.4%; Pred. No. 5.9e-10;
Matches 81; Conservative 58; Mismatches 110; Indels 70; Gaps 16;

QY 6 PLENQRLSFLLEKAI---TREAOQMKVNRKMP---SNQNVSPS---QRDRVIQWLAKLK 56
DB 49 PLQDLDSWEHEELVSLFTKEBOQK---QTPCTLSFGKTSVSPFAARKEAVDWILKVK 104
QY 57 YQFNLYPETEALASSLLDRFLATV---KAHPKYLSCIAISCFFLAAKTVEEDERIPVLK 113
DB 105 SCYGFTEPLTALAINYLDRFLSSHLFQEDKPMWQLVAVSCLSLAAKV--EETQVPLLD 162
QY 114 L-ARDSPCGSSSEILMERIILDKLNWDLHTATPLDPLHIFHAI-AVSTRPQLLSLPK 171
DB 163 LQVEDTKYLFKAKNIQKMWLLVMSLTKWRMNPVTPIISFLDHIVRRLG----- 209
QY 172 LSPSOHLAVLTK--OALLHMACNQLLOFRGSMALAMVLSLEMEKLIIP-----DWLSLTIE 224
DB 210 LTHVHWDFFKCEAMILCLVSDSRFVCYKPSVLATATMLHVDEIDPPNCIDYKSQLD 269
QY 225 LLQKAQMDSSQLIHCRELVA-----HHLSTLQSSSLPLNSVYVYRPLKHTLVTCDKGVFRL 279
DB 270 LLKTTKDDINE---CYELIVELAYDHH-----NKRKH-----DANETTT 305
QY 280 HPSSVPGP-DESKDNKPE 297
DB 306 NPVSPAGVIDFTCDSESSNE 324

RESULT 10
US-10-388-269-4
; Sequence 4, Application US/10388269
; Publication No. US20030221221A1
; GENERAL INFORMATION:
; APPLICANT: MURRAY, James Augustus Henry
; TITLE OF INVENTION: PLANTS WITH MODIFIED GROWTH
; FILE REFERENCE: 2121-0151P
; CURRENT APPLICATION NUMBER: US/10/388,269
; CURRENT FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-388-269-4

Query Match      9.6%; Score 188.5; DB 15; Length 373;
Best Local Similarity 23.1%; Pred. No. 1.4e-09;
Matches 81; Conservative 70; Mismatches 144; Indels 55; Gaps 13;

QY 8 ENQRLSFLLEKAITREAOQMKVNRKMPSNQNVSPSORDEVIQWLAKLYQFNLYPETFA 67
DB 72 EDEBLLSLFSK--EKETHCFNSFQ---DBSLCSARVDSVEWILKNGYVYGFSAITAV 125
QY 68 LASSLLDRFLATV---KAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDFSCGSS 124
DB 126 LAINYDFRFLTSLHYQDKPMWQLAAVATCLSLAAK-VEETQVPLLDLQVEDAKYVFEA 184
QY 125 SEILMERIILDKLNWDLHTATPLDPLHIFHAI-AVSTRPQLLSLPKLSPOHLAVLTK 183
DB 185 KTIORMELLVLSLKLWRMNPVTPLSLDHIIRRLGLRNNHWEF-----LRRCENL----- 235
QY 184 QLLHMACNQLLOFRGSMALAMVLSLEMEKLIIP--DWLSLTIELLQKAQMDSSQLIHCREL 242
DB 236 -LLSIMADCRFVYMPSPVLATAIMLVHIVHOPECNVDYQQLGLVLKINKKYNCCFEL 294
QY 243 VAHLSLTLQSSSLPLNSVYVYRPLKHTLVTCDKGVFRLHPSVPGPDESKDNKSEVPVRG 302
DB 295 ISE-----VCSKPISHKRKYENPSHS-----PSGVIDFIYSSSESSNDSDWLES 337
QY 303 TAAFYHHLPAASGCKQTSTKRKVEMEVDDFDYDGIKRLYNEDNVSENVGS 352
```

Db 338 TSSVF-----PVFKSRVQEQM-KLASSISRVF-----VEAVGS 371

RESULT 11

US-10-245-618-32
; Sequence 32, Application US/10245618
; Publication No. US20030143582A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; APPLICANT: Strohmaier, Heimo
; APPLICANT: Spruck, Charles
; APPLICANT: Sangfelt, Olle
; TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION
; FILE REFERENCE: TSRI 779.2
; CURRENT APPLICATION NUMBER: US/10/245,618
; PRIOR FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/404,116
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/322,947
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-245-618-32

Query Match 9.6%; Score 187.5; DB 14; Length 395;
Best Local Similarity 27.0%; Pred. No. 1.9e-09;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIOMLAKLYQFNLYPETFALASSLLD 74
Db 100 EVWKIMLNKETYLRDQHFLQHPLOPKMRAILLDMLMEVCEVVKLHRETFYLAQDFD 159
QY 75 RFLATVKAHPK-YLSCIAISCFFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMBELM 217
QY 134 ILDKLNWDLHTATPLDFLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQK 184
Db 218 IMKALKWRLSPLTIVSWLVNQVAYLNDLHEVLDPQYPOQIFI--QIAELLDCVLVD 275
QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLIIPDWLSLITBELLQAKQMDSSQL 236
Db 276 CLEFPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCY-KWMVPFAMVIR--ETGSSKL 331
QY 237 IHCRELV---AHLSTLOSSLPL 256
Db 332 KHFRGVADEDAHNITQTHRDSLDL 354

RESULT 12

US-10-245-618-46
; Sequence 46, Application US/10245618
; Publication No. US20030143582A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; APPLICANT: Strohmaier, Heimo
; APPLICANT: Spruck, Charles
; APPLICANT: Sangfelt, Olle
; TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION
; FILE REFERENCE: TSRI 779.2
; CURRENT APPLICATION NUMBER: US/10/245,618
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/404,116
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/322,947
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46

; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 62
; OTHER INFORMATION: Xaa = Any Amino Acid or none
US-10-245-618-46
Query Match 9.6%; Score 187.5; DB 14; Length 395;
Best Local Similarity 27.0%; Pred. No. 1.9e-09;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIOMLAKLYQFNLYPETFALASSLLD 74
Db 100 EVWKIMLNKETYLRDQHFLQHPLOPKMRAILLDMLMEVCEVVKLHRETFYLAQDFD 159
QY 75 RFLATVKAHPK-YLSCIAISCFFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMBELM 217
QY 134 ILDKLNWDLHTATPLDFLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQK 184
Db 218 IMKALKWRLSPLTIVSWLVNQVAYLNDLHEVLDPQYPOQIFI--QIAELLDCVLVD 275
QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLIIPDWLSLITBELLQAKQMDSSQL 236
Db 276 CLEFPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCY-KWMVPFAMVIR--ETGSSKL 331
QY 237 IHCRELV---AHLSTLOSSLPL 256
Db 332 KHFRGVADEDAHNITQTHRDSLDL 354

RESULT 13

US-10-245-618-47
; Sequence 47, Application US/10245618
; Publication No. US20030143582A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven
; APPLICANT: Strohmaier, Heimo
; APPLICANT: Spruck, Charles
; APPLICANT: Sangfelt, Olle
; TITLE OF INVENTION: HCDC4 MODULATES CYCLIN E DEGRADATION
; FILE REFERENCE: TSRI 779.2
; CURRENT APPLICATION NUMBER: US/10/245,618
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US 60/404,116
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 60/322,947
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 380
; OTHER INFORMATION: Xaa = Any Amino Acid or none
US-10-245-618-47

Query Match 9.6%; Score 187.5; DB 14; Length 395;
Best Local Similarity 27.0%; Pred. No. 1.9e-09;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
QY 25 QMKVNVVRK-----MPSNQVSPSQRDEVIOMLAKLYQFNLYPETFALASSLLD 74
Db 100 EVWKIMLNKETYLRDQHFLQHPLOPKMRAILLDMLMEVCEVVKLHRETFYLAQDFD 159
QY 75 RFLATVKAHPK-YLSCIAISCFFLAAKTVEDEIRPVLKVLARDSFCGSSSEILRMERI 133
Db 160 RYMATQENVVKTLLQLIGISLFLAAKL--BEIYPPKHLQFAYVTDGACSGDEILTMBELM 217
QY 134 ILDKLNWDLHTATPLDFLHIF-----HAIAVSTRPQLLFLSLPKLSPSHLAVLTQK 184
Db 218 IMKALKWRLSPLTIVSWLVNQVAYLNDLHEVLDPQYPOQIFI--QIAELLDCVLVD 275
QY 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLIIPDWLSLITBELLQAKQMDSSQL 236
Db 276 CLEFPYGILAAALYHFSSSEL-MQKVSQYQWCDIENCY-KWMVPFAMVIR--ETGSSKL 331
QY 237 IHCRELV---AHLSTLOSSLPL 256
Db 332 KHFRGVADEDAHNITQTHRDSLDL 354

Db 100 EVWKIMLNKEXTYLRDQHFLQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 159
 Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEEDERIPVLKVLARDSFCGCSSESILRMERI 133
 Db 160 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 217
 Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
 Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 275
 Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
 Db 276 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENC-V-KMWVPFAMVIR--ETGSSKL 331
 Qy 237 IHCRELV---AHLSTLQSSLP 256
 Db 332 KHFRGVADEDAHNIQTHRDSLDL 354

RESULT 14
 US-10-245-618-48
 ; Sequence 48, Application US/10245618
 ; Publication No. US20030143582A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven
 ; APPLICANT: Strohmaier, Heimo
 ; APPLICANT: Spruck, Charles
 ; APPLICANT: Sangfelt, Olle
 ; TITLE OF INVENTION: HCD4 MODULATES CYCLIN E DEGRADATION
 ; FILE REFERENCE: TSRI 779.2
 ; CURRENT APPLICATION NUMBER: US/10/245,618
 ; PRIOR FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: US 60/404,116
 ; PRIOR FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: US 60/322,947
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 48
 ; LENGTH: 395
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthesized
 ; NAME/KEY: VARIANT
 ; LOCATION: 62, 380
 ; OTHER INFORMATION: xaa = Any Amino Acid or none
 US-10-245-618-48

Query Match 9.6%; Score 187.5; DB 14; Length 395;
 Best Local Similarity 27.0%; Pred. No. 1.9e-09;
 Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
 Qy 25 QMKVNVK-----MPSNQVSPQRDEVIOWLAKLYQFNLYPETFALASSLLD 74
 Db 100 EVWKIMLNKEXTYLRDQHFLQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 159
 Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEEDERIPVLKVLARDSFCGCSSESILRMERI 133
 Db 160 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 217
 Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
 Db 218 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 275
 Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
 Db 276 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENC-V-KMWVPFAMVIR--ETGSSKL 331
 Qy 237 IHCRELV---AHLSTLQSSLP 256
 Db 332 KHFRGVADEDAHNIQTHRDSLDL 354

RESULT 15
 US-10-245-618-31
 ; Sequence 31, Application US/10245618
 ; Publication No. US20030143582A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Reed, Steven
 ; APPLICANT: Strohmaier, Heimo
 ; APPLICANT: Spruck, Charles
 ; APPLICANT: Sangfelt, Olle
 ; TITLE OF INVENTION: HCD4 MODULATES CYCLIN E DEGRADATION
 ; FILE REFERENCE: TSRI 779.2
 ; CURRENT APPLICATION NUMBER: US/10/245,618
 ; PRIOR FILING DATE: 2002-09-16
 ; PRIOR APPLICATION NUMBER: US 60/404,116
 ; PRIOR FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: US 60/322,947
 ; PRIOR FILING DATE: 2001-09-14
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 31
 ; LENGTH: 410
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-10-245-618-31

Query Match 9.6%; Score 187.5; DB 14; Length 410;
 Best Local Similarity 27.0%; Pred. No. 2e-09;
 Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;
 Qy 25 QMKVNVK-----MPSNQVSPQRDEVIOWLAKLYQFNLYPETFALASSLLD 74
 Db 115 EVWKIMLNKEXTYLRDQHFLQHPLOPKMRAILLDMLMEVCEVYKHLHRETFYLAQDFD 174
 Qy 75 RFLATVKAHPK-YLSCIAISCFPLAAKTVEEDERIPVLKVLARDSFCGCSSESILRMERI 133
 Db 175 RYMATQENVVKTLLQLIGISLFAAKL--EEIYPPKHLQFAYVTDGACSGDEILTMELM 232
 Qy 134 ILDKLNWDLHTATPLDPLHIF-----HAIIVSTRPQLLFLSLPKLSPSOHLAVLTQ 184
 Db 233 IMKALKWRLSPLTIVSWLVNVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLVD 290
 Qy 185 LLH-----CMACNQLQFRGSMALAMVS-----LEMEKLPDWLSLTIELLOKQAMDSSQL 236
 Db 291 CLEPPYGILAAALYHFSSEL-MQKVSQYQWCDIENC-V-KMWVPFAMVIR--ETGSSKL 346
 Qy 237 IHCRELV---AHLSTLQSSLP 256
 Db 347 KHFRGVADEDAHNIQTHRDSLDL 369

Search completed: February 11, 2005, 03:13:12
 Job time : 87.7775 secs

GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:59:54 ; Search time 28.9258 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 162

Sequence: 1 MKFPGPLENQLSFLLEKAI.....LSRQEGHASPDPPIQPVSVM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	902	46.0	178	2	J00264
2	271.5	13.8	249	2	cyclin G - rat
3	271.5	13.8	295	2	cyclin G1 - human
4	269.5	13.7	256	2	cyclin G - human
5	263.5	13.4	249	2	cyclin G - mouse
6	201.5	10.3	410	2	cyclin E - zebra f
7	196	10.0	361	2	cyclin D3-like pro
8	187.5	9.6	395	2	cyclin E - human
9	187	9.5	309	2	hypothetical prote
10	181.5	9.3	449	2	cyclin - common to
11	177.5	9.0	289	2	cyclin D2 - mouse
12	176.5	9.0	419	2	cyclin D - rice
13	176	9.0	291	2	cyclin D1 - Africa
14	176	9.0	471	2	cyclin B1 - yeast
15	175.5	8.9	359	2	cyclin - fission y
16	175.5	8.9	601	2	cyclin E type I -
17	175	8.9	386	2	cyclin 4, D-type -
18	174.5	8.9	372	2	cyclin D-like prot
19	174	8.9	288	2	cyclin D2 - rat
20	174	8.9	291	2	cyclin D1 - zebra
21	173.5	8.8	502	2	cyclin A-like prot
22	171.5	8.7	359	2	cyclin pucl - fission
23	171.5	8.7	456	2	cyclin II - maize
24	171	8.7	327	2	probable cyclin, 2
25	170.5	8.7	242	2	cyclin - rice
26	170.5	8.7	460	2	protein F2D10.10 [
27	169.5	8.6	441	2	mitosis-specific c
28	169.5	8.6	469	2	cyclin a2-type, mi
29	169	8.6	289	2	cyclin D2 - human

30 168.5 8.6 428 2 T04743
31 168 8.6 291 2 S57925
32 168 8.6 440 2 T07676
33 167.5 8.5 424 2 D57742
34 167 8.5 473 2 T03611
35 167 8.5 491 2 S14166
36 166.5 8.5 479 2 T04104
37 166.5 8.5 491 2 JC2497
38 164.5 8.4 262 2 T42986
39 164.5 8.4 291 2 JC4579
40 164.5 8.4 371 2 T02963
41 163.5 8.3 492 2 JC4828
42 162.5 8.3 498 2 D86298
43 162 8.3 443 2 T14916
44 161.5 8.2 376 2 T05420
45 161.5 8.2 408 2 A56186

ALIGNMENTS

RESULT 1

JE0264

cyclin I - human

C/Species: Homo sapiens (man)

C/Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004

C/Accession: JE0264

R/Zhu, X.; Naz, R.K.

Biochem. Biophys. Res. Commun. 249, 56-60, 1998

A/Title: Expression of a novel isoform of cyclin I in human testis.

A/Reference number: JE0264; MUID:98381026; PMID:9705831

A/Accession: JE0264

A/Molecule type: mRNA

A/Residues: 1-178 <ZHU>

A/Cross-references: UNIPROT:Q14094

C/Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 46.0%; Score 902; DB 2; Length 178;

Best Local Similarity 98.3%; Pred. No. 1.8e-70;

Matches 175; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy

1 MKFPGPLENQLSFLLEKAITREAOQMKVNVKRMPSNQNVSPORDEVIOMLKLYQFN 60

Db

1 MKFPGPLEDQKLSFLLEKAITREAOQMKVNVKRMPSNQNVSPORDEVIOMLKLYRPN 60

Qy

61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSCFC 120

Db

61 LYPETFALASLLDGLFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSCFC 120

Qy

121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHFAIAVSTRPQLLSPKLSPSQHL 178

Db

121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHFAIAVSTRPQLLSPKLSPSQHL 178

RESULT 2

S37693

cyclin G - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995

C/Accession: S37693

R/Tamura, K.; Katsoka, Y.; Jinno, S.; Nagata, A.; Ogiso, Y.; Shimizu, K.; Hayakawa, T.;

Oncogene 8, 2113-2118, 1993

A/Title: Cyclin G: a new mammalian cyclin with homology to fission yeast Cig1.

A/Reference number: S37693; MUID:93330551; PMID:8336937

A/Accession: S37693

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-249 <TAM>

A/Cross-references: EMBL:X70871

Query Match 13.8%; Score 271.5; DB 2; Length 249;

Best Local Similarity 31.8%; Pred. No. 7.9e-16;

Matches 77; Conservative 49; Mismatches 85; Indels 31; Gaps 7;


```
RESULT 6
S52288
C:Species: Brachydanio rerio (zebra fish)
C:Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 12-Jul-2004
C:Accession: S52288
R:Yarden, A.; Geiger, B.
submitted to the EMBL Data Library, December 1994
A:Reference number: S52288
A:Accession: S52288
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-410 <YAR>
A:Cross-references: UNIPROT:P47794; EMBL:X83594; NID:G643111; PIDN:CAA58574.1; PID:G6431
C:Superfamily: cyclin, A/B/D/E type
C:Keywords: cell cycle control

Query Match 10.3%; Score 201.5; DB 2; Length 410;
Best Local Similarity 27.1%; Pred. No. 1.7e-09;
Matches 80; Conservative 51; Mismatches 117; Indels 47; Gaps 10;

Qy 30 NVRKPSNQVSPQRDVIQWLAKLYQFNLYPETPALASSLLDRFLATVKAHPK-YLS 88
Db 132 DTRVWERHPNLPQKRAILLDNLMEVCEVYKLRHETFYLGODYFDRPWATQENVLKTQLQ 191
Qy 89 CIAISCFFLAAKTVEEDERIPVLKVLARDSPCGSSSEILMERIILDKLNDLHTATPL 148
Db 192 LIGISCLFIAAKM--EETYPKVHQFAVVTGACTEDDILSWEIIMKELNWSLSPLTPV 249
Qy 149 DFLHIFHAIIV--STRPOLLESPLKLSPSQHLAVLTQQLLHMACNQQLQPRGSMALAM 206
Db 250 AMLNIYQMAYLKRETAELVTAQYQATEVQ----IAELLDLCILDVRSLEFSYSLAASA 305
Qy 207 V-----SLEM-----EKLIPDWLSLTIELLQKQMDSSSLIHCRELVAAH 246
Db 306 LFHFSLELVIVKSLKWCDBECVRMVPFAMSI-----REAGSALKTFKGIADD 358
Qy 247 LSTLQSSLP-----LNSVYVYRPLKHTLVCTDKGVFRHLHSSVPQDFSKNSRPE 297
Db 359 MHNITQHPVLEWLGKHSYQ-----LVDISSQSRSPVPTGVLTPPSSE--KEE 406

RESULT 7
T45860
cyclin D3-like protein - Arabidopsis thaliana
N:Alternate names: protein F3A4.150
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C:Accession: T45860
R:Bargues, M.; Collado, M.C.; Navarro, P.; Terol, J.; Perez-Alonso, M.; Mewes, H.W.; May
submitted to the Protein Sequence Database, December 1999
A:Reference number: T23007
A:Accession: T45860
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <BAR>
A:Cross-references: UNIPROT:Q9SN11; EMBL:AL132978
A:Experimental source: cultivar Columbia; BAC clone F3A4
C:Genetics:
A:Map position: 3
A:Introns: 157/3; 225/1; 268/3
A:Note: F3A4.150

Query Match 10.0%; Score 196; DB 2; Length 361;
Best Local Similarity 25.8%; Pred. No. 4.3e-09;
Matches 76; Conservative 53; Mismatches 120; Indels 46; Gaps 11;

Qy 45 RDEVIQWLAKLYQFNLYPETPALASSLLDRFLATVKAH---PKYLSCIAISCFFLAAKT 101
Db 86 REKALDWIFKVKSHYGFNSLTALLAVNYFDRFITSRKFTQDKPWNLSQTLACLALAAKV 145
Qy 102 VEEDERIPVLKVL-----ARDSPCGSSSEILMERIILDKLNDLHTATPLDFL-HIFHA 156
```

```
Db 146 --BEIRVPFLDQVEEARYVF---EAKTQRMELLVLSTLDMRMHPVPTISFFDHIIR 200
Qy 157 IAVSTRPQLLPSLPKLSPSQHLAVLTQQLLHMACNQQLQPRGSMALALA-MVSLMEBKLI 215
Db 201 YSPKSHHQLEP-----LSRCESL-----LLSIIPDSRFLSPSVLATAMVSVIRDLKM 250
Qy 216 PDWLSLTIELLQKQMDSSSLIHCRELVAAHLSLTQSSSLPLNSVYVVRPLKHTLVCTDKG 275
Db 251 CDEAVYQSLMTLLKVDSEKVNKCYELVDHDSPSKKMMN-----WMQOPAS----- 297
Qy 276 VFRLLHPSVPGPDPSKDNKPEVVRGTAAFYHHLPAASGCKQTSTRKVKVEEMEV 330
Db 298 -----PIGVFDASFSSDSNESWVVSASAS-----VSSSPSEPLKRRRVOEQQM 343

RESULT 8
A40270
cyclin E - human
C:Species: Homo sapiens (man)
C:Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 12-Jul-2004
C:Accession: A40270; C40268
R:Koff, A.; Cross, F.; Fisher, A.; Schumacher, J.; Leguellec, K.; Philippe, M.; Roberts
Cell 66, 1217-1228, 1991
A:Title: Human cyclin E, a new cyclin that interacts with two members of the CDC2 gene f
A:Reference number: A40270; MUID:92005673; PMID:1833068
A:Accession: A40270
A:Molecule type: mRNA
A:Residues: 1-395 <KOF>
A:Cross-references: UNIPROT:P24864; GB:M73812
R:Lew, D.J.; Dulic, V.; Reed, S.I.
Cell 66, 1197-1206, 1991
A:Title: Isolation of three novel human cyclins by rescue of G1 cyclin (Cln) function in
A:Reference number: A40268; MUID:92005671; PMID:1833065
A:Accession: C40268
A:Molecule type: mRNA
A:Residues: 1-395 <LEW>
A:Cross-references: GB:M74093
C:Comment: This protein is one of the G1 type cyclins; it forms a complex with both prot
C:Genetics:
A:Gene: GDB:CCNE
A:Cross-references: GDB:128967; OMIM:123837
A:Map position: 19q12-19q12
C:Superfamily: cyclin, A/B/D/E type
C:Keywords: cell cycle control

Query Match 9.6%; Score 187.5; DB 2; Length 395;
Best Local Similarity 27.0%; Pred. No. 2.6e-08;
Matches 71; Conservative 48; Mismatches 105; Indels 39; Gaps 11;

Qy 25 QMKVNVVRK-----MPSNQNVSPQRDEVIQWLAKLYQFNLYPETPALASSLLD 74
Db 100 EVKIMLNKEKTYLRDQHFLEQHPQLQPKRAILLDNLMEVCEVYKLRHETFYLAQDFD 159
Qy 75 RFLATVKAHPK-YLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPCGSSSEILMERI 133
Db 160 RYMATQENVVKTLLQLIGISLSFLTAAL--BEIYPPKHLQFAYVYTDGACSGDEILTMELM 217
Qy 134 ILDKLNDLHTATPLDPLHIF-----HAIAVSTRPQLLPSLPKLSPSQHLAVLTQ 184
Db 218 IMKALKWRSLPLTIVSWINVMQVAYLNDLHEVLLPQYPOQIFI--QIAELLDLCVLDVD 275
Qy 185 LLH-----CMACNQQLQPRGSMALAMVS-----LEMEKLIPLDWLSLTIELLQKQMDSSQL 236
Db 276 CLEFPYGIILAAALYHFSSSEL-MQKSYGVQWCDIENCV-KMWVPFAMVIR--ETGSSKL 331
Qy 237 IHCRELV---AHLSTLQSSILPL 256
Db 332 KHFRGVADEAHNIQTHRDSLDL 354

RESULT 9
T16660
```

```

Db      303. TP-----SDQENMTFFFAELGLMYKITYRPSWLAASSVVAARSTLNK 350
Qy      215 IPDWLSLTIELLQKAQDSSQLIHCRE-LVAHLSTLQSSLPLNSVVYRPLKHTLVCTD 273
Db      351 TPLW---TQTLQHTGYSEDQLMECAKILSVYHLDAAESKL-----388
Qy      274 KGVFRLLHPSSVPGDFSKDMSKPEVPVRGTAAFPVHHLPAASGCCQQTSTKRVKEEMVDDF 333
Db      389 KAIYRKFS-----PDRGAVAF-----PPARNLLPTTT-TDAASLVLEEF 428
Qy      334 Y 334
Db      429 Y 429

RESULT 11
A41984
N:Alternate names: cyclin-like protein Cyl2
C:Species: Mus musculus (house mouse)
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Jul-2004
C:Accession: A41984; B40035
R:Kiyokawa, H.; Busquets, X.; Powell, C.T.; Ngo, L.; Rifkind, R.A.; Marks, P.A.
Proc. Natl. Acad. Sci. U.S.A. 89, 2444-2447, 1992
A:Title: Cloning of a D-type cyclin from murine erythroleukemia cells.
A:Reference number: A41984; MUID:92196134; PMID:1372445
A:Accession: A41984
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-289 <KTY>
A:Cross-references: UNIPROT:P30280; GB:M83749; NID:g192938; PIDN:AAA37519.1; P
A:Experimental source: erythroleukemia cells
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBI:88492, NCBIP:88493)
R:Matsumine, H.; Rousssel, M.F.; Ashmun, R.A.; Sherr, C.J.
Cell 65, 701-713, 1991
A:Title: Colony-stimulating factor 1 regulates novel cyclins during the G1 pha
A:Reference number: A40035; MUID:91235305; PMID:1827757
A:Accession: B40035
A:Status: Preliminary

```

[illegible]

```

QY 134 ILDKLNWDLHTATPDLFLHIFHAIIVSTRPQLLFSLPKLSPSOHLAVLTKQLLH-----187
Db 142 VLNKLKWDLASVTPPHDFIEHF-----LNKMP-----LTDTKQIIRKHAQTF 183
QY 188 ---CMACNQLQPRGSMALAMVSLWEKLI-----IPDWLSLTIELLQKAQMDSSQLI 237
Db 184 VALCATDVNFISNPPSMIAAGSVAAVQGLNGLNADSVSTQRLTLFLSQVILKCDPDCLR 243
QY 238 HCKELVAHHLSTLQSSL 254
Db 244 ACQEQIE---SLLESSL 257

RESULT 14
S14165
cyclin B1 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein G5967; protein YGR108W
C;Species: Saccharomyces cerevisiae
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 12-Jul-2004
C;Accession: S14165; S36659; A23700; S64415
R;Surana, U.; Robitach, H.; Price, C.; Schuster, T.; Fitch, I.; Fletcher, A.B.; ;
Cell 65, 145-161, 1991
A;Title: The role of CDC28 and cyclins during mitosis in the budding yeast S. c.
A;Reference number: S14165; MUID:91191554; PMID:1849457
A;Accession: S14165
A;Molecule type: DNA
A;Residues: 1-471 <SUR>
A;Cross-references: UNIPROT:P24868; EMBL:M65069; NID:g171234; PIDN:AAA34501.1;
R;Ghiara, J.B.; Richardson, H.E.; Sugimoto, K.; Henze, M.; Lew, D.J.; Wittenber
submitted to the EMBL Data Library, April 1991
A;Reference number: S36659
A;Accession: S36659
A;Molecule type: DNA
A;Residues: 1-471 <GHI>
A;Cross-references: EMBL:M62389; NID:g172537; PIDN:AAA35019.1; PID:g172539
R;Ghiara, J.B.; Richardson, H.E.; Sugimoto, K.; Henze, M.; Lew, D.J.; Wittenber
Cell 65, 163-174, 1991
A;Title: A cyclin B homolog in Saccharomyces cerevisiae: chronic activation of
A;Reference number: A23700; MUID:91191555; PMID:1849458
A;Accession: A23700
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 192-449 <GH2>
A;Cross-references: GB:M62389
R;Wedler, H.; Scharfe, M.; Wedler, E.; Wambutt, R.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64356
A;Accession: S64415
A;Molecule type: DNA
A;Residues: 1-471 <WED>
A;Cross-references: EMBL:Z72893; NID:gl323168; PIDN:CAA97112.1; PID:gl323169; M
A;Experimental source: strain S288C
C;Genetics:
A;Gene: SGD:CLB1; SCB1
A;Cross-references: SGD:S0003340; MIPS:YGR108W
A;Map position: 7R
C;Superfamily: cyclin, A/B/D/E type
C;Keywords: cell cycle control; transmembrane protein
F;375-391/Domain: transmembrane #status predicted <TMM>

Query Match 9.0%; Score 176; DB 2; Length 471;
Best Local Similarity 33.9%; Pred. No.3 3e-07;
Matches 42; Conservative 26; Mismatches 50; Indels 6; Gaps 3;

QY 28 KVNVRKMPNQNVPSQRDEVITQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYL 87
Db 228 KANLYK---HKNIK-QNRDILNVNIIKHKKFLLPETLYLAINIMDRFLCEEVQNLRL 283

QY 88 SCIAISCFPLAAKTVEEDRIPVLKVLARDSFCGSSSSSILRMERILDKLNWDLHTATP 147
Db 284 QLVGTSCLFIASK--YEETIYSPSIKHFAVETAGCSVEDIKGEKRFLEKDFQISFANP 341

```

QY 148 LDFL 151
 Db 342 MNFL 345

RESULT 15
 S36408
 cyclin - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 12-Jul-2004
 C:Accession: S36408; T40826; T39819
 R:Forsburg, S.L.; Nurse, P.
 submitted to the EMBL Data Library, August 1993
 A:Description: Analysis of the S. pombe cyclin puc1: evidence for a role in cell cycle
 A:Reference number: S36408
 A:Accession: S36408
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-359 <FOR>
 A:Cross-references: UNIPROT:P25009; EMBL:X74451; NID:G396596; PIDN:CAAS2460.1; PID:G3965
 R:Beck, A.; Reinhardt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, October 1998
 A:Reference number: Z21949
 A:Accession: T40826
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-359 <BEC>
 A:Cross-references: EMBL:AL032684; PIDN:CAA21817.1; GSPDB:GN00067; SPDB:SPBP8B7.32C
 A:Experimental source: strain 972h-; clone pl p8B7
 R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.
 submitted to the EMBL Data Library, April 1998
 A:Reference number: Z21882
 A:Accession: T39819
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-277 <LYN>
 A:Cross-references: EMBL:AL022599; PIDN:CAA18649.1; GSPDB:GN00067; SPDB:SPBC19F5.01C
 A:Experimental source: strain 972h-; cosmid c19F5
 C:Genetics:
 A:Gene: SPBP8B7.32c; puc1; SPDB:SPBC19F5.01c
 A:Map position: 2
 C:Superfamily: cyclin, G1 CLN1/CLN2/Puc1 type

Query Match 8.9%; Score 175.5; DB 2; Length 359;
 Best Local Similarity 24.4%; Pred. No. 2.5e-07;
 Matches 63; Conservative 54; Mismatches 100; Indels 41; Gaps 10;

QY 15 LLEKAITREAOQWKVNRKMFNSQNVSPSQDEVIQWLAKLYQPNLYPETFALASSLLD 74
 Db 100 IHHLLITRE-KNFLNLVHLSNQQPELRWSMRPALVNFIVEIHNGFDLSIDTLPISLMD 158
 QY 75 RFLATVKAHPKYLSCIAISCFPLAAKTVEEDERIPVLK-----VLARDSFCGCSSE 126
 Db 159 SYVSRRVYVYCHIQLVACVCLWIAKSFHETEDRVLPQLQELKACKNIYAEOLF----- 211
 QY 127 ILRMERIILKINWDLHTATPLDFLHIFHAJAVSTRPQLLSLPKL--SPSQHLAVLTQK 184
 Db 212 -IRMERHILDTLWDISITPTASYPVLDPIFFFLVDASMF-VPNLFKFPASKIA----- 264
 QY 185 LLHCWACNQLQFRGSMALAMVLSLEMEK-----LIP---DWLSLTIELLOKAQMDSSQL 236
 Db 265 ---CSVMNIVNEHVGSFL-LTHPSMESYRKODNFWLPEDLDITVTSYMNNGSKRYANE--- 317
 QY 237 IHCRLVAHLSTLQSSL 254
 Db 318 -ECTDLLFSSIGRISSIL 334

Search completed: February 11, 2005, 03:05:48
 Job time : 29.9258 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:45 ; Search time 948.767 Seconds
(without alignments)
2352.255 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPEPLENORLSFLEKAI.....LSRQGHASPCPPLPQVSVM 377

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/usPTO_spool/US09736250/runat_07022005_154923_20396/app_query.fasta_1.718
-DB=N Geneseq 16Dec04 -QFMT=fastap -SUFFIX=ring -MINMATCH=0.1 -LOPCL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blotsum2 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.qcgn 1 586 @runat_07022005_154923_20396 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq 16Dec04:*

1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	1260	3	Aaz37836 Human cyc
2	1962	100.0	1260	6	Abk83672 Human cdn
3	1962	100.0	1260	10	Adk61064 Ovarian c
4	1962	100.0	1260	11	Adi31573 Human cdn
5	1962	100.0	1260	13	Adr25465 Breast ca

6	1962	100.0	1328	2	AAT73937	Aat73937 DNA encod	
7	1962	100.0	1384	8	ACC47339	Acc47339 Human pro	
8	1962	100.0	1889	6	ABL87929	AbL87929 Human ova	
9	1962	100.0	1890	12	ADP10653	Adp10653 Reference	
10	1962	100.0	1890	13	ACN38124	Acn38124 Tumour-as	
11	1841	93.8	2755	5	ADL63374	AdL63374 Human ova	
12	1713.5	87.3	1651	9	AAD57247	Aad57247 Human CGD	
13	1529.5	78.0	903	12	ADNO1156	Adno1156 Human cel	
14	770.5	39.3	2146	5	ADL63082	AdL63082 Human ova	
c	15	763	38.9	804	2	AAX40003	Aax40003 Prostate
16	748	38.1	444	3	AAC01909	Aac01909 Human sec	
17	647	33.0	392	2	AAQ61358	Aaq61358 Human bra	
c	18	633	32.3	417	2	AAT26236	Aat26236 Human gen
c	19	621	31.7	516	5	ADL44155	AdL44155 Human ova
20	550	28.0	389	10	ADK61066	Adk61066 Ovarian c	
21	540	27.5	1493	2	AAZ41284	Aaz41284 Human nor	
22	517	26.4	329	2	AAT23729	Aat23729 Human gen	
23	502.5	25.6	1110	5	AAS82590	Aas82590 DNA encod	
24	502.5	25.6	2356	13	ADR10427	Adr10427 Full leng	
25	486	24.8	348	6	ABS69603	AbS69603 Novel mur	
c	26	466	23.8	536	10	ADF82253	Adf82253 Leukaemia
c	27	465	23.7	597	10	ADK61065	Adk61065 Ovarian c
c	28	433	22.1	409	10	ADF80870	Adf80870 Leukaemia
c	29	408	20.8	486	5	ADL43407	AdL43407 Human ova
c	30	377.5	19.2	426	5	ADL37023	AdL37023 Human ova
c	31	377.5	19.2	426	5	ADI71872	Adi71872 Human ova
32	346	17.6	447	4	AAS25071	Aas25071 Human ova	
33	346	17.6	447	5	AAH83716	Aah83716 Human ova	
34	326.5	16.6	1410	11	ADI31587	Adi31587 Human CDN	
35	326.5	16.6	2044	6	ABL61909	AbL61909 Colon ade	
36	326.5	16.6	2044	6	ABK84346	Abk84346 Human CDN	
37	326.5	16.6	2044	6	ABV78034	Abv78034 Hypoxia-r	
38	326.5	16.6	2044	10	ADH28975	Adh28975 Human chr	
39	326.5	16.6	2044	12	ADO19807	Ado19807 Human PRO	
40	326.5	16.6	2044	12	ADO19316	Ado19316 Human PRO	
41	326.5	16.6	2044	13	ADR25164	Adr25164 Breast ca	
42	326.5	16.6	2044	13	ADP54949	Adp54949 Human PRO	
43	326.5	16.6	2044	13	ADP23417	Adp23417 PRO polyp	
44	326.5	16.6	2044	13	ADR65826	Adr65826 Human pro	
45	326.5	16.6	2044	13	ADR66510	Adr66510 Human pro	

ALIGNMENTS

RESULT 1
AAZ37836
ID AAZ37836 standard; DNA; 1260 BP.
XX
AC AAZ37836;
XX
09-FEB-2000 (first entry)
XX
Human cyclin I nucleotide sequence.
XX
Cyclin-dependent kinase 2; CDK2; hsReq; hsReq-1; hsReq-2; cyclin I;
KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
KW atherosclerosis; tumour; ss.
XX
Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..1134
FT /*tag= a
FT /product= "Cyclin_I"
XX
XX
DN WO9925829-A2.
XX
XX
PD 27-MAY-1999.
XX
XX
PF 12-NOV-1998; 98WO-US024095.
XX
PR 13-NOV-1997; 97US-00969106.
XX

(CURA-) CURAGEN CORP.

XX Yang M, Nandabalan K, Schulz VP;

XX WPI; 2000-061923/05.

DR P-PSDB; AAY52185.

XX New complexes of the cyclin-dependent kinase 2 protein with its
PT interacting proteins, used to treat, e.g. atherosclerosis.

XX Example; Fig 2; 90pp; English.

XX This sequence is the human Cyclin I nucleotide sequence. Cyclin I is
CC expressed at almost constant levels throughout the cell cycle, and is
CC implicated in controlling cell cycle progression and transcriptional
CC control. Cyclins form complexes with cyclin-dependent kinases. CDK2,
CC cyclin-dependent kinase 2, is used in the invention which relates to
CC complexes of the CDK2 protein with other proteins, selected from cyclin
CC I, ERH, hReg, hReg-1 and hReg-2 (AAY52185-Y52188). CDK2 is expressed
CC late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S
CC transition. Compositions containing a CDK2 complex, an antibody targeting
CC the complex, and nucleotide sequences encoding CDK2 or its derivatives
CC can be used therapeutically. The complexes and their nucleotide sequences
CC can be used to treat diseases or disorders associated with increased or
CC decreased levels of the complex. Screening the complex, or a derivative
CC or a modulator of the complex for neoplastic activity by measuring the
CC survival or proliferation of cells from a malignant cell line when in
CC contact with the complex can be used to indicate if the complex has
CC anti-neoplastic activity. Screening for molecules that modulate the
CC formation of the complexes can be used for treating or preventing
CC atherosclerosis or atherosclerosis-associated disease by contacting cells
CC or using a test animal, in which tumour growth or regression is measured
CC to test whether anti-neoplastic activity is displayed. Diseases which can
CC be treated or prevented by molecule/s which modulate the function of the
CC complex include cancer, hyperproliferative disorders and atherosclerosis

XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1,92e-205 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x AAZ37836 (1-1260)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
DB 1 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
DB 61 ACTAGGGAAGCAGATGTGAAGTGAATGTGGGAAATAGCTTCAATCAAGATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
DB 121 TCTCATCCAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 180
QY 61 LeuTrpProGluThrPheAlaLeuAsnSerLeuLeuAspArgPheLeuAlaThrVal 80
DB 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 240
QY 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
DB 241 AAGGCTCATCAAAATCTGAGTTGATTCGAATCAGCTGTTTTCTAGCTGCCAAG 300
QY 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspPheCys 120
DB 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 360
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140

DB 361 GGATGTTCTCTCATCTGAAATTTTGAAGATGGAGAGAAATTATTCTGGATAAGTTCAATTGG 420
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB 421 GATCTTCCACACAGCCACACCAATTGGATTTTCTCATATATTTTCCATGTCATTCAGTGTCA 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCCAATTTGAGCCCACTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
DB 541 CTTTACCAGCAACTACTTCTGATGGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
DB 601 ATGCTTGTCTCTGGCCATGTTAGTCTGGAATGAGAACTCATTTCTGATGGCTTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
DB 661 CTTTACAATTGAACTGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTGTCGG 720
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
DB 721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTTAT 780
QY 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB 781 GTCTACCGTCCCTTCAGACACACCTGTGTGACCTGTGACAAAGAGTGTTCAGATTACAT 840
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
DB 841 CCCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGAGCCAGAGTCCAGTC 900
QY 301 ArgGlyThrAlaPheTrpHisLeuProAlaAsnValGlySerValCysGlyThrAspLeuSer 320
DB 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGGCAGACACTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyLysArgLeu 340
DB 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
DB 1021 TATAATGAGATAATGTCTCAGAAATGTGGTTCGTGTGTGGCACTGATTTATCAAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
DB 1081 CAAGAGGAGCATGCTCCCTTTGCCACCTTTGCCACCTGTTCCTGTCTCATG 1131
RESULT 2
ABK83672
ID ABK83672 standard; cDNA; 1260 BP.
XX AC ABK83672;
XX 14-AUG-2002 (first entry)
XX Human cDNA differentially expressed in granulocytic cells #243.
XX Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
XX granulocyte activation; chronic inflammation; allergy.
XX Homo sapiens.
XX WO200228999-A2.
PN

XX AC ADK61064;
 XX DT 06-MAY-2004 (first entry)
 XX DE Ovarian cancer-related DNA #219 with altered ovarian cancer expression.
 XX KW ds; Gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
 KW gene expression; primer; cancer.
 XX OS Homo sapiens.
 XX FN WO2003068054-A2.
 XX PD 21-AUG-2003.
 XX PF 13-FEB-2003; 2003WO-US004688.
 XX PR 13-FEB-2002; 2002US-0357031P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PA (SLOK) SLOAN KETTERING INST CANCER RES.
 XX Jazaeri AA, Boyd J, Liu ET;
 XX WPI; 2003-689589/65.
 XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
 PT like tumor by determining a pattern of expression in the ovarian tumor of
 PT several markers.
 XX Disclosure; SEQ ID NO 234; 137pp; English.
 CC The invention relates to a method of classifying an ovarian tumor as a
 CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
 CC pattern of expression in the ovarian tumor of several markers given in
 CC the specification; and (2) comparing a similarity of the pattern of
 CC expression of the markers in the ovarian tumor to a pattern of expression
 CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
 CC like or non-BRCA-like tumor. The method is useful for classifying an
 CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
 CC This sequence corresponds to an ovarian cancer -related gene having an
 CC altered pattern of expression in ovarian cancer. (Note: The sequence data
 CC for this patent did not form part of the printed specification but was
 CC obtained in electronic format from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences).
 XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 1,92e-205 Length: 1260
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x ADK61064 (1-1260)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATTGCTTTCCCTGTTGGAAAGGCAATC 60
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 61 ACTAGGAGACACAGATGGAAGTGAATGTGGGAAATGCTTCAATCAGATGTT 120
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrGlnPheAsn 60
 DB 121 TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180
 QY 61 LeuTyTrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80

DB 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 240
 QY 81 LysAlaHisProLysTyTrLeuSerCysValIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 DB 241 AAGCTCATCCAAATACTTGGATTGATTGCAATCAGCTGTTTTTCTTCCAGTCCCAAG 300
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTAGTACTAAAGGTATTGGCAGAGACAGTTTCTGT 360
 QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 361 GGATGTTCTCATCTGAATTTTTCAGAAATGAGAGAAATTTCTGGTAAGTGAATGG 420
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 421 GAICTTCACAGCCACCATTTGGATTTCTTCATATTTTCCATGTCATGTCAGTGTCA 480
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 481 ACTAGGCTCAGTTACTTTTCAGTTGCCCCAAATTCAGCCCATCTCAACATTTGGCAGTC 540
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 541 CTTACCAAGCAACTACTTCTGATGCTGCAACCACTTCGCAATTCAGAGGATCC 600
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAACTCATCTCGATGGCTTTCT 660
 QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 661 CTTACAAATTCGAATGCTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGTCGG 720
 QY 241 GluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyx 260
 DB 721 GAGCTTGTCACATCATCTTTCTACTCTGAGTCTTCTCTGCTCTGAAATTCGATTTAT 780
 QY 261 ValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 781 GTCTACCGTCCCTCAAGCACACCCCTGTCACCTGTGCACAAAGAGGTGTTCCAGATTACAT 840
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 841 CCTCTCTCTGTCAGGCCAGACTTCTCCAGAGACAAACAGCAGCCAGAGTGCACAGTC 900
 QY 301 ArgGlyThrAlaAlaPheTyTrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 DB 901 AGAGGTACAGAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCGCAGACCTCT 960
 QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyTrAspGlyIleLysArgLeu 340
 DB 961 ACTAAACGCAAGATAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1020
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 1021 TATAATGAAGATAATGTCTCAGAAAATGGGGTCTGTGTGTGGCATGATTTATCAAGA 1080
 QY 361 GlnGlyGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 DB 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGGCTGTCTCTGTCTATG 1131

RESULT 4
 ADI31573
 ID ADI31573 standard; cDNA; 1260 BP.
 XX AC ADI31573;
 XX 17-JUN-2004 (first entry)
 XX Human cDNA #899.
 XX Human; gene; ss; immunological response; immunopathological condition;

KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
XX Homo sapiens.
XX
XX US6607879-B1.
XX
XX 19-AUG-2003.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX
XX WPI, 2003-895307/82.
XX
XX A composition comprising a plurality of cDNAs, useful for detecting
XX altered expression of genes in an immunological response or for
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX or osteoarthritis.
XX
XX Claim 1; SEQ ID NO 899; 50pp; English.
XX
XX The invention relates to a composition comprising a plurality of cDNAs
XX for detecting the altered expression of genes in an immunological
XX response. The invention also relates to a method of diagnosing or
XX monitoring the treatment of an immunopathological condition in a sample,
XX comprising obtaining nucleic acids from a sample, contacting the nucleic
XX acids of the sample with an array comprising the plurality of cDNAs under
XX conditions to form one or more hybridisation complexes, detecting the
XX hybridisation complexes and comparing the levels of the detected
XX hybridisation complexes with the level of hybridisation complexes
XX detected in a non-diseased sample, where an altered level of the detected
XX hybridisation complexes correlates with the presence of an
XX immunopathological condition. Also disclosed are an expression profile
XX comprising a microarray and a plurality of detectable complexes and a
XX method for identifying a plurality of polynucleotide probes. The cDNAs
XX are useful as hybridisable array elements in a microarray for monitoring
XX the expression of target polynucleotides. The microarray can be used in
XX the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
XX osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX identifying agents for the treatment of the diseases. The microarray may
XX also be used in drug discovery and development, toxicological and
XX carcinogenicity studies, forensics or pharmacogenomics. The composition
XX may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX genomic fragments. This sequence represents a human cDNA of the
XX invention. Note: The sequence data for this patent did not form part of
XX the printed specification but was obtained in electronic format directly
XX from USPTO at seqdata.uspto.gov/sequence.html.
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred No.: 1-92e-205 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-1 (1-377) x ADI31573 (1-1260)

Qy 1 MetlysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40

Db 61 ACTAGGAAGCACAGATGTGAAAGTGAATGTGCGAAATAGCCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTAATGCTGGCTGGCCAAACTCAAGTACCAATCAAC 180
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGGAGAGAATTAATCTGGATAAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACCATTTGGAATTTCTCATATTTTCCATGTCATTTGAGTGTC 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTCCAAATTAAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 541 CTTTACCAGAACTACTTCTGATGGCTTGCACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTCTCTGGCCATGTTAGTCTGGAATGGAAACTCATTTCTGATGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACATTAAGCTGCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATTCATTCGCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 721 GAGCTTGTGGCACATCATCTTCTACTCTGCACTTCTCCCTGCTCTGAAATTCGTTTAT 780
Qy 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCTCCAGCCAGACACTTCTCCAGGACAAACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTrpHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGTCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGATAGAGGAAATGGAAGTGGATGATCTTATGATGGAATCAACGGGTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAAGTAATGCTCAGAAATGTGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTGTCACCTTTGTCAGCTGTGTTCTGTCTCATG 1131
RESULT 5
ADR25465

ADR25465 standard; DNA; 1260 BP.
ADR25465;
21-OCT-2004 (first entry)
Breast cancer prognosis marker #1326.
ds; breast cancer; prognosis; gene expression; diagnosis.
Homo sapiens.
WO2004065545-A2.
05-AUG-2004.
15-JAN-2004; 2004WO-US0001100.
15-JAN-2003; 2003US-00342887.
(ROSE-) ROSETTA INPHARMATICS LLC.
(NECA-) NETHERLANDS CANCER INST.
Van't Veer LJ, He Y;
WPI; 2004-593473/57.
Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
Disclosure; SEQ ID NO 1326; 226pp; English.
The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a marker used in the method of the invention.
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.92e-205 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0
US-09-736-250-1 (1-377) x ADR25465 (1-1260)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaile 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAAACAGAGATGCTTCTCTGTTGGAAAGCCAAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTCGAAAGTGAATGTGGGAAATGCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGATTTTGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTTGATGCAATCAGCTGTTTTCCTAGTCCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGTAAGATTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGATTTTCTCATATTTTCCATGTCATGTCAGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTTGCCTGCAACCACTTCTGCAATTCAGAGATCC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGGCTTGCCTGCAACCACTTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTTGGAATGAGAAACTCATTTCTGATGGCTTCT 660
Qy 221 LeuThrIleGlnLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACCAATGCACTGCTTTCAGAAAGCACAGATGATAGTCCAGATGTCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGTTGTGTCACATACCTTTTCTACTCTGAGTCTTCTGCTGCTTGAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCAGGCCAGACTTCTCCAAAGCAACAGCAAGGAGGAGTCCAGTCC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCCTTTTACCAATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAAATGTGGGTCTGTGTGTGCGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGTGCGCTGTTTCTGTCTCATG 1131
RESULT 6
AAT73937
ID AAT73937 standard; DNA; 1328 BP.
XX
XX AAT73937;
AC
XX
XX 02-DEC-1997 (first entry)
DT
XX
XX DNA encoding human cyclin I.
DE
XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.
XX
XX Homo sapiens.
XX

FH Key Location/Qualifiers
 FT CDS 69..1202
 XX /*tag= a
 XX
 XX W09712973-A1.
 XX 10-APR-1997.
 XX
 XX 07-OCT-1996; 96WO-JP002905.
 XX 05-OCT-1995; 95JP-00284663.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 XX Nakamura T;
 XX
 XX WPI; 1997-226217/20.
 XX P-PSDB; AAW21965.
 XX
 XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
 XX labelling method and cancer cell detection.
 XX
 XX Example 1; Fig 1; 45pp; Japanese.
 XX
 XX This sequence encodes human cyclin I. Antisense polynucleotides are
 XX useful for as probes and can be labelled and used for detection of
 XX neurones by hybridisation with mRNA for cyclin I (contained in the
 XX neurones and arising by the expression of the cyclin I gene in these
 XX cells). The gene can be used for detection of cancer cells by detecting
 XX the expression of the cyclin I gene in these cells. Also antibodies
 XX specific for the fragments of the protein (especially AAW21966) can be
 XX used for detection
 XX
 XX SQ Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;
 XX
 XX Alignment Scores:
 XX Pred. No.: 2,09e-205 Length: 1328
 XX Score: 1962.00 Matches: 377
 XX Percent Similarity: 100.00% Conservative: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX DB: 2 Gaps: 0
 XX
 XX US-09-736-250-1 (1-377) x AAT73937 (1-1328)
 XX
 XX 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 XX 69 ATGAAGTTTCAGGGCCCTTTGGAAAACACAGAGATTGCTTCTCTGTTGGAAAAGGCAATC 128
 XX 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 XX 129 ACTAGGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAAATGCCCTTCAAAATCAGAAATGTT 188
 XX 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 XX 189 TCTCCATCCCAAGAGAGATGAAGTGAATCAATGGTGGCCAAACCAAGTACCAATTCAC 248
 XX 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 XX 249 CTTTACCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTACCGTA 308
 XX 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 XX 309 AAGGCTCATCCAAAATACTTTCAGTTGTATTGCAATCAGCTGTCTTTTCTAGCTGCCAAG 368
 XX 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 XX 369 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAGGTATTGGCAAGAGACAGTTTCTGT 428
 XX 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 XX 429 GGATGTTCTCATCTGAAATTTTGAGATGAGAGAAATTTCTGGATAGTTGAATGG 488

141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 489 GATCTTTCACACAGCCACACCATTTGGATTTTCTCATATTTTCCATGTCATGTCAGTGTCA 548
 161 ThrArgProGlnLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 549 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCACTCAACCAATTTGGCAGTC 608
 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 609 CTTACCAAGCAACTACTTCTACTGTATGGCCCTGCAACCAACTTCTGCAATTCAGAGGATCC 668
 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
 669 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATATGAGAAATCTCATTTCTGATTTGGCTTTCT 728
 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 729 CTTACAATTGAACTGCTTTCAGAAAGCACAGATGATAGCTCCCAAGTTGATCCATTGTCGG 788
 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuProLeuAsnSerValTyr 260
 789 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTTAT 848
 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 849 GTCTACCGTCCCTCAAGCACACCTGTGTGACCAAGAGAGTTCAGATTACAT 908
 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 909 CCTCTCTGTCTCCAGGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTGCAGTC 968
 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 969 AGAGGTACACAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAGACACCTCT 1028
 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 1029 ACTAAACGCCAAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1088
 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 1089 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGGCACTGATTTATCAAGA 1148
 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 1149 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTTCTGTGTCATG 1199

RESULT 7
 ACC47339
 ID ACC47339 standard; cDNA; 1384 BP.
 XX
 AC ACC47339;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Human prostate selective polynucleotide Pr325.
 XX
 KW Prostate; molecular marker; cancer; cytostatic; gene therapy; human;
 XX gene; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 200..1333
 XX /*tag= a
 XX
 XX W02003014298-A2.
 XX
 XX 20-FEB-2003.
 XX
 XX 02-AUG-2002; 2002WO-US024431.
 XX

PR 03-AUG-2001; 2001US-0309470P.
 PR 30-OCT-2001; 2001US-0330747P.
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
 PI WPI; 2003-256562/25.
 DR P-PSDB; ABR39934.
 XX New polynucleotide, useful for preparing a composition for treating
 PT prostate disease, e.g., cancer.
 XX Claim 1; Page 147-149; 212pp; English.
 PS The invention relates to prostate selective polynucleotides and
 CC polypeptides. The polynucleotides are expressed in prostate and are
 CC useful as molecular markers, as drug targets, and for detecting,
 CC monitoring, preventing or treating diseases and conditions related to
 CC prostate, such as prostate cancers. Sequences ACC47325-356 represent
 CC specific examples of prostate specific polynucleotides
 XX
 SQ Sequence 1384 BP; 364 A; 329 C; 324 G; 367 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 2,23e-205 Length: 1384
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-736-250-1 (1-377) x ACC47339 (1-1384)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 200 ATGAAGTTTCAGGGCCCTTTGGAAAACAGAGATGTCTTTCCTGTGGAAAAGGCAATC 259

QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 260 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGAAAATGCCTTCAATCAGAATGTT 319

QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 320 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAACTCAAGTACCAATTCAAC 379

QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 380 CTTTACCAGAAAACATTTGCTGTGGTAGCAGTCTTTTGGATAGGTTTTTAGCTACCGTA 439

QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 DB 440 AAGGCTCATCAAAATACTTGCAGTTGTATTGCAATCAGCTGTTTTTTCCTAGCTGCCAAG 499

QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 500 ACTGTGTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTGGCAAGACAGATTCTGT 559

QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 560 GGAITGTCCTCATCTGAATTTTGGAAATGAGAGATTAATTCGGATAAGTTGAATGG 619

QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 620 GATCTTCACAGCCACACCATTTGATTTTCTTCATATTTTCCATGTCATTCAGTGCA 679

QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 680 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTTGGCAGTC 739

QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 740 CTTACCAAGCACTACTTCTACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCC 799

QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 800 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGAGAAACTCATCTCTGATTGCTTCT 859

QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 860 CTTACAATTCAACTGCTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTGTCGG 919

QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 920 GAGCTTGTGGCACATCACCTTTCTACTCTCAGTCTTCCCTGCTCTGAAATTCGGTTAT 979

QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 980 GTCTACCGTCCCTTCAGCACACCTTGTGTGACCTGTGACAAAGAGTGTTCAGATTACAT 1039

QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 1040 CCCTCCTCTGTCCAGGCCCAGACTTCTCCAGGACAAACAGAACCCAGAGTGCCAGTC 1099

QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 DB 1100 AGAGGTACAGCAGCCTTTTACCATCATCTCCCACTGCCAGTGGGTGCAAGCAGACTCT 1159

QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 DB 1160 ACTAAGCCAAAGTAGGAAATGGAAATGGAGTGTGATCTTCTATGATGGAATCAACGGCTC 1219

QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 1220 TATAATGAGATAATGTCTCAGAAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGA 1279

QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 DB 1280 CAAGAGGAGCATGCTTCCCTTGTGCCACTTTCAGCCTGTTTCTGTGTCATG 1330

RESULT 8
 ABL87929
 ID ABL87929 standard; DNA; 1889 BP.
 XX
 AC ABL87929;
 XX
 DT 17-MAY-2002 (first entry)
 XX
 DE Human ovarian cancer related DNA clone SEQ ID NO:10907.
 XX
 KW Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200192581-A2.
 XX
 PD 06-DEC-2001.
 XX
 PF 29-MAY-2001; 2001WO-US017756.
 XX
 PR 26-MAY-2000; 2000US-0207484P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Algate PA, Harlocker SL, Jones R;
 XX
 DR WPI; 2002-122075/16.
 XX
 PT Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide.
 XX
 PS Claim 1; SEQ ID NO 10907; 489pp; English.
 XX
 CC The present invention describes a composition (I) comprising: carriers

CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
 CC or antigen presenting cells that express (II). (I) has cytostatic
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
 CC detecting ovarian cancer in a patient's biological sample preferably
 CC serum or ovarian tissue. The method comprises contacting a biological
 CC sample from a patient with (IV), detecting the amount of polynucleotide
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff
 CC value and thereby detecting ovarian cancer in the patient, where the
 CC amount of polynucleotide hybridising to (IV) is detected preferably by
 CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
 CC useful for stimulating and/or expanding T cells specific for an ovarian
 CC tumour protein comprising contacting T cells with (III) or (II). (III) is
 CC useful in design and preparation of ribozyme molecules for inhibiting
 CC expression of the tumour polypeptides and proteins in tumour cells; and
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
 CC library using well known techniques

XX
 SQ Sequence 1889 BP; 473 A; 501 C; 436 G; 479 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 3,62e-205 Length: 1889
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x ABL87929 (1-1889)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 544 ATGAAGTTTCAGGCGCTTCGAAACCCAGAGATTGCTTTCTGTTGGAAAGGCAATC 603
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 604 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAAAATCAGAATGTT 663
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
 DB 664 TCTCCATCCAGAGAGATGAAGTAATTCATGCGTGGCCAACTCAAGTACCAATTCAAC 723
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 724 CTTTACCAGAAACATTGCTCTGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 783
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 DB 784 AAGGCTCATCCAAATACTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 843
 QY 101 ThrValGluAspGluArgGluProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 844 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGACAGATTTCTGT 903
 QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 904 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATATTCTGGATAAGTTGAAATTGG 963
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 964 GATCTTCACAGGCACACCATGGAATTTCTCATATTTTCCATGTCATGCGAGTGTCA 1023
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 1024 ACTAGGCTCAGTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1083
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 1084 CTTACCAAGCAACTACTTCTGATGTCCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220

DB 1144 ATGCTTCTCTGGCCATGGTTAGTCTGGAAATGGAGAAATCATTTCTGATTGCTTTCT 1203
 QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 1204 CTTACAAATGAATGCTTTCAGAAAGCACAGATGAGTAGCTCCCGATTGATCCATTGCGG 1263
 QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 1264 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAAATTCGGTTAT 1323
 QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 1324 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGAGGTTCAGATTACAT 1383
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 1384 CCCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGCAGAGTCCAGTC 1443
 QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 DB 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGTCCAGTGGGTGCAAGCAGACCTCT 1503
 QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 DB 1504 ACTAAACGCAAGTAGAGGAAATGGAAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1563
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 1564 TATAATGAAGATAATGTCTCAGAAATGTGGTTCGTGTGTGGCACTGATTATCAAGA 1623
 QY 361 GlnGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 DB 1624 CAAGAGGAGATGTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTGTCATG 1674
 RESULT 9
 ADP10653
 ID ADP10653 standard; DNA; 1890 BP.
 XX
 AC ADP10653;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Reference mRNA sequences for marker probe #330.
 XX
 KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2004042346-A2.
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 XX
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX
 PS Claim 80; SEQ ID NO 662; 1762pp; English.
 XX

CC The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC an individual. The methods are also useful in diagnosing and monitoring
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
 CC and monitoring of allograft rejection and other disorders.

XX
 SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3.62e-205 Length: 1890
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x ADP10653 (1-1890)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 545 ATGAAGTTTCAGGGCCCTTTGAAACCCAGAGATTGCTTTTCCTGTTGGAAAGGCCAATC 604
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 605 ACTAGGGAAGCACAGATGCGAAGTGAATGTCGGAAATGCTTCAATCAGATGTT 664
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 665 TCTCCATCCAGAGAGATGAAGTAATTCATGCTGGCTGGCCAACTCAAGTACCAATTCAC 724
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 725 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGATTTTATGCTACCGTA 784
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 Db 785 AAGGCTCATCCAAATACTTTCAGTTGATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 844
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 845 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAGGTAATTTGGCAAGACAGATTTCTGT 904
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 Db 905 GGATGTTCTCATCTGAATTTTGAGATGAGAGAAATTTCTGGATAAGTTGAATGG 964
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 965 GATCTTCACAGCCACACCATTTGATTTTCTATATTTTCCATGCGCATTCAGTGTCA 1024
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1025 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 1084
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1085 CTTACCAAGCAACTACTTTCATCTGATGGCTGGCAACCACTTCTGCAATTCAGAGATCC 1144
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 1145 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAACTCAATTCCTGATTGCTTCT 1204
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240

Db 1205 CTTACAAATTGAACCTGCTTCAGAAAGCAGACAGATGATAGCTCCACGTTGATCCATTGTGG 1264
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1265 GAGCTTGTGGACATCACTTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGTTAT 1324
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1325 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGGAGTGTTCAGATTACAT 1384
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1385 CCTCTCTCTGTCAGGCCACAGACTTCTCCAAGACACACAGCAGCAGAGTCCAGTC 1444
 Qy 301 ArgGlyThrAlaLysPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1445 AGAGTACAGAGCCTTTTACCATCATCTCCAGCTCCAGTGGGTGGGTCAGACACCTCT 1504
 Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
 Db 1505 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACCTTCTATGATGAATCAAACGGCTC 1564
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1565 TATAATGAAGATAATGTCTCAGAAAATGTGGTTCCTGTGTGGCACTGATTTATCAAGA 1624
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1625 CAAGAGGACATGCTTCCCTTGTCCACCTTGGAGGCTGTTCTCTGTCATG 1675

RESULT 10
 ACN38124
 ID ACN38124 standard; cdna; 1890 BP.
 XX
 AC ACN38124;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) CDNA DNA324488, SEQ ID NO:1449.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic; gene; ss.
 OS Homo sapiens.
 XX
 PN W02004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347921/32.
 XX
 DR P-PSDB; ABM80569.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 1; SEQ ID NO 1449; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)

CC polypeptides, and their related nucleic acids. The TAR polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAR nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAR nucleic
 CC acid; an antibody specific for a TAR polypeptide; a peptide or organic
 CC molecule which binds to a TAR polypeptide; fusion proteins comprising a
 CC TAR polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAR polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAR expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAR nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAR nucleic acid of the invention

XX SQ Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 3, 62e-205 Length: 1890
 Score: 1962.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 13 Gaps: 0

US-09-736-250-1 (1-377) x ACN38124 (1-1890)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 Db 545 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGCTTCTTCCTGTTGGAAAGCGCAATC 604
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 605 ACTAGGGAAGCACAGATGCGAAAGTGAATGTGGGAAATGCCTTCAAAATCAGATGTT 664
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 665 TCTCCATCCAGAGATGAAGTAAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 724
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 725 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTGGATAGTCTTTAGCTACCGTA 784
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 Db 785 AAGGCTCATCCAAAATACTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 844
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 845 ACTGTGAGGAAGATGAGAGAATTCAGTCTAAAGATGATTGGCAAGACAGATTTCTGT 904
 Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 Db 905 GGATGTTCTCTCATCTGAATTTTGGAAATGAGAGAATATTCTGGATGAATGGAATGG 964
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 965 GATCTTCACAGCCACACCATGAGATTTTCTCATATTTTCCATGCGCATTCAGTGTCA 1024
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1025 ACTAGGCGCTAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCGAGTC 1084
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1085 CTTACCAAGCAACTACTTCTACTGTATGGCTCGCAACCAACTCTCGCAATTCAGAGATCC 1144
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220

Db 1145 ATGCTTCTCTGGCCATGGTTAGTCTGGAATGGAAACTCATCTCTGATGCTTTCT 1204
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 Db 1205 CTTTACATTTGAATGCTTTCAGAAAGCACAGATGATAGTCCCGATTTGATTCGCG 1264
 Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1265 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTAT 1324
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1325 GTCTACCGTCCCTTCAAGCACACCCCTGTGACCTGTGACAAAGAGGTTCAGATTACAT 1384
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1385 CCCTCTCTGTCGCCAGCCCGACAGCTTCTCCAGGACAAACAGCAGAGTCCAGTC 1444
 Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 1445 AGAGGTACAGCAGCCCTTTTACCATCATCTCCAGTCCAGTGGGTGCAAGCAGACCTCT 1504
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1505 ACTAAACGCAAGTAGAGGAAATGGAAATGGAGTGGATGACTTCTATGATGGAATCAAACGGCTC 1564
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1565 TATAATGAAGTAAATGCTCAGAAATGTGGTCTCTGTGTGCACTGATTATCAAGA 1624
 Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1625 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGACCTTGTCTGTCTCATG 1675

RESULT 11
 ADL63374
 ID ADL63374 standard; DNA; 2755 BP.
 XX AC ADL63374;
 XX AC ADL63374;
 DT 20-MAY-2004 (first entry)
 XX Human ovarian cancer DNA marker #21586.
 DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200170979-A2.
 XX WO200170979-A2.
 PD 27-SEP-2001.
 XX 21-MAR-2001; 2001WO-US009126.
 PF 21-MAR-2001; 2000US-0191031P.
 XX 25-MAY-2000; 2000US-0207124P.
 PR 15-JUN-2000; 2000US-0211940P.
 PR 07-JUL-2000; 2000US-0216820P.
 PR 25-JUL-2000; 2000US-0220661P.
 PR 21-DEC-2000; 2000US-0257672P.
 XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
 XX Lee J, Lillie J;
 XX WPI; 2001-611502/70.
 XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian
 PT cancer cells as compared to their normal non-cancerous ovarian cells are
 PT used to characterize stage, grade, histological type of ovarian cancer.
 XX Disclosure; SEQ ID NO 21586; 106pp; English.
 PS

XX The invention relates to nucleic acid markers which are overexpressed in
 CC ovarian cancer cells as compared to their expression in normal (i.e. non-
 CC cancerous) ovarian cells. The invention also relates to polypeptides
 CC encoded by the markers, antibodies that selectively bind to the
 CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
 CC of developing ovarian cancer involving inhibiting expression of a gene
 CC corresponding to a marker of the invention and a method of treating a
 CC patient afflicted with ovarian cancer comprising providing to cells of
 CC the patient an antisense oligonucleotide complementary to a marker of the
 CC invention. The markers are useful for assessing if a patient is afflicted
 CC with ovarian cancer, which involves comparing the level of expression of
 CC a marker in a patient sample and a normal level of expression of the
 CC marker in a control non-ovarian cancer sample. A difference between the
 CC expression levels indicates ovarian cancer. The level of expression of a
 CC marker corresponds to a secreted protein or to a transcribed
 CC polynucleotide or its portion. The level of expression of the marker is
 CC assessed by detecting the presence in the sample, a protein or protein
 CC fragment corresponding to the marker. The presence of protein or protein
 CC fragment is detected using an antibody that specifically binds with the
 CC protein or protein fragment. Alternatively, the level of expression of
 CC the marker is assessed by detecting the presence of a transcribed
 CC polynucleotide which anneals with the marker or anneals with a portion of
 CC the polynucleotide comprising the marker, under stringent conditions. The
 CC marker is also used for monitoring the progression of ovarian cancer in a
 CC patient which involves detecting expression of the marker in a patient
 CC sample at a first point in time, repeating the method at a subsequent
 CC time and comparing the level of expression. The method is carried out
 CC using an ovarian tissue sample. A composition comprising a marker,
 CC polypeptide or antibody of the invention is used to treat ovarian cancer.
 CC This sequence represents a human ovarian cancer DNA marker of the
 CC invention.

XX SQ Sequence 2755 BP; 749 A; 673 C; 606 G; 727 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.36e-191 Length: 2755
 Score: 1841.00 Matches: 358
 Percent Similarity: 94.96% Conservative: 0
 Best Local Similarity: 94.96% Mismatches: 1
 Query Match: 93.83% Indels: 18
 DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x ADL63374 (1-2755)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 Db 847 ATGAAGTTTCCAGGCGCTTTTGGAAACCCAGAGATTGCTTTCTCTGTTGGAAGGCAATC 906
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 907 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 966
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 967 TCTCCATCCAGAGAGATGAAGTAATTCATATGGCTGGCCAACTCAAGTACCAATTCAC 1026
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 1027 CTTTACCAGAAACATTTGCTGCTGGCTAGCAGTCTTTTGGATAGGTTTATAGCTACCGTA 1086
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 Db 1087 AAGGCTCATCT----- 1098
 Qy 101 ThrValGluGluAspGluArgGileProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 1099 -----GAGGAAGATGAGAGATTCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 1152
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 Db 1153 GGATGTTCTCATCTGAAATTTTGAGAAATGAGAGATTTATCTGGATAAGTGAATGG 1212

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 1213 GATCTTCACACAGCCACACCATTTGGATTTTCTTCATATTTTCCATGCGATGCGTCA 1272
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 1273 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1332
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 Db 1333 CTTACCAAGCACTACTTCTGATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 1392
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 1393 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTTCT 1452
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 Db 1453 CTTTACCAATGCACTGCTTCAGAAAGCACAGATGATAGCTCCAGATTTGATCCATTTGCGG 1512
 Qy 241 GluLeuValAlaHisLeuHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 1513 GAGCTTGTGGCAGCATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGGTTAT 1572
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 1573 GTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 1632
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 1633 CCCTCTCTCTGCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGCACAGTC 1692
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuSerGlyCysLysGlnThrSer 320
 Db 1693 AGAGGTACAGAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1752
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1753 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAACGCTC 1812
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1813 TATAATGAGATAATGTCTCAGAAAATGTGGGTCTGTGTGTGCGCATGATTTATCAAGA 1872
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1873 CAAGAGGAGACATGCTTCCCTTGTCTACCTTTCAGCGCTGTTTCTGTCAAG 1923
 RESULT 12
 AAD57247
 ID AAD57247 standard; cDNA; 1651 BP.
 XX
 AC AAD57247;
 XX 06-NOV-2003 (first entry)
 XX Human CGDD-27 cDNA.
 DE
 XX Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytosolic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic; gene; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH

XX DE Human cell growth, differentiation, and death-associated coding seq #15.
 XX KW human; cell growth; cell differentiation; cell death; CGDD;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; polycythemia vera; psoriasis; cancer;
 KW neurological disorder; Cushing's syndrome; hypothyroidism;
 KW Pick's disease; Huntington's disease; Parkinson's disease;
 KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
 KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
 KW reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
 XX OS ds.
 XX OS Homo sapiens.
 XX PN WO2004031364-A2.
 XX PD 15-APR-2004.
 XX PF 03-OCT-2003; 2003WO-US031441.
 XX PR 03-OCT-2002; 2002US-0416205P.
 XX PR 25-OCT-2002; 2002US-0421521P.
 XX PR 21-NOV-2002; 2002US-0428376P.
 XX PR 23-DEC-2002; 2002US-0436258P.
 XX PR 10-JAN-2003; 2003US-0439282P.
 XX PR 13-FEB-2003; 2003US-0447578P.
 XX PA (INCY-) INCYTE CORP.
 XX PA (BURR/) BURRILL J D.
 XX PI Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
 PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
 PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
 PI Yang YG, Gietzen KU, Hatalia AJA;
 XX WPI; 2004-330172/30.
 DR P-PSDB; ADN01131.
 XX New isolated polypeptides associated with cell growth, differentiation
 PT and death, useful for diagnosing, treating or preventing e.g.
 PT arteriosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
 PT diabetes mellitus or infertility.
 XX Claim 5; SEQ ID NO 40; 213pp; English.
 XX The invention comprises the amino acid and coding sequences of human
 CC proteins that are associated with cell growth, differentiation, and death
 CC (CGDD). The DNA and protein sequences of the invention are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of CGDD, such as: cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
 CC polycythemia vera, psoriasis and cancers), developmental disorders (e.g.
 CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
 CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, Parkinson's disease and multiple sclerosis),
 CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
 CC contact dermatitis and diabetes mellitus), and reproductive disorders
 CC (e.g. infertility, endometriosis and uterine fibroid). The present DNA
 CC sequence encodes a human CGDD-associated protein of the invention.
 XX SQ Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;

Alignment Scores:
 Pred. No.: 4,64e-158 Length: 903
 Score: 1529.50 Matches: 300
 Percent Similarity: 79.58% Conservative: 0
 Best Local Similarity: 79.58% Mismatches: 0
 Query Match: 77.96% Indels: 77
 DB: 12 Gaps: 1

US-09-736-250-1 (1-377) x ADN01156 (1-903)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 2 ATGAAGTCTCCAGGCGCTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAAGCAATC 61
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 62 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCTTCAATCAAGATGTT 121
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 122 TCTCCATCTCCAGAGAGATGAAGTAATCAATGGCTGCCAACTCAAGTCAACATTCAC 181
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 182 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTTAGCTACCGTA 241
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 DB 242 AAGGCTCATCCAAATACTTGAATTTGAGATGAGAGAAATTATTCTGGATAGTTGAATTGG 301
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 302 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGTATTGCCAAGACACAGTTCTGT 361
 QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
 DB 362 GGATGTTCTCATCTGAAATTTTGAGATGAGAGAAATTATTCTGGATAGTTGAATTGG 421
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 422 GATCTTCACACAGCCACCATTTGGATTTTCTTCATATT----- 460
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 460 ----- 460
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
 DB 460 ----- 460
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 460 ----- 460
 QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 461 -----ATGATAGCTCCAGTTGATCCATTGTCGG 490
 QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 491 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTTAT 550
 QY 261 ValTyrArgProLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 551 GTCTACCGTCCCTCAAGCACACCTGGTACCTGTGACAAAGAGAGTTCAGATTACAT 610
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 611 CCTCTCTCTGCCAGGCCAGACTTCTCCAAGGACAAACAGCAGCAGAGTCCAGTCC 670
 QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaLaserGlyCysLysGlnThrSer 320
 DB 671 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCCAGCACCTCT 730
 QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyValLysArgLeu 340
 DB 731 ACTAACGCAAGATGAGGAAATGGAAGTGGATGAGTCTTATGATGGAATCAACAGCGTC 790
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 791 TATAATGAAGATATGCTCAGAAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 850

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 851 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGAGCTGTTTCTGTCATG 901

RESULT 14

ADL63082
ID ADL63082 standard; DNA; 2146 BP.

AC ADL63082;

DT 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #21294.

DE Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

KW Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

PR 25-MAY-2000; 2000US-0207124P.

PR 15-JUN-2000; 2000US-0211940P.

PR 07-JUL-2000; 2000US-0216820P.

PR 25-JUL-2000; 2000US-0220661P.

PR 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

PA Lee J, Lillie J;

PI WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian

CC cancer cells as compared to their normal non-cancerous ovarian cells are

CC used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 21294; 106pp; English.

CC The invention relates to nucleic acid markers which are overexpressed in
CC ovarian cancer cells as compared to their expression in normal (i.e. non-
CC cancerous) ovarian cells. The invention also relates to polypeptides
CC encoded by the markers, antibodies that selectively bind to the
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk
CC of developing ovarian cancer involving inhibiting expression of a gene
CC corresponding to a marker of the invention and a method of treating a
CC patient afflicted with ovarian cancer comprising providing to cells of
CC the patient an antisense oligonucleotide complementary to a marker of the
CC invention. The markers are useful for assessing if a patient is afflicted
CC with ovarian cancer, which involves comparing the level of expression of
CC a marker in a patient sample and a normal level of expression of the
CC marker in a control non-ovarian cancer sample. A difference between the
CC expression levels indicates ovarian cancer. The level of expression of a
CC marker corresponds to a secreted protein or to a transcribed
CC polynucleotide or its portion. The level of expression of the marker is
CC assessed by detecting the presence in the sample, a protein or protein
CC fragment corresponding to the marker. The presence of protein or protein
CC fragment is detected using an antibody that specifically binds with the
CC protein or protein fragment. Alternatively, the level of expression of
CC the marker is assessed by detecting the presence of a transcribed
CC polynucleotide which anneals with the marker or anneals with a portion of
CC the polynucleotide comprising the marker, under stringent conditions. The
CC marker is also used for monitoring the progression of ovarian cancer in a
CC patient which involves detecting expression of the marker in a patient
CC sample at a first point in time, repeating the method at a subsequent
CC time and comparing the level of expression. The method is carried out
CC using an ovarian tissue sample. A composition comprising a marker,
CC polypeptide or antibody of the invention is used to treat ovarian cancer.
CC This sequence represents a human ovarian cancer DNA marker of the

CC invention.

XX Sequence 2146 BP; 662 A; 392 C; 432 G; 660 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 6.38e-74 Length: 2146
Score: 770.50 Matches: 154
Percent Similarity: 91.18% Conservative: 1
Best Local Similarity: 90.59% Mismatches: 12
Query Match: 39.27% Indels: 3
DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x ADL63082 (1-2146)

Qy 210 GluMetGluLysLeuLeuProAspTrpLeuSerLeuThrLeuGluLeuGlnLysAla 229
Db 815 GAGCAGCCTATGTTTAAATTAATGATCAACTGTGTGGCTTTT---TTTTTTTCTCGCC 871
Qy 230 GlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisLeuSerThr 249
Db 872 CAGATGGATAGCTCCCGAGTTGATCCATTGTGCGGAGCTTGTGGCAGCATCACCTTTCTACT 931
Qy 250 LeuGlnSerSerLeuProLeuAsnSerValTyArgProLeuLysHisThrLeu 269
Db 932 CTGCAGTCTTCCCTGCCCTCTGAATTCGTTTATGTCTACCGTCCCTCAAGCAGCACCTG 991
Qy 270 ValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPhe 289
Db 992 GTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTC 1051
Qy 290 SerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyHisHis 309
Db 1052 TCCAAGGACAAACAGCAGCCAGAGTGCAGAGTCCAGAGTACAGCAGCTTTTACCATCAT 1111
Qy 310 LeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGluGluMetG 329
Db 1112 CTCCAGCTCCCGAGTGGGTGCAAGCAGACTCTTACTAAACGCAAGTAGAGAAATGG 1171
Qy 329 luValAspAspPheTyArgGlyLysArgLeuTyArgGluAsnValSerGluA 349
Db 1172 AAGTGGATGACTTCTATGATGGAATCAACGGCTCTATATAGATAATGTCTCAGAAA 1231
Qy 349 snValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysP 369
Db 1232 ATGTGGTCTTGTGTGTGGCACTGATTATCAAGACAAGAGGAGCATGCTTCCCTTTGTC 1291
Qy 369 roProLeuGlnProValSerValMet 377
Db 1292 CACCTTTGACGCTGTTTCTGTGTCATG 1317

RESULT 15
AAAX4003/c
ID AAAX4003 standard; DNA; 804 BP.
XX AC AAAX4003;
XX DT 02-JUL-1999 (first entry)
XX DE Prostate cancer associated gene.
XX KW Cancer associated antigen; diagnosis; research; treatment; human;
XX KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX KW prostate cancer; ss.
XX OS Homo sapiens.
XX PN WO9904265-A2.
XX PD 28-JAN-1999.
XX PF 15-JUL-1998; 98WO-US014679.
XX PR 17-JUL-1997; 97US-00896164.

```
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides - isolated
XX using sera from cancer patients, used to develop products for the
XX diagnosis, monitoring or treatment of cancers.
XX
XX Claim 67; Page 630; 787pp; English.
XX
XX The invention relates to a method for diagnosing a disorder characterised
XX by expression of a human cancer associated antigen precursor coded for by
XX a nucleic acid molecule (NAM). The method comprises: (a) contacting a
XX biological sample isolated from a subject with an agent that specifically
XX binds to the NAM, an expression product or a fragment of an expression
XX product complexed with an HLA molecule; and (b) determining the
XX interaction between the agent and the NAM or the expression product as a
XX determination of the disorder. The products and methods can be used in
XX the diagnosis, monitoring, research, or treatment of conditions
XX characterised by the expression of various cancer associated antigens.
XX The invention provides nucleic acid sequences and encoded polypeptides
XX which are cancer associated antigen precursors expressed in human breast
XX cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
XX lung cancer
XX
XX SQ Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;
```

```
Alignment Scores:
Pred. No.: 9.18e-74 Length: 804
Score: 763.00 Matches: 161
Percent Similarity: 94.25% Conservative: 3
Best Local Similarity: 92.53% Mismatches: 7
Query Match: 38.89% Indels: 5
DB: 2 Gaps: 0

US-09-736-250-1 (1-377) x AAX40003 (1-804)

Qy 207 ValSerLeuGluMetGluLeu-1lePro-AspTpo-LeuSerLeuThrIleGluLeu 225
Db 710 GTTAGTCTGAAATGGANGAACTCCATTCCNGGATGGGCTTTCTCTTACAAATTGANCTG 651

Qy 226 LeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHis 245
Db 650 CTTCAGAAAGC-CAGATGNATAGTCCAGTTGATCCATGTCGGAAGCTTGG-GCACAT 593

Qy 246 HisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeu 265
Db 592 CACCTTTNTACTCTGCAGCTCTTCCTGCTGCTGAATTCGGTTATGTTACCGTCCCTC 533

Qy 266 LysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValPro 285
Db 532 AAGCACACCCCTGGTGACCTGTGCAAAAGGAGTGTTCAAGATTACATCCCTCTCTGTCCCA 473

Qy 286 GlyProAspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAla 305
Db 472 GGCCACAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGCCAGTCAGAGGTACAGCAGCC 413

Qy 306 PheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysVal 325
Db 412 TTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAAAGTA 353

Qy 326 GluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsn 345
Db 352 GAGGAATGGGAATGGATGACTTTCTATGATGAATCAACCGGCTCTATATGAAGATAAT 293
```

```
Qy 346 ValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAla 365
Db 292 GTCTCAGAAATGTGGGTTCTGTGTGTGGCACTGATTTATCAAGACAAGAGGACATGCT 233

Qy 366 SerProCysProProLeuGlnProValSerValMet 377
Db 232 TCCCTTGTCCACCTTTGCAGCCTGTTTCTGTGTCATG 197
```

Search completed: February 11, 2005, 03:41:45
Job time : 964.767 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:24:00 ; Search time 301.793 Seconds
(without alignments)
2044.039 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKPFGPLENQLRSLLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat 07022005 154924 20422/app query.fasta_1.718
-DB=Issued Patents NA -OPWT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOPECL=0
-LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.cgn 1 1 93 @runat 07022005 154924 20422 -NCFU=6 -ICPU=3
-NO MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FCAPOP=6
-FCAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCFUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	1133	3	US-09-054-492B-2
2	1962	100.0	1260	2	US-08-969-106-5
3	1962	100.0	1260	4	US-09-338-125-5
4	1962	100.0	1260	4	US-09-023-655-899
5	748	38.1	444	4	US-09-513-999C-1907
6	326.5	16.6	1410	4	US-09-023-655-913
7	326.5	16.6	2039	4	US-09-949-016-1852
8	271.5	13.8	1576	4	US-09-949-016-4342
9	271.5	13.8	1578	4	US-09-949-016-578
10	271.5	13.8	1602	4	US-09-023-655-912
11	269.5	13.7	2212	4	US-09-023-655-948
12	204	10.4	1214	2	US-09-092-770-7

13	204	10.4	1214	3	US-09-222-851-7	Sequence 7, Appli
14	204	10.4	1215	2	US-09-092-770-1	Sequence 1, Appli
15	204	10.4	1215	3	US-09-222-851-1	Sequence 1, Appli
16	204	10.4	2637	4	US-09-949-016-5313	Sequence 5313, Ap
17	202	10.3	1212	2	US-09-092-770-2	Sequence 2, Appli
18	202	10.3	1212	2	US-09-092-770-17	Sequence 17, Appli
19	202	10.3	1212	2	US-09-222-851-2	Sequence 2, Appli
20	202	10.3	1212	3	US-09-222-851-17	Sequence 17, Appli
21	196	10.0	13424	4	US-09-949-016-13594	Sequence 13594, A
22	193	9.8	1414	4	US-09-404-296B-9	Sequence 9, Appli
23	188.5	9.6	1679	4	US-09-404-296B-3	Sequence 3, Appli
24	188	9.6	1680	1	US-08-706-539-1	Sequence 1, Appli
25	188	9.6	1680	1	US-08-522-166-1	Sequence 1, Appli
26	188	9.6	1680	1	US-08-488-382A-1	Sequence 1, Appli
27	188	9.6	1680	1	US-08-385-142-1	Sequence 1, Appli
28	188	9.6	1680	2	US-08-480-912-1	Sequence 1, Appli
29	188	9.6	1680	3	US-09-027-007-1	Sequence 1, Appli
30	188	9.6	1680	4	US-09-023-655-1049	Sequence 1049, Ap
31	188	9.6	1692	1	US-08-485-859-1	Sequence 1, Appli
32	187.5	9.6	1101	3	US-08-895-707-5	Sequence 5, Appli
33	187.5	9.6	1158	3	US-08-895-707-8	Sequence 8, Appli
34	187.5	9.6	1179	1	US-08-706-539-3	Sequence 3, Appli
35	187.5	9.6	1179	3	US-09-027-007-3	Sequence 3, Appli
36	187.5	9.6	1188	1	US-08-706-539-2	Sequence 2, Appli
37	187.5	9.6	1188	3	US-09-027-007-2	Sequence 2, Appli
38	183	9.3	304	4	US-09-513-999C-29894	Sequence 29894, A
39	176	9.0	1951	3	US-08-895-707-1	Sequence 1, Appli
40	171.5	8.7	1311	1	US-08-706-539-4	Sequence 4, Appli
41	171.5	8.7	1311	3	US-09-027-007-4	Sequence 4, Appli
42	170.5	8.7	1632	4	US-09-404-296B-31	Sequence 31, Appli
43	169	8.6	1129	4	US-09-920-760-3	Sequence 3, Appli
44	169	8.6	1911	2	US-08-246-361A-3	Sequence 3, Appli
45	169	8.6	1911	4	US-09-023-655-1022	Sequence 1022, Ap

ALIGNMENTS

RESULT 1
US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-09-054-492B-2

Alignment Scores:

Pred. No.: 1.52e-236 Length: 1133
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-054-492B-2 (1-1133)

QY 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
DB 1 ATGAAGTTTCAGGGCCCTTCGAAACCCAGAGATTGTTCTTCCTGTTGGAAAGGCCAATC 60
QY 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
DB 61 ACTAGGGAAGCACAGATGTGAAGTGAATGTGGAAATGGCTTCAATCAGATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
DB 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCAAC 180
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
DB 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGTACCGTA 240
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
DB 241 AAGGCTCATCAAATATCTGAGTGTATTCATTCGATCAGCTGTTTTCCTAGTCCCAAG 300
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
DB 301 ACTGTGAGGAAGATGAGAGAATCCAGTACTAAGAGTATTTGGCAAGACAGATTCTGT 360
QY 121 GlyCysSerSerSerGluIleuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
DB 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAATATTCGGATPAAGTTGAATGG 420
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
DB 421 GATCTTCACAGCCACACCATTCGATTTCTTCATATTTTCCATGCTCCATTCAGTGTC 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
DB 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
DB 541 CTTACAGCAACTACTCTCACGTATGGCTGCACCAACTCTGCAATTCAGAGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
DB 601 ATGCTTGCTCTGCCATGTTAGTCTGGAATGGAGAACTCATCTCGATTGGCTTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
DB 661 CTTACAAATGAATGCTTCAGAAACACAGATGGATAGCTCCAGTTGATCCATTTGTCGG 720
QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
DB 721 GAGCTTGTCGACATCACCTTTCTACTCTGAGTCTTCCTGCTCTGAAATTCGTTAT 780
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
DB 781 GTCTACCGTCCCTCAAGCACACCCCTGGTGTGACCTGTGACAAAGAGAGTGTTCAGATTAC 840
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300

DB 841 CCTCTCTGTCTCCAGGCCAGACTTCTCAAGGACAAACAGCAAGCCAGAGTCCAGTTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
DB 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
DB 961 ACTAAACGCCAAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACGGCTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
DB 1021 TATAATGAAGATAATGTCTCAGAAAATGGGGTCTGTGTGGGCTACTGATTTATCAAG 1080
QY 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
DB 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTCTCATG 1131

RESULT 2

US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-08-969-106-5

Alignment Scores:
Pred. No.: 1.83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-1 (1-377) x US-08-969-106-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGlnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGGAAGCACAGATCGAAGTGAATGTGGGAAATGCCCTTCAATCAGAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAAGTATTCATGGCTGGCCAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTATTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATATCTGAGTTGTATTCATCAGCTGTTTTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGTATTGGCAGAGACAGTTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAAATTTCTGGATAAGTTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCAATGGATTTCTTCATATTTTCCATGCCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTTCAGTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCTACGTATGGCTGCAACCAACTCTTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTGTGCTGGCCATGTTAGTCTGGAAATGGAGAACTCATTCCTGATTGGCTTCT 660

Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAITGAACCTCTTCAGAAACACAGATGGATAGTCTCCAGTTGATCAATGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTCGTGTGACCTGTGCAAAAGGAGTCTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCAGGCGCCAGACTCTCCAGAGCAACAGCAAGCCAGAGTGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaIleSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGATCTCTATGATGGTAATCAACGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATATGGGTCTCTGTGTGGCAGCTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTTCTGTGATG 1131

RESULT 3

US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-09-338-125-5

Alignment Scores:
Pred. No.: 1.83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-338-125-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGlnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGGAAGCACAGATCGAAGTGAATGTGGGAAATGCCCTTCAATCAGAATGTT 120

```
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATAGTGGCTGGCCAAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTGTATTCATTCAGCTGTCTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAATTTATCTGGATAAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTACACAGCCACCAATGGAATTTCTCATATTTCCATGTCATGCAATGCAAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACGTATGGCTTGCACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAAACTCATCTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTGTGATTCATTCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCCTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAGAGAGTGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCTCCAGGCCAGAGCTTCTCCAAGGACACAGCAAGCCAGAAAGTGCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisIleuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCGCTTTTACCATCATCTCCAGCTGCTGAGTGGTGCAAGCAACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGATGAAATCAAGCGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTTCGTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGACGCTGTCTTCTGTCTATG 1131
```

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:

```
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HERewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 899:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1260 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g1183161  
; US-09-023-655-899
```

Alignment Scores:
Pred No.: 1,83e-236 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-023-655-899 (1-1260)

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCTTTGGAAAACACAGAGATTGCTTTCTCTGTTGGAAAAGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAACACAGAGATGTGGAAGTGAATGTCGGAAAATGCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATAGTGGCCAAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTGTATTCATTCAGCTGTCTTTTCTAGCTGCCAAG 300
```

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db |||||
Qy 301 ACTGTGAGGAGATGAGAGATTCCAGTACTAAAGGTAATTGGCAAGACAGATTCTGT 360
Db |||||
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db |||||
Qy 361 GGATGTCCTCATCTGAATTTTGAAGATGAGAGAAATATCTGGATAGATTGAATGG 420
Db |||||
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db |||||
Qy 421 GATCTTCACAGACACACACATTGGATTTCTTCATATTTTCCATGGCCATTGGCAGTGCA 480
Db |||||
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db |||||
Qy 481 ACTAGGCTCAGTACTTTTTCAGTTTGGCCAAATGGAGCCCATCTCAACATTTTGGCAGTC 540
Db |||||
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db |||||
Qy 541 CTTACCAAGCACTACTTCTGATGCTGATGCTGCAACCACTCTGCAATTCAGAGGATCC 600
Db |||||
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db |||||
Qy 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGAGAACTCATCTCGATTGGCTTTCT 660
Db |||||
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db |||||
Qy 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCCCACTTCATTCATTTGTCGG 720
Db |||||
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db |||||
Qy 721 GAGCTTGGGCACATCACTTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGTTAT 780
Db |||||
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db |||||
Qy 781 GTCTACCGTCCCTCAAGCACACCTGGTGTGACCTGTGACAAAGAGGTTCAGATTACAT 840
Db |||||
Qy 281 ProSerValProGlyProAspPheSerLysAspSerLysProGluValProVal 300
Db |||||
Qy 841 CCTCTCTGTGCCAGGCCAGACTTCTCCAAAGACAAACAGCAAGCCAGAGTCCAGTC 900
Db |||||
Qy 301 ArgGlyThrAlaAlaPheTyrHisIleuProAlaIleSerGlyCysLysGlnThrSer 320
Db |||||
Qy 901 AGAGTACAGAGAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTCAAGCACCTCT 960
Db |||||
Qy 321 ThrLysArgLysValGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db |||||
Qy 961 ACTAACGCAAGTAGAGGAATGGAATGGAATGATGATCTTATGATGGAATCAACGGCTC 1020
Db |||||
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db |||||
Qy 1021 TATAATGAAGATAATGTCTCAGAAATGTGGGTCTGTGTGGCACTGATTTATCAAGA 1080
Db |||||
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db |||||
Qy 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCCTGTTCTGTGATG 1131
Db |||||

RESULT 5

US-09-513-999C-1907
; Sequence 1907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59. US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 1907
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..444
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-1907

Alignment Scores:

Pred. No.: 2.18e-84 Length: 444
Score: 748.00 Matches: 147
Percent Similarity: 99.32% Conservative: 0
Best Local Similarity: 99.32% Mismatches: 1
Query Match: 38.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-1907 (1-444)

Qy 113 ValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGluArg 132
Db 1 GTATTGGCAKAGACAGATTCTGTGGATGTTCTCATCTGAAATTTTGGATGGAGAGA 60
Qy 133 IleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHis 152
Db 61 ATTATTCTGGATAGTTGAATTGGATCTTTCACAGCCACACCATTTGGATTTTCTTCAT 120
Qy 153 IlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeu 172
Db 121 ATTTTCCATCCCATTTGAGTGTCAACTAGGCCTCAGTTACTTTTTCAGTTTGGCCAAATTTG 180
Qy 173 SerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsn 192
Db 181 AGCCATCTCAACATTTGGCAGTCTTACCAGCNACTACTTCACTGTATGGCCTGCAAC 240
Qy 193 GlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGlu 212
Db 241 CAATCTTGCAAATTCAGAGATCCATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAG 300
Qy 213 LysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAsp 232
Db 301 AAATCTATCTCCTGATTGGCTTTCTTTACAATTTGAATGCTTTCAGAAAGCACAGATGGAT 360
Qy 233 SerSerGlnLeuIleHisCysArgGluLeuValAlaHisIleLeuSerThrLeuGlnSer 252
Db 361 AGTCCCAAGTTGATCCATTTGCGGAGCTTGTGGACATCACCTTTCTACTCTGCACTCT 420
Qy 253 SerLeuProLeuAsnSerValTyr 260
Db 421 TCCCTGCTCTGAAATTCGGTTAT 444

RESULT 6

US-09-023-655-913
; Sequence 913, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 913:
SEQUENCE CHARACTERISTICS:
LENGTH: 1410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1236234
US-09-023-655-913

Alignment Scores:	
Pred. No.:	2,056-30
Score:	326.50
Percent Similarity:	55.08%
Best Local Similarity:	36.44%
Query Match:	16.64%
DB:	4
Length:	1410
Matches:	86
Conservative:	44
Mismatches:	73
Indels:	33
Gaps:	7

US-09-736-250-1 (1-377) x US-09-023-655-913 (1-1410)

31	ValArgLysMetProSerAsnGlnAsn---ValSerProSerGlnArgAspGluValIle	49
Qy	
357	ATTGAGGCTACCCCGAGAAATGATAACACTTTTGTGTCCAGGATTGAGAAATGCCAAAGTT	416
Db	
50	GlnTrpLeuAlaLysLeuLysTyrcLnPheAsnLeuTytrProGlnThrPheAlaLeuAla	69
Qy	
417	GAAGATTTTAAGAGATTAGCCAACTTTTTCGATCTTGCACCTGAAACTTTTGTCCCTGGCT	476
Db	
70	SerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTytrLeuSerCys	89
Qy	
477	GTCNAATATTTGGACAGGTCTTGGCTCTTATGAGGTGAACCTTAACAATTTGTCTTGC	536
Db	
90	IleAlaIleSerCysPhePheLeuAlaLysThrValGluGluAspGluArgIlePro	109
Qy	
537	ATTGGAGTCTGTCTTTTTTGTGGCTGCTAGAAATAGTTGAAGAAGACTGCAATATTCCA	596
Db	
110	valLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArg	129
Qy	
597	TCCACTCATGATGTGATCCGGATTAGTCAGTGTAAATGTACTGCTCTGCATATAAACGG	656
Db	
130	MetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAsp	149
Qy	
657	ATGAAAAAATATTTTCAGAAAAATTCACATATGAAATTTGGNAGCTACTACTGCCTTAAC	716
Db	
150	PheLeuHisIlePheHisAlaIleAlaVal-----SerThrArgProGlnLeuLeu	166
Qy	
717	TTTTTGCATTTATACCATCTATTATATCTTTGTCTCATCTTCAGAAAGCAAGAAATCTGT	776
Db	

```

Qy 167 PheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeu 186
Db 777 ---AGCCTTGATAACTAGAA-----GCT 797

Qy 187 HisCysMetAlaCysAsnGlnLeuLeuGlnPhe-----ArgGlySerMetLeuAla 203
Db 798 CAGCTGAAGAGCTGCAACTGCCGACTCATCTTTCAAAGCAAAACCATCTGTATTAGCC 857

Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 858 TTGTGCTCTCAATTGGAAGTGAAACTTTG-----AAATCTCTGT 899

Qy 224 GluLeuLeuGln-----LysAlaGlnMetAspSerSerGlnLeu 236
Db 900 GAATTACTGGAAATCTCTTGCTAGTTTAAAAAACATTCACAGATTAAATGACACTGAGTTC 959

Qy 237 IleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSer 252
Db 960 TTCTACTGGAGAGAGTTGGTTTCTAAATGCCGTAGCCGAGTATTCTTCT 1007

RESULT 7
US-09-949-016-1852
; Sequence 1852, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1852
; LENGTH: 2039
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-1852

Alignment Scores:
Pred. No.: 3,966-30 Length: 2039
Score: 326.50 Matches: 114
Percent Similarity: 46.25% Conservative: 71
Best Local Similarity: 28.50% Mismatches: 138
Query Match: 16.64% Indels: 78
DB: 4 Gaps: 14

US-09-736-250-1 (1-377) x US-09-949-016-1852 (1-2039)

Qy 31 ValArgLysMetProSerAsnGlnAsn---ValSerProSerGlnArgAspGluValIle 49
Db 256 ATTGAGGCTACCCCGAGAAATGATAACAATTGTGTCCAGGATTGAGAAATGCCAAAGTT 315

Qy 50 GlnTrpLeuAlaLysLeuLysTytrGlnPheAsnLeuTytrProGluThrPheAlaLeuAla 69
Db 316 GAAGATTAAAGAGTTTAGCCAACTTTTGGATCTTGCACTGAAACTTTTGCTCTGGCT 375

Qy 70 SerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTytrLeuSerCys 89
Db 376 GTCAATATTTTGGACAGGTTCTTGCTCTTATGAGGTTGAAACCTTAAACATTTGTCTTGC 435

Qy 90 IleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluLeuAspGluArgIlePro 109
Db 436 ATTGAGTGCTGTTCTTTTCTGCTGCTAGATAGATTGAAGAGACGTGCAATATTCCA 495

Qy 110 ValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArg 129

```



```
Qy 65 ThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisPro 84
Db 425 ACATTTCTAGCTGTGCTTTTCTGGACAGATCTCTGTCTAAATGAAGGTACAGCC 484
Qy 85 LysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGlu 104
Db 485 AAGCACCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 544
Qy 105 AspGluArgIleProValLeuLysValLeuAlaArgPheSerPheCysGlyCysSerSer 124
Db 545 GAAAGGAATGTCCTATGGCACTGACTGTGATCCGAATAAGTCAATATAGGTTTACGGTT 604
Qy 125 SerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThr 144
Db 605 TCAGACTTGTATGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 664
Qy 145 AlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGln 164
Db 665 ACTACTGCTTCAATTTCTGCACTGTATTTATTTCACTCTCTCAAGAGAACTTGCACCT 724
Qy 165 LeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGln 184
Db 725 -----GAAAGGAGAAATAGCATTAAATTTTGAAGACTAGAAGCTCAA 766
Qy 185 LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeu 204
Db 767 CTGAAGCATCTCATTCGAGATCATATTTTCTAAAGCAAAAGCCTTCTGTGTGGCATTG 826
Qy 205 AlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGlu 224
Db 827 TCTATCATGATGATAGATCCAGCAGACAGAGTGTGTAGATTAACAGAGGATAGAA 886
Qy 225 LeuLeuGlnLys---AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 887 TGTCTTCAGAAACATTCACAGATAAATGCGCAGAGATCTGACCTTCTGCGCAAGAGCTGTA 946
Qy 244 AlaHisHisLeuSerThrLeuGlnSer-----SerLeuPro----- 255
Db 947 TCCAAATGTTTAACTGAATATTCATCAATAAAGTGTTCCTCAACCAAAATGTTTCAGAGTTG 1006
Qy 256 -----LeuAsnSerValTyrValTyrArgProLeuLysHisThr 268
Db 1007 AAATGGATGTTTCTGGCGGTACTGCGCGCAATTAAGCATAGC 1051

RESULT 11
US-09-023-655-948
; Sequence 948, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
```

```
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 948:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI431875
; US-09-023-655-948
```

```
Alignment Scores:
Pred. No.: 6.89e-23 Length: 2212
Score: 269.50 Matches: 68
Percent Similarity: 55.71% Conservative: 49
Best Local Similarity: 32.38% Mismatches: 86
Query Match: 13.74% Indels: 7
DB: 4 Gaps: 2
```

US-09-736-250-1 (1-377) x US-09-023-655-948 (1-2212)

```
Qy 45 ArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGlu 64
Db 167 AGGACACTTGAAGTAAAGATCTTCTTAGCTAACTCAGTCTTCTGGCTTTGACACAGAG 226
Qy 65 ThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisPro 84
Db 227 ACATTTCTAGCTGTGATTTACTGACAGATCTCTGTCTAAATGAAGGTACAGCC 286
Qy 85 LysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGlu 104
Db 287 AAGCACCTGGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGTGTGGT 346
Qy 105 AspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSer 124
Db 347 GAAAGGAATGTCCCATTTGGCAACTGACTTGCATCAATAGTCAATATATGTTTACGGTT 406
Qy 125 SerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThr 144
Db 407 TCAGACTTGTATGAGATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT 466
Qy 145 AlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGln 164
Db 467 ACTACTGCTTCAATTTCTGCACTGTATTTATTTCACTCTCTTCAAGAGAACTTGCACCT 526
Qy 165 LeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGln 184
Db 527 -----GAAAGGAGAAATAGCATTAAATTTTGAAGACTAGAAGCTCAA 568
Qy 185 LeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeu 204
Db 569 CTGAAGCATGTCTATTCAGGATCATATTTTCTAAAGCAAAAGCCTTCTGTGTGGCATTG 628
Qy 205 AlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGlu 224
Db 629 TCTATCATGATGATAGATCCAGCAGACAGAGTGTGTAGAGTTAAACAGAGGATAGAA 688
Qy 225 LeuLeuGlnLys---AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 689 TGTCTTCAGAAACATTCACAGATAAATGCGCAGAGATCTGACCTTCTGCGCAAGAGCTGTA 748
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSer 253
Db 749 TCCAAATGTTTAACTGAATATTTCAATAT 778
```

```

RESULT 12
US-09-092-770-7
; Sequence 7, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1214
; TYPE: RNA
; ORGANISM: Human
US-09-092-770-7

Alignment Scores:
Pred. No.: 4.2e-15 Length: 1214
Score: 204.00 Matches: 85
Percent Similarity: 43.81% Conservative: 60
Best Local Similarity: 25.68% Mismatches: 111
Query Match: 10.40% Indels: 76
DB: 2 Gaps: 15

US-09-736-250-1 (1-377) x US-09-092-770-7 (1-1214)
QY 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCGUCCCGCGUGCCGAC-----CUGUCCGGGUGUCUCAA----- 333
QY 24 AlaGlnMetTyrLysValAsnValArgLysMetProSer----- 36
Db 334 ---GAAGUUUGG---CUGAACAUUGGAAAGAAUCCCGUUAACGUAACGACAAACAC 387
QY 37 -----AsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
Db 388 UUCGAAAGUUCGACUCCCGACCGGACCGGACCGAGAUCCGUAUCCGUGGACUGGCG 447
QY 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerLeu 72
Db 448 CUGAAGUUCGAAAGUUUACACCCUGCAGCGUGAAGAAACUUCUACCGCAGGACUUC 507
QY 73 LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 UUCGACCGUUUACUGCUGACCCAGAAAGACAUCAACAAACAAACGUGCUGACGUGG 567
QY 92 IleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 AUCACCCUCCUGUUAUCUGCUUCCAAACUG-----GAAGAAAUUCUACCGUCCAAACUG 621
QY 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAGGAUUUCGCUAGUUUACGACGCGUGUGUCCGAAAGAAUCCGUAUCCGUAUGGAA 681
QY 132 ArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CUGAUCAUCCUGAAGUUCUGAAUUGGAAUUGGACUGGCGGUGUCCGUAUCCGUGGUG 741
QY 152 HistPheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 742 AACCGUUCUGCAGGUUGACGUCUGAAGACGACCGUCCGAAAGUUCUG-----CUGCCG 795
QY 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGUAC-----UCCAGGAAACCUUACUACAGUCCGACGAGGUGG----- 837
QY 191 CysAsnGlnLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 191 CysAsnGlnLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210

838 -----GACGUGGCAUCCUGGCUAUCGACUCCUGGAA 870
QY 211 MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 UUCAGUACCGUAUCCUGACCGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 930
QY 227 GlnLysAlaGln---MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHis 245
Db 931 AAAAAAGUCCCGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUGGUG 990
QY 246 HisLeuSerThrLeuGlnSerSerLeuProLeu-----AsnSerValTyr 260
Db 991 UUCGUUAACGUGUUAUAACUCCUCCCGGUUAAACUGAAAAACUUAACAAAAAUAUCCCG 1050
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1051 AUGGA-AGACCGUCACAAUCA-----GAC 1076
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1077 CCACCAACUACUCCGCG-----UAU 1097

RESULT 13
US-09-222-851-7
; Sequence 7, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/222,851
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: 09/092,770
; EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1214
; TYPE: RNA
; ORGANISM: Human
US-09-222-851-7

Alignment Scores:
Pred. No.: 4.2e-15 Length: 1214
Score: 204.00 Matches: 85
Percent Similarity: 43.81% Conservative: 60
Best Local Similarity: 25.68% Mismatches: 111
Query Match: 10.40% Indels: 76
DB: 3 Gaps: 15

US-09-736-250-1 (1-377) x US-09-222-851-7 (1-1214)
QY 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCGUCCCGCGUGCCGAC-----CUGUCCGGGUGUCUCAA----- 333
QY 24 AlaGlnMetTyrLysValAsnValArgLysMetProSer----- 36
Db 334 ---GAAGUUUGG---CUGAACAUUGGAAAGAAUCCCGUUAACGUAACGACAAACAC 387
QY 37 -----AsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
Db 388 UUCGAAAGUUCGACUCCCGACCGGACCGGACCGAGAUCCGUAUCCGUGGACUGGCG 447
QY 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerLeu 72
Db 448 CUGAAGUUCGAAAGUUUACACCCUGCAGCGUGAAGAAACUUCUACCGCAGGACUUC 507

```

Qy 73 LeuaspArgPheLeuAlaThrVallys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 UUCGACCGUUAUGAUGCUGACCGAGAAAGACAUCAACAAAAACAUCAUGCUGAUCG 567
Qy 92 IleSerCysPheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 AUCACCUCCUGUUAUGCUGUCCAAACUG-----GAAGAUAUCUACGCUCCGAACUG 621
Qy 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAGGAUUAUGCUUACGACCGGUGCUGUCCGGAAGAGACAUCAUCUGGUAUGGAA 681
Qy 132 ArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CUGAUAUCUCCGAAAGCUGAAUUGGAACUGGCGGUGUACCAUCUCCUGGUG 741
Qy 152 HisIlePheHisAlaIle---AlaValSerThrArgProGlnLeuPheSerLeuPro 170
Db 742 AACCUUGUUCUGAGGUGAGCUGCUGAAAGACGUGCUGGAAAGUUCUG-----CUGCG 795
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGUAC-----UCCACGAAACCUCAUCAGACGUGCUGGUG-----837
Qy 191 CysAsnGlnLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 838 -----GACCUUGUGCAUCUCCUGGUGUACGACUCCUGGAA 870
Qy 211 MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 UUCGACGUAUGUUAUGAUGCUGCUGCUGGUGCUGCUGCUGCUGCUGCUGGAA 930
Qy 227 GlnLysAlaGln---MetAspSerSerGlnLeuHisCysArgGluLeuValAlaHis 245
Db 931 AAAAAGCUGGUGUUGAUGGAGGACUCCUCCGGAUGGUGGUGGUGGUGGUGGUG 990
Qy 246 HisLeuSerThrLeuGlnSerLeuProLeu-----AsnSerValTyr 260
Db 991 UUCGUUAACGUGUUAUUAUCCACCUCCCGGUAUAAACUGAAAAAUAUCCCG 1050
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1051 AUGGA-AGACCGUACACAUCCA-----GAC 1076
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1077 CCACACCAUCCUGGC-----UAU 1097
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuPro 311
Db 1098 CGUGAAGAAGUUAACUACAUCAACACACCUCCG 1130

RESULT 14

US-09-092-770-1
; Sequence 1, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119a1 Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092,770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1215
; TYPE: DNA
; ORGANISM: Human
US-09-092-770-1

Alignment Scores:

Pred. No.: 4,21e-15 Length: 1215
Score: 204.00 Matches: 75
Percent Similarity: 47.60% Conservative: 54
Best Local Similarity: 27.68% Mismatches: 96
Query Match: 10.40% Indels: 46
DB: 2 Gaps: 12

US-09-736-250-1 (1-377) x US-09-092-770-1 (1-1215)

Qy 4 ProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThrArgGlu 23
Db 295 CCTCACCTTGGCTGAT-----TTAAGCTGGGATGTTCAAAA-----333
Qy 24 AlaGlnMetTrpLysValAsnValArgLysMetProSer-----36
Db 334 ---GAAGCTGG---CTAAACATGTTAAAAAGAGAGACAGATATGTTTCATGACAAACAT 387
Qy 37 -----AsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
Db 388 TTGAAAGTTCTGCATTCTGACCTTGGAAACACAGATGAGGTCCATATCTTAGACTGGCTT 447
Qy 53 AlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSerSerLeu 72
Db 448 TTAGAGTATGTGAGTATACACATTCATAGGGAACATTTATCTTGCACAGACTTT 507
Qy 73 LeuAspArgPheLeuAlaThrValLys---AlaHisProLysTyrLeuSerCysIleAla 91
Db 508 TTTGATAGATTATGTTGACACAAAGGATATAATAAATATGCTTCAACTCATTTGA 567
Qy 92 IleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeu 111
Db 568 ATTACCTCATTTATTCATTGCTTCCAAACTT-----GAGGAATCTATGCTCTCTAAACTC 621
Qy 112 LysValLeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGlu 131
Db 622 CAAGAGTTGCTTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 681
Qy 132 ArgIleIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeu 151
Db 682 CTCATTATATAAGGCTTTAAATGGAACCTTTGCTCTGTAAACAATCATCTCTCTGGCTA 741
Qy 152 HisIlePheHisAlaIle---AlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 742 AATCTCTTCTCCAAAGTTGATGCTCTTAAAGATGCTCTCTAAAGTTCTT-----CTACCT 795
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 796 CAGTAT-----TCTCAGGAACATTCATCAAAATAGCTCAGCTTTTA-----837
Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 838 -----GATCTGTGTATTCTAGCCATTGATTCATTAGAG 870
Qy 211 MetGluLysLeuIleProAspTrpLeuSerLeu-----ThrIleGluLeuLeu 226
Db 871 TTCCAGTACAGAAATACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 930
Qy 227 GlnLysAlaGln---MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHis 245
Db 931 AAGAAAGCCTCAGGTTTGGAGTGGAGCAGTATTTTCAGAAATGTTGATGTTGATGTTGATGTT 990
Qy 246 HisLeuSerThrLeuGlnSerSerLeuProLeu 256
Db 991 TTTGCTCAATGTAGTAAAAAGTACTAGTCCAGTG 1023

RESULT 15

US-09-222-851-1
; Sequence 1, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 11, 2005, 05:55:30 ; Search time 1613.1 Seconds
(without alignments)
1379.008 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKRFGPLENORLSFLEKAL.....LSRQEGHASPPLQPVSVVM 377

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
Searched: 5378673 seqs, 2950229984 residues
Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154926_20490/app.query.fasta_1.718
-DB=Published Applications NA -QFMT=fastap -SUFFIX=rnnpb -MINMATCH=0.1
-LOOPECL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HRAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09736250 @CGN 1 1 582 @runat_07022005_154926_20490
-NCPU=6 -ICPU=3 -NO WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1962	100.0	1134	12	US-09-736-250-2
2	1962	100.0	1260	17	US-10-172-118-1326
3	1962	100.0	1260	17	US-10-342-887-1326
4	1962	100.0	1260	17	US-10-641-643-893
5	1962	100.0	1889	9	US-09-867-701-10907
6	1841	93.8	2755	10	US-09-814-353-21586
7	811	41.3	490	17	US-10-242-535A-30212
8	811	41.3	490	17	US-10-085-783A-30212
9	770.5	39.3	2146	10	US-09-814-353-21294
10	731	37.3	444	17	US-10-242-535A-16032
11	731	37.3	444	17	US-10-085-783A-16032
12	638	32.5	389	17	US-10-242-535A-6834
13	638	32.5	389	17	US-10-085-783A-6834
14	625	31.9	369	17	US-10-242-535A-33391
15	625	31.9	369	17	US-10-085-783A-33391
16	621	31.7	516	10	US-09-814-353-18045
C 17	486	24.8	348	9	US-09-728-445-666
18	414	21.1	350	17	US-10-242-535A-20816
19	414	21.1	350	17	US-10-085-783A-20816
20	408	20.8	486	10	US-09-814-353-17297
C 21	377.5	19.2	426	10	US-09-814-353-4614
C 22	377.5	19.2	426	10	US-09-814-353-10913
23	367	18.7	387	9	US-09-796-692-3935
24	367	18.7	387	14	US-10-040-862-3935
25	367	18.7	387	17	US-10-057-475B-3935
26	367	18.7	387	17	US-10-154-884B-3935
27	367	18.7	387	18	US-10-764-324-3935
28	346	17.6	447	9	US-09-777-564-1252
29	346	17.6	447	14	US-10-015-219-1252
30	331	16.9	666	17	US-10-240-425-64
31	326.5	16.6	1410	17	US-10-641-643-913
32	326.5	16.6	2044	10	US-09-873-670C-246
33	326.5	16.6	2044	15	US-10-171-581-243
34	326.5	16.6	2044	17	US-10-170-385-322
35	326.5	16.6	2044	17	US-10-172-118-1025
36	326.5	16.6	2044	17	US-10-240-425-1439
37	326.5	16.6	2044	17	US-10-342-887-1025
38	326.5	16.6	2692	13	US-10-002-600-15
39	326.5	16.6	5811	13	US-10-002-600-15
40	321	16.4	420	9	US-09-960-352-9810
41	315.5	16.1	889	9	US-09-867-701-10906
42	284	14.5	288	17	US-10-242-535A-57578
43	284	14.5	288	17	US-10-085-783A-57578
C 44	281.5	14.3	477	10	US-09-814-353-5374
C 45	281.5	14.3	477	10	US-09-814-353-11661

ALIGNMENTS

RESULT 1
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736, 250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2

```

; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 9,44e-231 Length: 1134
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x US-09-736-250-2 (1-1134)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTTGAAACCCAGAGATTGCTTTTCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAGACAGATGCGAAGTGAATGTGCGAAGATGCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGATGAAGTAATTCATGTGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaIleuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGATGTTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTGTATTCATGCATCAGCTGTTTTCTTACGTGCCAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGATTCAGTACTAAAGGTATTTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAAATGAGAGAAATTTCTGGATGAATGAAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACACCATGGAATTTCTTATATTTTCCATGCAATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTGGCAACCAACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCATGTTAGTCTGGAATGAGAAACTCAATTCCTGATGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTCAATGTAACATGCTTTCAGAAAGCACAGATGATAGTCTCCCATGTTGATCCATTTGCGG 720

Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCAGATCATCTTCTACTCTGAGTCTTCTCCCTGCTGTAATTCGCTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTGTGACAAAGGAGTGTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300

```

```

Db 841 CCCTCCTCTGTCCAGGCCCCAGACTTCTCCAAGACAAACAGCAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGACACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAGTAGAGGAATGGAAGTGGATGACTTCTTATGATGAATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTTGTCCACCTTTTGAGCCTGTTCTGTCTCATG 1131

RESULT 2
US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 1.12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-172-118-1326 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTTGAAACCCAGAGATTGCTTTTCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAGACAGATGCGAAGTGAATGTGCGAAGATGCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGATGAAGTAATTCATGTGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGATGTTTTAGCTACCGTA 240

```


Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATCTTGGATTGATTGCAATCAGCTGTTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGATTTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAATGAGAGAAATTTCTGGATAAGTTCAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCACACCATTCGATTTCTCATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTCTCTGGCCATCGTTAGTCTGGAATGAGAAACTCATTCCTGATGCGTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGACCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGGCACATCACTTCTACTCTGCACTTCCCTGCTCTGAAATTCGGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGAGCACACAGCAGCAGAGTGGCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCCAAGTAGAGGAATGGAATGGATGATGACTTCTATGATGGAATCAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAGATAATGCTCAGAAATTTGGGGTCTGTGTGTGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCCTGTTCTGTGTCATG 1131

RESULT 3

US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene

; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:

Pred. No.: 1,12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-342-887-1326 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGCGCTTTGGAAACACAGAGATTGCTTTCTTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGCGAAATGCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATAGGTGGCCAAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTTGGATTGATTGATTCAGTCTGATTCAGTCTGTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGTATTTGGCAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTGAGAATGAGAGAAATTTCTGGATAAGTTCAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCACACCATTCGATTTCTCATATTTTCCATGTCATTCAGTGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCACTGATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTCTCTGGCCATCGTTAGTCTGGAATGAGAAACTCATTCCTGATGCGTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240

Db 661 CTTACATTAAGTCTTTCAGAAAGCACAGATGATGATCCAGTTGATCCATTCGCG 720
Qy
Db 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTGTGGGACATCCTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspLysSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCGCCAGACTTCTCCAAAGCACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspPheTyrAspGlyLysLeuArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGATGATGATGATGATGATGATGAT 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAAGATAATGCTTCAGAAATGTGGGTTCTGTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAGAGGGACATGCTTCCCTTGTCCCTTTGACCTTTGACGCTGTTTCTGTGATG 1131

RESULT 4

US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 5.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641.643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: G1183161
; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :
US-10-641-643-899

Alignment Scores:
Pred. No.: 1,12e-230 Length: 1260
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-641-643-899 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCTTTGGAAACCCAGAGATTGCTTTCTGTGTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGGCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTAATTCATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTATCCAGAAACATTTGCTCTGGGTAGCAGTCTTTTGGATAGGTTTATAGTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACITTGAGTTGATTTGCAATCAGCTGTTTCTTCTAGTGGCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTTAAGGTATTTGCAAGAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCTCATCTGAAATTTTGAGAAATGAGAGAAATTAATCTGGATAAGTTGAA 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGGATTTTCTCATATTTTCCATGCCATGCAAGTCA 480
Qy 161 ThrArgProGlnLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCACTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 541 CTTTACCAAGCACTACTTCTACTGTATGGCTTGAACCAACTTCTCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGAGAAACTCAATCTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACAAATGAACTGCTTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCCATTTGCG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTGTGAGTCTTCCCTGCTCTGAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300

```
Db 841 CCCTCCTCTGTCAGGCCAGACTTCTCCAGGACACACAGCAAGCCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaPheTyHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCACTCCAGCTGCCAGTGCGGTGCAGCAGCCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyAspGlyLeuLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACCTTCTATGATGGAATCAACAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATTAATGAAGATAATGCTCAGAAATGTTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGAGCTGTTCTGTGATG 1131

RESULT 5
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.457
; CURRENT APPLICATION NUMBER: US/09/867,701
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907

Alignment Scores:
Pred. No.: 2,19e-230 Length: 1889
Score: 1962.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x US-09-867-701-10907 (1-1889)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 544 ATGAAGTTTCCAGGGCCTTTGGAAACCCAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 603
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGAAGCACAGATGGAAGTGAATGTCGGAAATGCCTTCAATCAGATGTT 663
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCATCCAGAGAGATGAAGTGAATTCATGGCTGGCCAAACTCAAGTACCAATCAAC 723
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 783
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 784 AAGGCTCATCAAAATACTTGAAGTGTATTCGAATCAGCTGTTTTTCTAGCTGCCAAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTTATTGGCAAGAGACAGTTTTCTGT 903
```

```
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCTCATCTGAAATTTTGAAGATGAGAGAATTATTTCTGGATAAGTTGAATTGG 963
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCCACAGAGCCACCATTTGATTTCTTCATATTTTCCATGTCATTGCGAGTGCA 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTCCAAATGAGCCCATCTCAACATTTGGCAGTC 1083
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1084 CTTACCAAGCAACTACTTCTGATGSCCTGCAACCAACTTCTGCAATTCAGAGGATCC 1143
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGTCTGCGCATGGTTAGTCTGGAATGGAAGAACTCATCTCTGATTGGCTTCT 1203
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTACAATTGAATGCTTTCCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 1263
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTTGTGGCACATCACCCTTTCTACTCTGCAGTCTTCCCTCGCTCTGAAATTCGCTTAT 1323
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTTCAAGCACACCCCTGGTCACTGTGACAAAGGAGTGTTCAGATTACAT 1383
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCTCCTCTGTCCAGGCCAGACTTCTCCAGGACACAGCAAGCCAGAGTCCAGTC 1443
Qy 301 ArgGlyThrAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCGCAAGCAGACCTCT 1503
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyAspGlyIleLysArgLeu 340
Db 1504 ACTAAACGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1563
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATTAATGAAGATAATGCTCAGAAATGTTGGTCTGTGTGGCAGCTGATTTATCAAGA 1623
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGAGCTGTTTCTGTGATG 1674
```

RESULT 6

```
US-09-814-353-21586
; Sequence 21586, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: M01-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
```

; PRIOR APPLICATION NUMBER: US 60/216,820
 ; PRIOR FILING DATE: 2000-07-07
 ; PRIOR APPLICATION NUMBER: US 60/220,661
 ; PRIOR FILING DATE: 2000-07-25
 ; PRIOR APPLICATION NUMBER: US 60/257,672
 ; PRIOR FILING DATE: 2000-12-21
 ; NUMBER OF SEQ ID NOS: 22037
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 21586
 ; LENGTH: 2755
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-814-353-21586

Alignment Scores:
 Pred. No.: 3,27e-215 Length: 2755
 Score: 1841.00 Matches: 358
 Percent Similarity: 94.96% Conservative: 0
 Best Local Similarity: 94.96% Mismatches: 1
 Query Match: 93.83% Indels: 18
 DB: 10 Gaps: 1

US-09-736-250-1 (1-377) x US-09-814-353-21586 (1-2755)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
 DB 847 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGTCTTTCTCTGTTGAAAAGGCAATC 906
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 907 ACTAGGGAAGCACAGATGTGAAGTGAATGTGGGAAATGGCTTCAAAATCAGAAATGTT 966
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 967 TCTCCATCCAGAGAGATGAATTAATCAATGGCTGGCCAACTCACTACCAATTCAC 1026
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 1027 CTTTACCAGAAACATTTTCTGCTGGCTAGCAGTCTTTTGGATAGTGTCTTTAGCTACCGTA 1086
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
 DB 1087 AAGGCTCATCTT----- 1098
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
 DB 1099 -----GAGGAAGATGACAGAAATCCAGTACTAAAGTATTGGCAAGACAGATTTCTGT 1152
 QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 DB 1153 GGATGTTCTCATCTGAAATTTTGAGAAATGGAGAGAAATATTCTGGATAAGTTGAAATGG 1212
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 1213 GATCTTCACAGCCACACCAATGGATTTCTTCAATATTTTCCATGCAATTCAGTGTCA 1272
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 1273 ACTAGGCCCTCAGTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1332
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
 DB 1333 CTTTACCAGCAACTACTTCTCATGTATGGCTTGGCCGCAACCAACTTCTGCAATTCAGAGGATCC 1392
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 DB 1393 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTCTGATGGCTTCT 1452
 QY 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
 DB 1453 CTTCAATTTGAATGCTTTCAGAAAGCACAGATGATAGTCCCACTGGATTCATTCATTCG 1512
 QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260

DB 1513 GAGCTTGTGGCACATCACCTTTTCTACTCTGCAGTCTTCCCTCGCCTCTGAATTCGGTTAT 1572
 QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 1573 GTCTACCGTCCCTTCAAGCACACCCCTGGTCACTGTGACAAAGGAGTGTTCAGATTACAT 1632
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 1633 CCTTCTCTGTCCAGGCCCCAGACTTCTCCAGGACCAACAGCAAGTCCAGTCCAGTC 1692
 QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 DB 1693 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGTCCAGTGGGTGGTCAAGCAGACCTCT 1752
 QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLeuArgLeu 340
 DB 1753 ACTAAACGCAAGTAGAGGAAATGGAAAGTGGAGTCTTATGATGGAATCAAAACGGCTC 1812
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 DB 1813 TATAATGAAGATATATGTCTCAGAAAATGTGGTCTGTGTGGCAGTGTATTCATCAAGA 1872
 QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 DB 1873 CAAGAGGACATGCTTCCCTTGTCTACCTTTCAGCCTGTTTCTGTCTCATG 1923

RESULT 7

US-10-242-535A-30212
 ; Sequence 30212, Application US/10242535A
 ; Publication No. US20040013663A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ChondroGene Inc.
 ; APPLICANT: Liew, C.C.
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 ; FILE REFERENCE: 4231/2005
 ; CURRENT APPLICATION NUMBER: US/10/242,535A
 ; CURRENT FILING DATE: 2002-09-12
 ; PRIOR APPLICATION NUMBER: US 10/085,783
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/305,340
 ; PRIOR FILING DATE: 2001-07-13
 ; PRIOR APPLICATION NUMBER: US 60/275,017
 ; PRIOR FILING DATE: 2001-03-12
 ; PRIOR APPLICATION NUMBER: US 60/271,955
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 58994
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 30212
 ; LENGTH: 490
 ; TYPE: DNA
 ; ORGANISM: Human
 US-10-242-535A-30212

Alignment Scores:
 Pred. No.: 1,39e-89 Length: 490
 Score: 811.00 Matches: 157
 Percent Similarity: 98.77% Conservative: 4
 Best Local Similarity: 96.32% Mismatches: 2
 Query Match: 41.34% Indels: 0
 DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-30212 (1-490)

QY 114 LeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArgMetGluArgIle 133
 DB 1 ATGGCCAGAGAGAGTTCCTGGATGTTCTCTCATCTGAAATTTGAGAAATGGAGAGATT 60
 QY 134 IleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
 DB 61 ATTCGATAGGTTGAATGGGATCTTTACAGCCACACCATTTGGATTTTCTTCATATT 120
 QY 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173

Db 121 TTCCATGCAATTCAGTGTCAACTAGGCTCAGTTACTTTTCAGTTTCCCAAAATTGAGC 180
Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuHisCysMetAlaCysAasnGln 193
Db 181 CCATCTCAACATTGGCAGTCTTACCAAGCAACTACTTCACTGTATGGCTGCAACCAA 240
Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
Db 241 CTTCTGCAATTCAGAGGATCCATGCTTCTGCGCATGGTGTAGTCTGGAAATGGAGAA 300
Qy 214 LeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db 301 CTCATTCCTGATGGCTTCTTACAAATTTGAATGCTTTCAGAAAGCACAGATGATAGC 360
Qy 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 361 TCCAGTGTATCCATTGTCGGAGCTTGTGGCACATCACCTTCTCTCGAGTCTTCC 420
Qy 254 LeuProLeuAasnSerValTyrrArgProLeuLysHisThrLeuValThrCysAsp 273
Db 421 CTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGCACACCCCTGGTGCCTGTGAC 480
Qy 274 LysGlyVal 276
Db 481 AAAGGAGTG 489

RESULT 8

US-10-085-783A-30212
; Sequence 30212, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-30212

Alignment Scores:
Pred. No.: 1.39e-89 Length: 490
Score: 811.00 Matches: 157
Percent Similarity: 98.77% Conservative: 4
Best Local Similarity: 96.32% Mismatches: 2
Query Match: 41.34% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-30212 (1-490)

Qy 114 LeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGluArgIle 133
Db 1 ATGTGCCACAGAGAAGTTTCTGTGGATGTTCTCATCTGAATTTTTCAGAAATGGAGAAAT 60
Qy 134 IleLeuAspLysLeuAasnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
Db 61 ATTCTGGATAGGTGAATTTGGATCTTTACACAGCACACCATTTGGATTTCTTCATATT 120
Qy 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173
Db 121 TTCCATGCAATTCAGTGTCAACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATTGAGC 180

Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuHisCysMetAlaCysAasnGln 193
Db 181 CCATCTCAACATTGGCAGTCTTACCAAGCAACTACTTCACTGTATGGCTGCAACCAA 240
Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
Db 241 CTTCTGCAATTCAGAGGATCCATGCTTCTGCGCATGGTGTAGTCTGGAAATGGAGAA 300
Qy 214 LeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db 301 CTCATTCCTGATGGCTTCTTACAAATTTGAATGCTTTCAGAAAGCACAGATGATAGC 360
Qy 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 361 TCCAGTGTATCCATTGTCGGAGCTTGTGGCACATCACCTTCTCTCGAGTCTTCC 420
Qy 254 LeuProLeuAasnSerValTyrrArgProLeuLysHisThrLeuValThrCysAsp 273
Db 421 CTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGCACACCCCTGGTGCCTGTGAC 480
Qy 274 LysGlyVal 276
Db 481 AAAGGAGTG 489

RESULT 9

US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294

Alignment Scores:
Pred. No.: 1.55e-83 Length: 2146
Score: 770.50 Matches: 154
Percent Similarity: 91.18% Conservative: 1
Best Local Similarity: 90.59% Mismatches: 12
Query Match: 39.27% Indels: 3
DB: 10 Gaps: 1

US-09-736-250-1 (1-377) x US-09-814-353-21294 (1-2146)

Qy 210 GluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuGlnLysAla 229
Db 815 GAGCAGCTATGTATTAATTAATGATCACTGTGTGGCTTTT---TTTTTTTCTCGGCC 871

QY 230 GlnMetAspSerSerGlnLeuHisCysArgGluLeuValAlaHisHisLeuSerThr 249
Db 872 CAGATGGATAGCTCCAGTTGATCCATGTCGGAGCTGTGCCACATCACCTTTCTACT 931
QY 250 LeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuHisHisThrLeu 269
Db 932 CTGCGAGTCTTCCCTGCTCTGAAATCCGTTTATGCTACCGTCCCTCAAGCACACCCCTG 991
QY 270 ValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPhe 289
Db 992 GTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTCGCCAGGCCAGACTTC 1051
QY 290 SerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHis 309
Db 1052 TCCAAAGGACAAACAGCAAGCCAGGAGTCCAGTACAGGCTTATCCATCAT 1111
QY 310 LeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGlnGluMetG 329
Db 1112 CTCCAGAGCTGCCAGTGGGTGCAAGCAGCTTCTTACTAAACGCAAGTAGAGGAATGG 1171
QY 329 LuValAspAspPheTyrAspGlyLysArgLeuTyrAsnGluAspAsnValSerGluA 349
Db 1172 AAGTGGATGACTTCTATGATGGAATCAACGGCTCTATAAGATATATGTCAGAAA 1231
QY 349 snValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysP 369
Db 1232 ATGTGGGTCTGTGTGGCACTGATTTATCAAGACAAGAGGAGCATGCTTCCCTTGTG 1291
QY 369 toProLeuGlnProValSerValMet 377
Db 1292 CACCTTTCAGCCTGTTTCTGTGCATG 1317

RESULT 10

US-10-242-535A-16032
; Sequence 16032, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-16032

Alignment Scores:
Pred. No.: 8,43e-80 Length: 444
Score: 731.00 Matches: 145
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 37.26% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-16032 (1-444)

QY 124 SerSerGluLeuLeuArgMetGluArgGlyLeuLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGATGGAGAAATTTCTGGATAAGTTGAATGGATCTTCAC 62

QY 144 ThrAlaThrProLeuAspPheLeuHisHisPheHisAlaLeuValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGATTTCTTCATATTTCCATGCCATTGCAGTGTCAACTAGGCT 122
QY 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCACTTTGGCCCAATTTGAGCCCATCTCAACATTTGGCAGTCTTTACCAAG 182
QY 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAATCTTCTACTGTATGGCTGCAACCACTCTGCAATTCAGAGATCCATGCTTGTCT 242
QY 204 LeuAlaMetValSerLeuGluMetGlyLysLeuLeuProAspTrpLeuSerLeuThrIle 223
Db 243 CTGSCCATGGTTAGTCTGGAAATGAGAACTCATCTCTGATTTGGCTTTCTTACAAAT 302
QY 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuVal 243
Db 303 GAATCTGCTTCAGAAAGCACAGATGATAGCTCCAGTTGATCCATTTGTCGGAGCTTGTG 362
QY 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 363 GCATCATCACCTTCTCTCTGAGTCTTCCCTGCTCTGAAATTCGTTTATGCTACCCG 422
QY 264 ProLeuLysHisThrLeuVal 270
Db 423 TCCCTCAAGCACACCTCTGGTG 443

RESULT 11

US-10-085-783A-16032
; Sequence 16032, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-16032

Alignment Scores:
Pred. No.: 8,43e-80 Length: 444
Score: 731.00 Matches: 145
Percent Similarity: 98.64% Conservative: 0
Best Local Similarity: 98.64% Mismatches: 2
Query Match: 37.26% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-16032 (1-444)

QY 124 SerSerGluLeuLeuArgMetGluArgGlyLeuLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGATGGAGAAATTTCTGGATAAGTTGAATGGATCTTCAC 62
QY 144 ThrAlaThrProLeuAspPheLeuHisHisPheHisAlaLeuValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGATTTCTTCATATTTCCATGCCATTGCAGTGTCAACTAGGCT 122
QY 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183

Db 123 CAGTTACTTTTCAGTTGGCCCAATTGAGCCCATCTCAACATTTGGCGAGTCCTTACCAAG 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuLeuLeuProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCCATGGTTACTGTGGAATCGAAGAACTCATCTGATTTGGCTTTCTTCTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuVal 243
Db 303 GAACCTGTTTCAAGAAGACAGATGGATAGTCCAGTTGATCCATTTGCGGAGCTTGTG 362
Qy 244 AlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 363 GCACATCACCTTTCTACTGTGAGTCTTCCCTGCTCTGAAATCCGTTTATGTTCTACCCG 422
Qy 264 ProLeuLysHisThrLeuVal 270
Db 423 TCCCTCAAGCACACCTCGGTG 443
RESULT 12
US-10-242-535A-6834
; Sequence 6834, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-6834
Alignment Scores:
Pred. No.: 1.93e-68 Length: 389
Score: 638.00 Matches: 128
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 1
Query Match: 32.52% Indels: 1
DB: 17 Gaps: 0
US-09-736-250-1 (1-377) x US-10-242-535A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTTCTGTTGGAAAGGCAATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGACACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAAGATGTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 121
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241

Db 122 CCATCCAGAGAGATGAGTAATTCAATGCTGCGCCAACTCAAGTACCATTCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101
Db 242 GCTCATCCCAAAATACTTGAATGTATTGCAATCAGCTGTTTTTCTTAGCTGCCAAGACT 301
Qy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe-CysG1 121
Db 302 GTTGAGGAAGATGAGAGAAATTCAGTACTAAAGGTATTGGCAGAGACAGTTTCTGNGGG 361
Qy 121 YCysSerSerSerGluIleLeuArgMet 130
Db 362 ATGTTCTCTCATCTGAAATTTTGAGATG 389
RESULT 13
US-10-085-783A-6834
; Sequence 6834, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US 10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-6834
Alignment Scores:
Pred. No.: 1.93e-68 Length: 389
Score: 638.00 Matches: 128
Percent Similarity: 98.46% Conservative: 0
Best Local Similarity: 98.46% Mismatches: 1
Query Match: 32.52% Indels: 1
DB: 17 Gaps: 0
US-09-736-250-1 (1-377) x US-10-085-783A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTTCTGTTGGAAAGGCAATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGACACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAAGATGTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 122 CCATCCAGAGAGATGAGTAATTCAATGCTGCGCCAACTCAAGTACCATTCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCCAGAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTCTTTTACCGTAAAG 241

Qy	82	AlaHisProLysTyrIleuSerCysIleAlaIleSerCysPheLeuAlaAlaLysThr	101
Db	242	GCTCATCCAAATACTTGAGTTGTATTGCAATCAGCTGTTTTCTTAGCTGCCAAGACT	301
Qy	102	ValGluGluAspGluArgIleProValIleuLysValIleuAlaArgAspSerPhe-CysG	121
Db	302	GTTGAGGAAGATCAGAGAATCCAGTACTAAAGTATTGCCAAGAGACAGTTTCTGNGGG	361
Qy	121	yCysSerSerGluIleLeuArgMet	130
Db	362	ATGTTCTCATCTGAAATTTTGAAATG	389

RESULT 14

```

US-10-242-53391
; Sequence 33391, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew. C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-33391

```

RESULT 15

```

US-10-085-783A-33391
; Sequence 33391, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)-(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)-(25)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-33391

Alignment Scores:
Pred. No.:          7.07e-67          Length:          369
Score:              625.00            Matches:         119
Percent Similarity: 99.17%            Conservative:     1
Best Local Similarity: 98.35%          Mismatches:      1
Query Match:        31.86%            Indels:          0
DB:                  17                Gaps:            0

US-09-736-250-1 (1-377) x US-10-085-783A-33391 (1-369)

QY      208  SerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGln 227
Db      4   AGTCGGAAATGGAGAAACTNTTCCTGATGGCTTTCTCTTACAATTGAACGTGCTTCAG 63

QY      228  LysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeu 247
Db      64  AAAGCACAGATGGATAGCTCCAGTTGATCCATTGTCGGAGCTTGTGGCACATCACCTT 123

QY      248  SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHis 267
Db      124  TCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGGTTTATGTCCTACCGTCCCTCAGAC 183

QY      268  ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyPro 287
Db      184  ACCCTGGTGAACCTGTGACAAAGGAGTGTTTCAGATTATCATCCCTTCCTCTGTCCAGGCCCA 243

QY      288  AspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyr 307

```

Db	244	GACTTCTCCAAGGACACAGCAGCCAGAAAGTGCCAGTCAGAGGTACAGCAGCCTTTTAC	303
Qy	308	HisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGlu	327
Db	304	CATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGAA	363
Qy	328	Met	328
Db	364	ATT	366

Search completed: February 11, 2005, 10:20:36
 Job time : 1619.1 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:23:50 ; Search time 5876.76 Seconds
(without alignments)
2441.859 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPEPLENQLSLLEKAI.....LSROEGHASPPLQPVSV 377

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154924_20414/app query.fasta_1.718
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 4385 @runat_07022005_154924_20414 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1:	gb est1.*
2:	gb est2.*
3:	gb_hcc.*
4:	gb_est3.*
5:	gb_est4.*
6:	gb_est5.*
7:	gb_est6.*
8:	gb_gss1.*
9:	gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1509	97.3	1134	9 AY412158	Homo sapi
2	1851	94.3	2348	3 BC029328	Mus muscu
3	1841	93.8	2045	3 AK050465	Mus muscu
4	1817	92.6	2739	3 AK079476	Mus muscu
5	1746	89.0	1110	9 AY412160	Mus muscu
6	1593	81.2	1085	7 CR754276	CR754276
7	1577	80.4	967	7 CN647834	ILLUMIGEN
8	1535	78.2	992	7 C0646424	ILLUMIGEN
9	1456	74.2	920	5 BQ673277	AGENCOURT

10	1442	73.5	983	7	CN646807	ILLUMIGEN
11	1440	73.4	920	5	BUS28295	AGENCOURT
12	1431.5	73.0	963	5	BUS38306	AGENCOURT
13	1424	72.6	841	7	CF552849	AGENCOURT
14	1416	72.2	906	6	CD107527	AGENCOURT
15	1415.5	72.1	936	5	BUS01311	AGENCOURT
16	1413.5	72.0	903	5	BUS56287	AGENCOURT
17	1406	71.7	865	5	BUI88239	AGENCOURT
18	1402	71.5	830	5	EX437607	EX437607
19	1402	71.5	853	5	BUI59699	AGENCOURT
20	1401.5	71.4	890	4	BI858571	603389030
21	1400.5	71.4	946	5	BUS58083	AGENCOURT
22	1399.5	71.3	931	5	BUS01596	AGENCOURT
23	1397	71.2	891	5	BUI51205	AGENCOURT
24	1391	70.9	844	4	BG215999	RST35685
25	1383	70.5	854	4	BG182134	RST998 At
26	1375.5	70.1	909	5	BUS7546	AGENCOURT
27	1363.5	69.5	976	4	BG757286	602715271
28	1359	69.3	899	6	CD358716	AGENCOURT
29	1354	69.0	914	5	BQ894247	AGENCOURT
30	1350	68.8	978	4	BM463752	AGENCOURT
31	1345.5	68.6	849	4	BG758079	602712239
32	1337	68.1	884	5	BUI88938	AGENCOURT
33	1335	68.0	946	7	CN647001	ILLUMIGEN
34	1334	68.0	918	5	BQ673252	AGENCOURT
35	1325	67.5	821	4	BI651160	603297638
36	1320	67.3	932	5	BQ669046	AGENCOURT
37	1317	67.1	775	4	BM016042	603642469
38	1305	66.5	790	4	BG198062	RST17446
39	1302	66.4	862	5	BUI49962	AGENCOURT
40	1300	66.3	885	5	BQ671998	AGENCOURT
41	1294	66.0	764	4	BG205510	RST24889
42	1293.5	65.9	764	6	CB962746	AGENCOURT
43	1288	65.6	767	4	BG213835	RST33455
44	1285.5	65.5	933	5	BUI51731	AGENCOURT
45	1285	65.5	963	7	CN803219	ILLUMIGEN

ALIGNMENTS

RESULT 1	LOCUS	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
AY412158	LOCUS	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
DEFINITION	AY412158	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
ACCESSION	AY412158	AY412158	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
VERSION	AY412158.1	GI:39768123	Homo sapiens CCNI gene, genomic survey sequence.	1134 bp	DNA	linear	GSS 16-DEC-2003
KEYWORDS	SS.		Homo sapiens (human)	1134 bp	DNA	linear	GSS 16-DEC-2003
SOURCE	SS.		Homo sapiens (human)	1134 bp	DNA	linear	GSS 16-DEC-2003
REFERENCE	1	(bases 1 to 1134)	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.	1134 bp	DNA	linear	GSS 16-DEC-2003
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			1134 bp	DNA	linear	GSS 16-DEC-2003
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios			1134 bp	DNA	linear	GSS 16-DEC-2003
JOURNAL	Science 302 (5652), 1960-1963 (2003)			1134 bp	DNA	linear	GSS 16-DEC-2003
PUBMED	14671302			1134 bp	DNA	linear	GSS 16-DEC-2003
REFERENCE	2	(bases 1 to 1134)	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.	1134 bp	DNA	linear	GSS 16-DEC-2003
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarival, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferreria, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.			1134 bp	DNA	linear	GSS 16-DEC-2003
TITLE	Direct Submission			1134 bp	DNA	linear	GSS 16-DEC-2003
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			1134 bp	DNA	linear	GSS 16-DEC-2003
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			1134 bp	DNA	linear	GSS 16-DEC-2003
FEATURES	Location/Qualifiers			1134 bp	DNA	linear	GSS 16-DEC-2003
source	1. .1134			1134 bp	DNA	linear	GSS 16-DEC-2003

```
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
<1_>1134
/gene="CCNI"
/locus_tag="HCW4464"
```

gene

ORIGIN

Alignment Scores:

```
Pred. No.: 3,93e-193 Length: 1134
Score: 1909.00 Matches: 368
Percent Similarity: 97.61% Conservative: 0
Best Local Similarity: 97.61% Mismatches: 9
Query Match: 97.30% Indels: 0
DB: 9 Gaps: 0
```

US-09-736-250-1 (1-377) x AY412158 (1-1134)

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAAACCCAGAGATTGCTTTCTCTGTTGGAAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAATGCCCTTCAAATCAGAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGATGAATTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCGTAGCAGTCTTTTGGATAGTGTTTTACGTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLays 100
Db 241 AAGCCTCATCCANAATACTTGAAGTGTATTGCAATCAGCTGTTTTTCTAGTCGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGGGAAGATGAGAGAAATTCAGTACTAAAGTATTGGCAGAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAAGTGAATTGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTACACAGCCACACCATTTGATTTCTTATATTNNCCATGCCATTGCAGTGCTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGAGAAACTCATTTCTGATTGCTTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACATTTGACTGCTTCAGAAAGCAGACAGNNNNNNNNNNNNNNNNNNNNNNATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCCTCTGAAATTCGGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCCGTCCCTCAAGCACACCCCTGGTGACCTGTGTGACAAAGGAGTGTTCAGATTACAT 840
```

```
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTCTCCAGGCCCCAGACTTCTCCAGGACACACAGCAGCCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGTCCAGTGGGTGCGACGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAGTGGATCTTCTATGATGAATCAACAGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGCTCAGAAATGTGGTCTGTGTGTGGCACTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCGCCTGTTCTGTCTCATG 1131
```

RESULT 2

```
BC029328 2348 bp mRNA linear HTC 12-OCT-2004
LOCUS Mus musculus cyclin I, mRNA (cdna clone IMAGE:3583701).
DEFINITION BC029328
ACCESSION BC029328.1 GI:20381070
VERSION HTc.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
```

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2348)

REFERENCE

1 (bases 1 to 2348)
Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Pange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahy, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2348)

Director MGC Project.

Direct Submission

TITLE

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK

COMMENT
Contact: MGC help desk
Email: cgaaps-xemail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 10 Row: i Column: 3
This clone has the following problem: no 5' EST match.

FEATURES

Location/Qualifiers
1..2348
/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3583701"
/tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by biopsy."
/clone_lib="NCI CGAP_Mam1"
/lab_host="DH10B"
/note="vector: pCMV-SPORT6"

ORIGIN

Alignment Scores:
Pred No.: 1 99e-186 Length: 2348
Score: 1851.00 Matches: 355
Percent Similarity: 97.08% Conservative: 11
Best Local Similarity: 94.16% Mismatches: 11
Query Match: 94.34% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x BC029328 (1-2348)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaile 20
Db 160 ATGAAGTTTCAGGACCTTGGAAACACAGAGATTGCTCTCTGTTGGAAAGGCAATC 219
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 220 TCCAGGGAAGCCAGATGTGGAGGTGAATGTGCCGAAATATACCTACAAATCAGAATGTT 279
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysLeuLysTrpGlnPheAsn 60
Db 280 TCTCCATCCAGAGAGATGAATTAATCAATGTTGGCCAACTCAATACCATGTTCAAC 339
Qy 61 LeuTrpProGluTrpPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 340 CTCTATCCAGAAACATTTGCTCTGCCAAGCAGTCTTTTGATAGATGTTTGTAGCTACAGTA 399
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 400 AAAGCCCATCCAAATATTTGAATTTGATTTGCAATCAGCTGTTTTTTTCTGGCTGCTAAG 459
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 460 ACTGTTGAGGAAGATGAGAAATTTCCAGTGTCAAGGTATTGGCAAGACAGATTTCTGT 519
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 520 GGATGTTCTCATCTGAGATTTTGAGATGAGAGAAATTTCTGGATAAATTCGAATGG 579
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 580 GATCTTCACCGGTACACCAATGGATTTTCTTCACATTTTCCATGTCATTCGCGGTGCA 639
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 640 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 699
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 700 CTGACCAAGCAGCTGCTTCACTGTATGGCTTGCACCACTCTCTGCAGTTCAAGGGTCC 759
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220

Db 760 ATGCTTGCTCTGCCCATTGGTTAGTCTGGAATGAGAAATCATCTCTGATGCTTCCT 819
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 820 CTTACGATTGAATGCTTTCAGAAAGCACAGATGCAGAGCTCCAGATTGATCCACTGCG 879
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 880 GAGCTGTGGCATATCACCTTTCTGCTCTGCAGTCTGCCCTGCTCTAAATTCGTTTAT 939
Qy 261 ValTrpArgProLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 940 GTCTACCGTCCCTCAAGCACACCTGTTAACTGTGACAAAGAGCATTCATTAATCAT 999
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1000 CCTCTCTCTCTCAGGCCAGATTTCTCCAGGACAAACAGAACCCAGAAGTCCAGTC 1059
Qy 301 ArgGlyThrAlaAlaPheTrpHisLeuProAlaHisLeuProAlaHisLeuGlnThrSer 320
Db 1060 CGAGGTCCAGCAGCTTCCACCTGTCATCTCCCGCTGCCAGTGGGTGCAAGCAACCTCT 1119
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyIleLysArgLeu 340
Db 1120 GCTAAACGGAAGATGGAGGAGATGGAGGTGGATGACTTCTACGATGGGATCAACGGCTC 1179
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1180 TATAATGAGGACCAATGGTCTCGAGATGTGGTCTGTATGTGGCACTGATTTATCAAG 1239
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1240 CAAGAGGGCCATGTTCCCTCTGTCACCTTTCAGCTTGTCTGTCTCATG 1290
RESULT 3
AK050465 2045 bp mRNA linear HTC 03-APR-2004
LOCUS Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DEFINITION enriched library, clone:C820001G04 product:cyclin I, full insert
sequence.
AK050465
AK050465.1 GI:26341217
VERSION HTC; CAP trapper.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE
3 Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE
PUBMED
REFERENCE
AUTHORS20530913
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)

JOURNAL
REFERENCE
AUTHORS

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

JOURNAL
REFERENCE
AUTHORS

6 (bases 1 to 2045)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imocani, K., Ishii, Y., Ito, K., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toyota, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp).
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Cells were provided by Hiroo Iwata (Department of Reproductive Materials Field of Tissue Engineering Institute for Frontier Medical Sciences, Sakyoku-ku, Kyoto, 606-8507, Japan) whose assistance we gratefully acknowledge.

Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>

URL: <http://fantom.gsc.riken.jp/>.

FEATURES

SOURCE

1..2045
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:C820001G04"
/db_xref="taxon:10090"
/clone="C820001G04"
/cell_type="islet cells"
/tissue_type="pancreas"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
628..1761
/note="unnamed protein product; cyclin I (MGI:1341077, GB|NM_017367, evidence: BLASTN, 98%, match=1534)
putative"

CDS

/codon_start=1
/protein_id="BAC34271.1"
/db_xref="GI:26341218"
/translation="MKPPGLEHRLSSLLERAIISREAOVKVNPVPIPTONVPSQ
RDEVIQWLAKLYQFNLYPETFAALLSRRIIDKLNWDHTATPDLFLHIFRAIVS
EEDKIPVLKVLARDSFCGSSSEILMERIILDKLNWDHTATPDLFLHIFRAIVS
ARPLQLSLKPSQSLAVLTITKQLHCMAQNQLQFPGSMALAVSLEMEKILPDW
LPTITLQKQMDSSQLIHRELVAYHLHALQSALPLNSVYVYVPLKHLTKLIDKGA
FKLHPSSVSGPDSKNSKEPVRGPAFHLPLPAASGCKQTSAKRKRVEEMVEDDFY
DGIKRLYNEDNGPENVSGVGTDLISREGHASFPCPIQPVSM"

ORIGIN

Alignment Scores:
Pred. No.: 1.88e-185 Length: 2045
Score: 1841.00 Matches: 353
Percent Similarity: 96.55% Conservative: 11
Best Local Similarity: 93.63% Mismatches: 13
Query Match: 93.83% Indels: 0
DB: 3 Gaps: 0
US-09-736-250-1 (1-377) x AK050465 (1-2045)
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 628 ATGAAGTTTCCAGGACCTTTGGAAACACACAGATTGCTCTCTGTTGGAAAGGCAATC 687
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 688 TCCAGGGAAGCCAGAGTGTGGAAGGTGAATGTGCCGAAAATACCTCAAAATCAGAAATGTT 747
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTytrGlnPheAsn 60
Db 748 TCTCCATCCAGAGAGATGAGTAATTCATGTGTGCCAAACTCAATACCAAGTTCAC 807
QY 61 LeuTytrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 808 CTCTATCCAGAAACATTTGCTCTGCGCAAGCAGTCTTTTGGATAGGTTTTTAGCTACAGTA 867
QY 81 LysAlaHisProLysTytrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 868 AAGGCCCATCCAAAATATTGTAATTTGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 927
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 928 ACTGTTGGAAGATGAGAAATTCAGTCTTAAGGTATTGCGACAGACAGACAGTTCTGT 987
QY 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 988 GGATGTTCTCATCTCAGATTTTGAGATGGAGAGAAATTTATCTGGATAAATGAATTGG 1047
QY 141 AspLeuHisThrAlaThrProLeuAppPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 1048 GATCTTCACACGGCTACACATTTGATTTTTCACATTTCCATGCCATTGCGGTGTC 1107
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1108 GCTAGGCTTCAGTTACTTTTCAGTTTGGCCAAATTCAGCCCATCTCAACATTTGGCAGTC 1167
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 1168 CTGACCAAGCAGCTGCTTCACTGTATGGCTTGCACCAACTTCTGCAGTTTCAAGGGTCC 1227
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1228 ATGCTTGTCTTGCCCATGTTAGTCTGGAAATGGAGAAACTCATCTCTGATTGGCTTCCT 1287
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1288 CTTTACGATTGAACCTGCTTCAGAAAGCACAGATGGACAGCTCCAGTTGATCCACTGCG 1347
QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTytr 260
Db 1348 GAGCTGGTGGCATATCACCTTTCTGCTCTGCAGTCTGCGCTGCTGCTTAAATTCGTTTAT 1407
QY 261 ValTytrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1408 GTCTACCGTCCCTCAAGCACACCTCTGGTAACCTGTGACAAAGAGCATTCATATTACAT 1467
QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1468 CCTCTCTGTCTCAGGCCAGATTCTCCAAGGACCAACAGCAAGCAAGAGTGCAGTC 1527
QY 301 ArgGlyThrAlaAlaPheTytrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320

Db 1528 CGAGGTCAGCAGCCTTCCACCTGCATCTCCCGCTGCCAGTGGTGCAAGCAACCTCT 1587

Qy 321 ThrLyAsArgLysValGluGluMeGluValAspAspPheTyrAspGlyIleIysArgLeu 340
 Db 1588 GCTAAACGGAAGTGGAGGAGATGGAGTGATGACCTTCTACGATGGGATCAAGCGGCTC 1647

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1648 TATTAATGAGGACAATGGTCTGGAAGATGGGTCTGTATGTGGCATTGATTTATCAAG 1707

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
 Db 1708 CAAGAGGCCATGCTTCCCGCTGCCACCTTGCAGCCTGTTCGTGATG 1758

RESULT 4
 LOCUS AK079476
 DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
 enriched library, clone: A130017J05 product: cyclin I, full insert
 sequence.

ACCESSION AK079476
 VERSION AK079476.1 GI:26098528
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Mech. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kitsumi, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
 FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research
 Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation
 of 60,770 full-length cDNAs
 JOURNAL Nature 420, 563-573 (2002)
 MEDLINE 12027399
 PUBMED 12027399

REFERENCE 6
 AUTHORS Fukuda, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,
 Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
 Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N.,

Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
 Muramatsu, M. and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
 Physical and Chemical Research (RIKEN), Laboratory for Genome
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
 RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
 Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp,
 URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
 Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome
 Encyclopedia Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.
 Division of Experimental Animal Research in Riken contributed to
 prepare mouse tissues.
 Please visit our web site for further details.
 URL: http://genome.gsc.riken.jp/
 URL: http://fantom.gsc.riken.jp/.

FEATURES
 source
 1..2739
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="FANTOM DB:A130017J05"
 /db_xref="taxon:10090"
 /clone="A130017J05"
 /tissue_type="thymus"
 /clone_lib="RIKEN full-length enriched mouse cDNA library"
 /dev_stage="16 days neonate"
 misc_feature
 567..1701
 /note="cyclin I (MGD|MG1:1341077, GB|NM_017367, evidence:
 BLASTN, 98%, match=1534)
 putative"
 2723..2728
 /note="putative"
 2739
 /note="putative"
 ORIGIN
 Alignment Scores:
 Pred. No.: 1..182 Length: 2739
 Score: 1817.00 Matches: 351
 Percent Similarity: 95.77% Conservative: 11
 Best Local Similarity: 92.86% Mismatches: 15
 Query Match: 92.61% Indels: 1
 DB: 3 Gaps: 0
 US-09-736-250-1 (1-377) x AK079476 (1-2739)
 Qy 1 MetLyAsPheProGly-ProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaI 20
 Db 567 ATGACGTTTCAGAGCCCTTGGAAACCCAGAGATTGCTCTCTGTGGAAAGGCAAT 626
 Qy 20 eThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVa 40
 Db 627 CTCGAGGGAAGCCAGATGTTGGAAGGTGAATGTGCCGACATACCTACCAATCATGT 686
 Qy 40 lSerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAs 60
 Db 687 TTCTCCATCCAGAGAGATGAAGTAATTAATGATGTAATGCAATCAGCTGTTTTCTGGCTGCTAA 746
 Qy 60 nLeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVa 80
 Db 747 CCTCTATCCAGAACATTTGCTCTGGCAAGGAGCTTTTGGATAGGTTTTTAGCTACAGT 806
 Qy 80 lLysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLaLy 100
 Db 807 AAAAGCCCATCCAAAATATTGAATGATGTAATGCAATCAGCTGTTTTTCTGGCTGCTAA 866
 Qy 100 sThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCy 120

```
Db 867 GACTGTTGAGGAAGATGAGAAATTCAGTCTAAAGGTATTGGCAAGACAGACTTCTG 926
Qy 120 sGlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTr 140
Db 927 TGGATGTTCTCACTGAGATTTTGGAGATGGAGAGATTTCTCGATATAATTTGAATG 986
Qy 140 pAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSe 160
Db 987 GGATCTTCACACGCTACACCATTTGATTTCTTTCACATTTTCCATGCGGTGTC 1046
Qy 160 rThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVa 180
Db 1047 AGCTAGGCTCAGTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGT 1106
Qy 180 lLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySe 200
Db 1107 CCTGACCAAGCAGCTGCTTCACTGATGGCTGCAACCACTTCTGAGTTTCAAGGTC 1166
Qy 200 rMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSe 220
Db 1167 CATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAACTCATTTCTGATTTGCTTCC 1226
Qy 220 rLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysAr 240
Db 1227 TCTTACGATTTGAATGCTTTCAGAAAGCACAGATGGACAGCTCCAGTTGTATCCACTGTG 1286
Qy 240 gGluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTy 260
Db 1287 GGAGCTGGTGCAATACACTTTTCTGCTCGATGCTGCGCTGCTCTAAATTCGGTTA 1346
Qy 260 rValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHi 280
Db 1347 TGTCTACGCTCCCTCAAGCACACCTTGTAACCTGTGACAAAGAGCAATTCAAATTACA 1406
Qy 280 sProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVa 300
Db 1407 TCCCTCTCTCTCTCAGGCCAGATTTTCTCAAGCAACACAGCAAGCGAGTGCAGT 1466
Qy 300 lArgGlyThrAlaAlaPheTyHisLeuProAlaAlaSerGlyCysLysGlnThrSe 320
Db 1467 CCGAGTCCAGCAGCTTCCAGTGCATCTCCCGCTGCCAGTGGTGCAAGCAAACTC 1526
Qy 320 rThrLysArgLysValGluGluMetGluValAspAspPheTyArgLysArgLe 340
Db 1527 TGTAAACCGAAAGTGGAGGAGATGGAGTGGATGACTTCTACGATGGATCAAGCGCT 1586
Qy 340 uTyAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerAr 360
Db 1587 CTATAATGAGGACAAATGCTCTGGAATGTGGGTCTGTATGTGGCACTGATTTATCAAG 1646
Qy 360 gGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1647 GCAAGAGGGCCATGCTCCCTGCTCCACCTTTCAGCCCTGTTTCTGTGATG 1698

RESULT 5
LOCUS AY412160
DEFINITION Mus musculus CCNI gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY412160
VERSION AY412160.1 GI:39768125
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1110)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1110
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
<1..>1110
/genes="CCNI"
/locus_tag="HCM4464"

ORIGIN
Alignment Scores:
Pred. No.: 1,07e-175 Length: 1110
Score: 1746.00 Matches: 345
Percent Similarity: 94.43% Conservative: 11
Best Local Similarity: 91.51% Mismatches: 14
Query Match: 88.99% Indels: 9
DB: Gaps: 1

US-09-736-250-1 (1-377) x AY412160 (1-1110)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGACCTTTGGAAACCAGAGATTGTTCTCTGTTGGAAGGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 TCCGAGGAGAGCCAGATGTGGAAGGTGAATGTCCGAAAATACCTACAAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysLysTyArgPheAsn 60
Db 121 TCTCCATCCACAGAGATGAAGTAATTCATATGTTGGCCAACTCAAAATACCAATTCAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTCTATCCAGAAACATTTGCTCTGGCAAGCAGCTTTTGGATAGGTTTTTGTCTACAGTA 240
Qy 81 LysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAAGCCCATCAAAATATTGTAATTGATTGCAATCAGCTGTTTTTTCTGGCTGCTAAG 300
Qy 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTCTAAAGGTATTGGCAAGACAGCTTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAGATTTTGGAGATGGAGAGATTTATTTCTGGATAATTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACGCTACCATTTGGATTTTCTTTCACA--TTCCATGCCATTTGGGTGTCA 478
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 479 GCTAGGCTCAGTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGT 538
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 539 CTGACCAAGCAGCTGCTTCTGATGCTGCTGCAACCACTTCTGCACTTTCAGAGGTGCC 598
```

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

```
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTyrLeuSer 220
Db 599 ATGCTTCTCTCGGCATGTTAGTCTGGAATGAGAAACTCATCTCGATTGCTTCTCT 658
Qy 221 LeuThrileGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 659 CTTACGATTGACATGCTTCAGAAAGCACAGAC-----TGTCGG 696
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 697 GAGCTGGTGGCATATCACCTTCTCTGCTGTCAGTCTGCTCTCTAAATTCGGTTAT 756
Qy 261 ValTyrArgProLeuLysHisLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 757 GTCTACCGTCCCTCAAGCACACCTGTGTACCTGTGCAAAAGGAGCATTCAAATTTACAT 816
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 817 CCTCTCTCTGCTCAGGCCAGATTTCTCCAGGACACACAGCCAGAGTCCAGTCC 876
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaSerGlyCysLysGlnThrSer 320
Db 877 CGAGTCCAGCAGCGCTTCCACCTGTCATCTCCCGCTGCCAGTGGGTGCAAGCAAACTCT 936
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysArgLeu 340
Db 937 GCTAAACGGAAGTGGAGGAGATGGAGTGGATGACCTTCTACGATGGGATCAAGCGCTC 996
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 997 TATATGAGGACATGTCCTGAGATGTTGGTCTGTATGTGGCAGCTGATTTATCAAGG 1056
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1057 CAAGAGGCGCCATGCTTCCCTGTCACCTTTGCGAGCTGTTCTGTCATG 1107

RESULT 6
LOCUS CR754276 1085 bp mRNA linear EST 02-SEP-2004
DEFINITION Rattus norvegicus muscle Sprague-Dawley Rattus norvegicus
cDNA clone GP0AAA12ZH09, mRNA sequence.
ACCESSION CR754276
VERSION CR754276.1 GI:51866233
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (Bases 1 to 1085)
AUTHORS Cros, N., Tkatchenko, A.V., Pisani, D.F., Leclerc, L., Leger, J.J.,
Marini, J.F. and Dechesne, C.A.
TITLE Analysis of altered gene expression in rat soleus muscle atrophied
by disuse
JOURNAL J. Cell. Biochem. 83 (3), 508-519 (2001)
MEDLINE 21479502
PUBMED 11596118
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Genoscope sequence ID: GP0AAA12ZH09CPL.
Location/Qualifiers
1. 1085
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="GP0AAA12ZH09"
/sex="Female"
/tissue_type="muscle"
/clone_lib="Rattus norvegicus muscle Sprague-Dawley"
/notes="Vector: pCR11-TOPO; Pietu G., Cros N., Leger J.J.,
```

Dechesne C.A. Subtracted library from atrophied and control soleus muscles subtraction was performed according to Diatchenko et al. (Diatchenko L, Lau YF, Campbell AP, Chenchik A, Moqadam F, Huang B, Lukyanov S, Lukyanov K, Gurekaya N, Sverdlov ED, Siebert PD. Suppression subtractive hybridization: a method for generating differentially regulated or tissue-specific cDNA probes and libraries. Proc Natl Acad Sci U S A. 1996; 93 :6025-30) Rats were female Sprague Dawley between 200 and 220g. Soleus muscle atrophy was performed by 14 days of hindlimb suspension."

ORIGIN

Alignment Scores: 2.45e-159 Length: 1085
Pred. No.: 1593.00 Matches: 318
Score: 1593.00
Percent Similarity: 94.54% Conservative: 11
Best Local Similarity: 91.38% Mismatches: 18
Query Match: 81.19% Indels: 3
DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CR754276 (1-1085)

```
Qy 31 ValArgLysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValIleGln 50
Db 1 GTACCAAAATATCTCAAAACCAGATGTTTCTCCATCCAGAGAGACGATA-ATTGAG 59
Qy 51 TrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSer 70
Db 60 TGGTTGGCCAACTCAATACCACTTCACTTATCCAGAAACATTTTGTCTGCGAAGC 119
Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
Db 120 AGTCTTTGGATAGTGTGTTAGCTACAGTAAAGCTCATCCAAATATTTGAATGTATT 179
Qy 91 AlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
Db 180 GCATATCAGCTGTTTTTCTGGCTGTCTAAGACTGTTGAAGAAGATGAGAAATTTCCAGTG 239
Qy 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArgMet 130
Db 240 CTTAAAGGTATTGGCAAGACAGAGTCTTCTGTGGATGTTCTCTCATCTGAGATTTTCCAGATG 299
Qy 131 GluArgIleLeuLeuAspLysLeuAsnTyrAspLeuHisThrAlaThrProLeuAspPhe 150
Db 300 GAGAGAAATTTATCTGGATAAAATTGAATTTGGGATCTTCCACAGCCACACCATTTGGATTTT 359
Qy 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 360 CTTTCAATTTTCCATGCTTCAAGAGTCCATGCTTCACTAGGCTTCACTTTTTCAGTTTGCCC 419
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 420 AGATTGAGCCCGTCTCAACACTTGGCAGTCTCTGACTAAGCAGCTACTTCACTGATGSGCC 479
Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
Db 480 TGCAACCAACTTCTGCAGTTTCAAGAGTCCATGCTTCTGCTGGCCATGGTTAGTCTGGAA 539
Qy 211 MetGluLysLeuLeuProAspTyrLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
Db 540 ATGAGAAACTCATTTCCCGATTTGCTTCTCTTCAATTTGAACCTGCTTCAAGAACACAG 599
Qy 231 MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisHisLeuSerThrLeu 250
Db 600 ATGGACAGCTCCCAAGTTGATCCCACTGTCTGGAGCTGGTGGCATATCACCTTCTGCTCTG 659
Qy 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
Db 660 CAGTCTTCCCTGCTCTAAATTTCCGTTTATGCTTACCGTCCCTTCAAGACACACCTGGTG 719
Qy 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
Db 1085
```

Db 720 ACCTGTGCAAAAGGAGCGTTCAANTATACATCCCTCTCTATCTCAGGCCAGATTCTCC 779
 QY 291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeu 310
 Db 780 AAGGACACAGACAGCCAGAGTGGCAGTCCAGAGTCCAGAGCTTCCACCTCCATCTC 839
 QY 311 ProAlaAlaSerGlyCysGlyGlnThrSerThrLysArgLysValGluGluMetGluVal 330
 Db 840 CCTGCTGTGAGTGGTGCAGCATACCTCTGCTAAACGMAAGTGGAGGAGATGGAGGTG 899
 QY 331 AspAspPhe-TyrAspGlyLysArgLeuTyrHisGlnAspAsnValSerGluAsnVa 350
 Db 900 GACGACTTGTAAATGACGGGATCAACGGCTCTTATAACGA-GACAGTGTGTCGGAATGT 958
 QY 350 LcylSerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysProPr 370
 Db 959 GGGCTCTGTGTTTGCATGATTATCCAGACAGAGGGGCCATGCCCTCCCTGTCCACC 1018
 QY 370 oLeuGlnProValSerValMet 377
 Db 1019 TTTGCGAGCTGTATCTGTAATG 1040

RESULT 7

CN647834

LOCUS

DEFINITION ILLUMIGEN MCQ 29127 Katze MMPL2 Macaca mulatta cDNA clone
 IBUW:7202 5' similar to Bases 1 to 967 highly similar to human
 CCNI (Hs.369110), mRNA sequence.

ACCESSION

CN647834

VERSION

CN647834.1

KEYWORDS

EST.

SOURCE

Macaca mulatta (rhesus monkey)

ORGANISM

Macaca mulatta

REFERENCE

Katze,M.G., Thomas,M., Korth,M., Iadonato,S.P. and Magnus,C.L.

Large-scale Rhesus Macaque cDNA Sequencing

Unpublished (2003)

Contact: C. Magnus

Illumigen Biosciences Inc.

2203 Airport Way S, Suite 450, Seattle, WA 98134, USA

Tel: 2063780400

Fax: 2063780408

Email: cmagness@illumigen.com

Sequenced on 2004.03.25. 786 Q20 bases.

PCR Primers

FORWARD: CCCTCACTAAGGGAACAAA

BACKWARD: CACTATAGGCGAATTGGGTA

Insert Length: 967 Std Error: 0.00

Plate: CL000123 row: A column: 11

Seq primer: CCCTCACTAAGGGAACAAA

POLYA=No.

FEATURES

source

1..967

/organism="Macaca mulatta"

/mol_type="mRNA"

/strain="Indian"

/db_xref="taxon:9544"

/clone="IBUW:7202"

/sex="male"

/dev_stage="newborn infant"

/lab_host="E. coli SOLR"

/clone_lib="Katze MMPL2"

/note="Organ: placenta; Vector: Uni-ZAP XR; Site 1: EcoR

I; Site 2: Xho I; Created from Stratagene ZAP-CDNA

Synthesis kit (catalog #200400) and ZAP-CDNA Gigapack III

Gold Cloning Kit (Catalog #200450)"

ORIGIN

Alignment Scores:

Pred. No.:

1.06e-157 Length: 967

Score: 1577.00 Matches: 302
 Percent Similarity: 99.67% Conservative: 1
 Best Local Similarity: 99.34% Mismatches: 1
 Query Match: 80.38% Indels: 0
 DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CN647834 (1-967)

QY 74 AspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIleAlaIleSer 93
 Db 1 GACAGGTTTTTAGTACTCCGTAAGGCTCATCCAAATACCTTGAGTTGTATTCGAATCAGC 60
 QY 94 CysPhePheLeuAlaLysThrValGluGluAspGluArgIleProValLeuLysVal 113
 Db 61 TGTITTTTCTAGCTGCCAGACTGTTGAGGAGATGAGAGAAATTCAGTACTTAAGGTA 120
 QY 114 LeuAlaArgAspSerPheCysGlyCysSerSerGluIleLeuArgMetGluArgIle 133
 Db 121 TTGGCAAGAGACAGTTTCTGTGGATGTTCTCATCTCGAAATTTTGAAGATGGAGAATT 180
 QY 134 IleLeuAspLysLeuAenTTPAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
 Db 181 ATTCTGGATAGTTGAATGGGATCTTCACAGCCACACCATTTGGATTTTCTTCATATT 240
 QY 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173
 Db 241 TTCCATGCTATTGGGTATCACTAGGCTCAGTTACTTTTTCAGTTTGCCCAATTCAGC 300
 QY 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGln 193
 Db 301 CCATCTCAATTTGGCAGTCTTACCAGCAACTACTTCACCTGTATGGCTGCAACCA 360
 QY 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLys 213
 Db 361 CTCTGCAATTCAGAGATCCATGCTGCTCTGCCATGTTAGTCTGGAATTCGAGAAA 420
 QY 214 LeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
 Db 421 CTTATTCTTAATTTGGCTTTCTCTTACAAATTGAATGCTTTCAGAAAGCACAGATGGATAGC 480
 QY 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSer 253
 Db 481 TCCAGTGTGATCCACTGTGCGGAGCTGTGTGCCACATCACCTTTCTACTCTGCAGTCTTC 540
 QY 254 LeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAsp 273
 Db 541 CTGCCTCTAAATTTCCGTTTATGTTCTACCGTCCCTCAAGCACACCTCTGTGACTGTGAC 600
 QY 274 LysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsn 293
 Db 601 AAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGACAAC 660
 QY 294 SerLysProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAla 313
 Db 661 AGCAAGCCAGAAGTGCAGGTACAGAGTACAGACCTTTTACCATCATCTCTCCAGTGTCC 720
 QY 314 SerGlyCysLysGlnThrSerThrLysArgLysValGluGluMetGluValAspAspPhe 333
 Db 721 AGTGGGTGCAGAGAGACCTCTGCTAAACGAAAGTAGAGAGATGGAAGTGCATCTTC 780
 QY 334 TyrAspGlyLysLysArgLeuTyrAsnGluAspAsnValSerGluAsnValGlySerVal 353
 Db 781 TATGATGAATCAAAAGGGCTCTATAATGAAGATAATGTCTCAGAAAAATGTGGTCTGTG 840
 QY 354 CysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCysProLeuGlnPro 373
 Db 841 TGTGGCAGTGAATTTATCAAGCAAGAGGGACATGCTTCCCTTGTCCACCTTTTGACGCT 900
 QY 374 ValSerValMet 377
 Db 901 GTTCTGTCTCATG 912

RESULT 8

C0646424 992 bp mRNA linear EST 23-JUL-2004
 LOCUS ILLUMIGEN MCQ 39156 Katze MPPB2 Macaca mulatta cDNA clone
 DEFINITION IBTUM:23419 5' similar to Bases 612 to 991 highly similar to human
 Unigene Hs.518825, mRNA sequence.
 C0646424
 C0646424.1 GI:50567918
 EST.
 KEYWORDS
 SOURCE
 ORGANISM
 Macaca mulatta (rhesus monkey)
 Macaca mulatta
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 Cercopithecinae; Macaca.
 1 (bases 1 to 992)
 Katze.M.G., Thomas.M., Korth.M., Iadonato.S.P. and Magness.C.L.
 Large-scale Rhesus Macaque cDNA Sequencing
 Unpublished (2003)
 CONTACT: C. Magness
 Illumigen Biosciences Inc.
 2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
 Tel: 2063780400
 Fax: 2063780408
 Email: cmagness@illumigen.com
 Sequenced on 2004.05.25 741 Q20 bases. Library Preparation: Prof.
 Michael Katze Lab at University of Washington DNA Sequencing:
 Illumigen Biosciences Inc. For further information, see
 http://www.macaque.org
 PCR PRIMERS
 FORWARD: CCCTCACTAAAGGAACAAAA
 BACKWARD: CACTATAGGCGAATGGGTA
 Insert Length: 992 Std Error: 0.00
 Plate: C000214 row: F column: 05
 Seq primer: CCCTCACTAAAGGAACAAAA
 POLYA-Yes.
 FEATURES
 Location/Qualifiers
 1..992
 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBTUM:23419"
 /sex="male"
 /tissue_type="blood"
 /cell_type="PBMC"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katze MPPB2"
 /note="Vector: pDONR 222; Site 1: BsrG I; Site 2: BsrG I;
 Created from CloneMiner cDNA Library Construction kit
 (catalog #18249-029)"
 ORIGIN
 Alignment Scores:
 Pred. No.: 3.44e-153 Length: 992
 Score: 1535.00 Matches: 308
 Percent Similarity: 96.06% Conservative: 9
 Best Local Similarity: 93.33% Mismatches: 8
 Query Match: 78.24% Indels: 5
 DB: 7 Gaps: 0
 US-09-736-250-1 (1-377) x C0646424 (1-992)
 QY 13 SerPheLeuLeuGluValAlaIleThrArgGluAlaGlnMetTrpLysValAsnValArg 32
 DB 6 TCTTCTCTGTTGGAAAGGCAATCACTAGGAGGCGAGATGTGGAAGTGAATGTGGG 65
 QY 33 LysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValIleGlnTrpLeu 52
 DB 66 AAAATGCTTCAATCAGAAATGTTTCTCCATCCAGAGAGATGAAGTAATCAATGGCTG 125
 QY 53 AlalysLeuLysTyGlnPheAsnLeuTyProGluThrPheAlaLeuAlaSerSerLeu 72
 DB 126 GCCAAACTCAAGTACCAATTCACCTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTT 185

QY 73 LeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrlSerCysIleAlaIle 92
 DB 186 TTGGACAGAGTTTGTAGTACCGTAAAGGCTCATCCAAATACTTGTAGTGTATGCAATC 245
 QY 93 SerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProValLeuLys 112
 DB 246 AGCTGTTTTTCTTAGCTGCCAAGACTGTTGAGAAAGATGAGAGAAATCCAGTACTAAG 305
 QY 113 ValLeuAlaArgAspSerPheCysGlyCysSerSerGluLeuLeuArgMetGluArg 132
 DB 306 GTATTGGCAAGACAGACTTTCTGTGGATGTTCTCATCTGAAATTTTGAGAAATGGAGAGA 365
 QY 133 IleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHis 152
 DB 366 ATTATTCTGATAAGTTGAATTTGGATCTTTCACACAGCCACACCATTTGGATTTTCTTCAT 425
 QY 153 IlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeu 172
 DB 426 ATTTTCCATGCTATTTGGGTATCAACTAGGCTCAGTTACTTTTCAGTTTGCCCAAAATG 485
 QY 173 SerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsn 192
 DB 486 AGCCCATCTCAATTTGGCAGTCTTACCAGCAACTACTTCACTGTATGGCTGCAAC 545
 QY 193 GlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGlu 212
 DB 546 CAACCTCTGCAATTCAGAGATCCATGCTTGTCTGCGCATGTTAGTCTGGAAATGGAG 605
 QY 213 LysLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAsp 232
 DB 606 AAACCTTATCTTAATTTGGCTTTCTTACAAATTTGAATGCTTTCAGAAAGCACAGATGAT 665
 QY 233 SerSerGlnLeuLeuHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSer 252
 DB 566 AGCTCCCACTGATCCACTGTGGGAGCTTGTGGACATCACCTTTTCTACTCTGCAGTCT 725
 QY 253 SerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCys 272
 DB 726 TCCCTGCTCTAAATTCGGTTTATGCTACGCTCCCTCAATCACACGCTGTGACCTGT 785
 QY 273 AspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAsp 292
 DB 786 GACAAAGAGTGTTCAGATTACATCCCTCTTCTGTCAGGCGCCAGACTTTTCTCCAGAC 845
 QY 293 AsnSerLysProGluValProValArgGly-ThrAlaAla-PheTyrHisHisLeuProA 312
 DB 846 AACAGCAGCCAAAGTGGCCAGTCAAGGTTACAGCAGCCTTTTACCATCTTCTCCCA 905
 QY 312 laAla-SerGlyCysLysGln-ThrSerThrLysArgLysValGluMetGluValAs 331
 DB 906 CTGCCAGGGGGTGCAAGCAAAACCTCTGCCAAACGCAAAAAAAGAGAAAGAAATGGA 965
 QY 331 p-AspPheTyrAspGlyIle 337
 DB 966 AAGAAATTTCTATGAAGGAATC 985
 RESULT 9
 B0673277
 LOCUS B0673277 920 bp mRNA linear EST 15-JUL-2002
 DEFINITION AGENCOURT_8354951 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275333
 5', mRNA sequence.
 ACCESSION B0673277
 VERSION B0673277.1 GI:21784111
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 920)
 NTH-MGC http://mgs.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)


```
/clone_lib="Katze WMBR"
/notes="Organ: brain; Vector: Uni-ZAP XR; Site 1: EcoR I;
Site 2: Xho I; Created from Stratagene ZAP-cDNA Synthesis
kit (catalog #200400) and ZAP-cDNA Gigapack III Gold
Cloning kit (Catalog #200450)"

ORIGIN
Alignment Scores:
Pred. No.: 3.06e-143 Length: 983
Score: 1442.00 Matches: 281
Percent Similarity: 98.95% Conservativeness: 3
Best Local Similarity: 97.91% Mismatches: 0
Query Match: 73.50% Indels: 0
DB: 7 Gaps: 0

US-09-736-250-1 (1-377) x CN646807 (1-983)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 122 ATGAAGTTTCCAGGCTTGGAAACCCAGAGATTGCTTCTCTGTTGGAAAGGCATC 181
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 182 ACTAGGGAAGCCAGATGTGGAAAGTGAATGCGGAAATGCTTCAATCAGATGTT 241
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 242 TCTCCATCCAGAGATGAAGTAATCAATGGTGCCCAACTCAAGTACCAATTCAAC 301
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 302 CTTTACCAGAAACATTTGCTGCTGAGCAGTCTTTTGACAGGTTTTAGCTACCGTA 361
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 362 AAGGCTCATCAAAATCTAGTGTATGCAATCAGCTGTTTTTCTAGCTGCCAAG 421
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 422 ACTGTTGAGGAAGATGAGAAATTCAGTATCAAGGTAATGGCAAGACAGTTCCTGT 481
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 482 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTAATCTGGATAAGTTGAAATGG 541
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 542 GATCTTCACAGCCACCACTTGGATTTCTCATATTTTCCATGCTATTTGCGGTATCA 601
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 602 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 661
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 662 CTTACCAAGCAACTACTTCACTGTATGCTGCAACCAACTCTGCAATTCAGAGGATCC 721
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 722 ATGCTTGCTCTGGCCATGTTAGTCTGGAAATGAGAAACTTATCTCTAATTTGGCTTCT 781
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 782 CTTACAATTGAATGCTTCAGAAAGCACAGATGATAGTCCCAAGTTCATCCAGTCTCGG 841
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 842 GAGCTTGTCGACATCACTCTTACTCTGAGTCTTTCCCTGCTCTAAATTCCTGTTAT 901
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 902 GTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGGAATGTTCAAAATTACTT 961

281 ProSerSerValProGlyPro 287
662 CCTCTCTGTGTCCACGCCCA 982

RESULT 11
BUS28295
LOCUS BUS28295
DEFINITION BUS28295 920 bp mRNA linear EST 13-SEP-2002
AGENCOURT_1018275 NIH_MGC_101 Homo sapiens cDNA clone
IMAGE:6538220 5', mRNA sequence.
BUS28295
VERSION BUS28295.1 GI:22838736
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 920)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2702 row: g column: 20
High quality sequence stop: 651.
Location/Qualifiers
1..920
/organism="Homo sapiens"
/db_mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6538220"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."

ORIGIN
Alignment Scores:
Pred. No.: 4.51e-143 Length: 920
Score: 1440.00 Matches: 291
Percent Similarity: 95.77% Conservativeness: 3
Best Local Similarity: 94.79% Mismatches: 11
Query Match: 73.39% Indels: 3
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BUS28295 (1-920)

Qy 11 ArgLeuSerPheLeuLeuGluLysAlaIleThrArgGluAlaGlnMetTrpLysValAsn 30
Db 2 AGATTTGTTCTTCTGTTGGAAAGGA-ATCCTAGGGAAGCAGAGATGTGGAAAGTGAAT 60
Qy 31 ValArgLysMetProSerAsnGlnAsnValSerProSerGlnArgAspGluValIleGln 50
Db 61 GTGCGGAAATGCTTCAATCAGATGTTTCTTCATCCAGAGATGAGATGAATTCATCA 120
Qy 51 TrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAlaLeuAlaSer 70
Db 121 TGGCTGGCCAACTCAAGTACCAATCAACCTTTACCCAGAAACATTTGCTCTGGTAGC 180
Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
```


181 AGTCTTTGGATAGTGTCTTTAGTACCTACCGTAAGGCTCATCCAAATACTTCAGTTGATT 240
 Qy
 91 AlalileSerCysPheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
 Db
 241 GCAATCAGCTGTTTTTCTAGCTGCCAAGACTGTTGAGGAAGATGAGAGAAATCCAGTA 300
 Qy
 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluLeuLeuArgMet 130
 Db
 301 CTAAGGTATTTGGCAGAGACAGTTCTCTGTGGATGTTCTCATCTGAAATTTTGAAGATG 360
 Qy
 131 GluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
 Db
 361 GAGAGAAATATCTCGATAGTGAATGGGATCTTCACACAGCCACACCATTCGATTTT 420
 Qy
 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
 Db
 421 CTTATATTTTCCAGGCAATGTCAGTGTCACTAGGCTTCAGTTACTTTTCAGTTTCC 480
 Qy
 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
 Db
 481 AAATTTAGCCCATCTCAACATTTGGCAGTCTTACCAAGCACTTCTTCACTGTATGGCC 540
 Qy
 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
 Db
 541 TGCAACCAACTTCTGCAATTCAGAGATCCATGCTTCTGGCCATGGTTAGTCTGAA 600
 Qy
 211 MetGluLysLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
 Db
 601 ATGAGAAACTCATCTCTGATGTCCTTCTTCAACATTTGAACCTGCTTCAGAAAGCACAG 660
 Qy
 231 MetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisLysLeuSerThrLeu 250
 Db
 661 ATGATAGTCCCAAGTTGATCCATTTGTCGGAGCTTGTGGCACAATCACTTTTACTCTG 720
 Qy
 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
 Db
 721 CAGTCTTCCCTGCTCTGAAATTCGGTTATGCTTACCTCCCTTCAAGCACACCTCGGTG 780
 Qy
 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
 Db
 781 ACCCTGTGACAGGAGGTTCAGATTACATCCCTCTCTGTCACCAAGCCCAACTTCTCC 840
 Qy
 291 LysAsnSerLys-ProGluValProValArgGlyThrAlaAla-PheTyrHisHisL 310
 Db
 841 AAGGACAACAGCAAGCCAGATGCCAGTCCGAGCAGACAGCAGCCCTTTTACCATCATC 900
 Qy
 310 euProAlaAlaSerGly 315
 Db
 901 TTCCAGTTGCCAATGGG 917

RESULT 12
 BU538306
 LOCUS
 DEFINITION AGENCOURT_10181155 NIH_MGC_107 Homo sapiens cDNA clone
 IMAGE:6568838 5', mRNA sequence.
 BU538306
 VERSION BU538306.1 GI:22848747
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 963)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-x@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Plate: LNCM2755 row: c column: 14
 High quality sequence stop: 646.
 Location/Qualifiers
 1..963
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6568838"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_107"
 /notes="Organ: breast; Vector: pOTB7; Site: 1: EcoRI; Site: 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 3 94e-142 Length: 963
 Score: 1431.50 Matches: 291
 Percent Similarity: 94.21% Conservative: 2
 Best Local Similarity: 93.57% Mismatches: 11
 Query Match: 72.96% Indels: 7
 DB: 5 Gaps: 1

US-09-736-250-1 (1-377) x BU538306 (1-963)

Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
 Db 3 AAGTTTCCAGGGCTTTGGAAAACCCAGAGATTGCTTCTGTTGTGAAAAGGCAATCACT 62
 Qy 22 AtgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
 Db 63 AGGGAAGCACAGATGTGGAAAGTGAATGCGGAAATGCTTCAATCAGAAATGTTCT 122
 Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
 Db 123 CCATCCAGAGAGATCAAGTAATTCATTCGTCGCCAAACTCAAGTACCAATTCACCTT 182
 Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
 Db 183 TACCCAGAAACATTTTCTGCTAGCAGCTCTTTTGGATAGGTTTTTAGCTACCGTAAAG 242
 Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
 Db 243 GCTATCCAAATVACTTGTGATGTATGCATCAGCTGTTTTTCTAGCTGCAAGACT 302
 Qy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
 Db 303 GTTGAGGAAGATGAGAGAAATTCAGTACTAAAGTATTGGCAAGACACAGTTTCTGTGGA 362
 Qy 122 CysSerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAsp 141
 Db 363 TGTTCCTCATCTGAAATTTTGAATGGAGAGAAATTAATTCGTGATAGTGAATGGAT 422
 Qy 142 LeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThr 161
 Db 423 CTTACACAGCCACACCATTTGATTTCTCATATTTTCCATGCTTTCAGCTCACT 482
 Qy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
 Db 483 AGGCTTCAGTACTTTTTCAGTTTGGCCAAATTCAGCCCATCTCACATTTGGCAGTCTT 542
 Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuPheArgGlySerMet 201
 Db 543 ACCAAGCACTACTTTCACCTGTATGGCTGCAACCAACTTCTGCAATTCAGAGATCCATG 602

Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSerLeu 221
 |||||
 Db 603 CTTCCTCTGGCCATGGTGTAGTCTGAAATGAGAACTCATTCCTGATGGCTTCTCTT 662
 |||||
 Qy 222 ThrileGluLeuLeuGlnLysAlaGlnMetAspSerGlnLeuLysCysArgGlu 241
 |||||
 Db 663 ACAATTGACCTGCTTCAGAAAGCAGATGATAGTCCCGAGTTGATCCATTGCGGGAG 722
 |||||
 Qy 242 LeuValAlaHisLeu-SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVa 261
 |||||
 Db 723 CTTCGTGGCACATCACCTTTCTACTCTGCAGTCTTCCTCGCTCTGAAATTCGGTTATGT 782
 |||||
 Qy 261 lTyrArgProLeuLysHisThrLeuValThrCysAspLysGly-ValPheArgLeuHisP 281
 |||||
 Db 783 CTACCGTCCCCCTCAGCACACCTCGGTGACCTGTGACAAAGAAAGTGGTCAGATTACATC 842
 |||||
 Qy 281 roSerSerValPro-GlyProAspPheSerLysAsp-AsnSerLysProGluValProVa 300
 |||||
 Db 843 CCTCTCTGTGTCAGGGCCCGAGCTTCTCCAGGACAAACAGCAAGCCACAGA----- 894
 |||||
 Qy 300 lArgGlyThrAlaAlaPheTyrHis 308
 |||||
 Db 895 -AGTGGCCAGTCCAGAGGGTACCAC 918
 |||||

RESULT 13

CF552849

LOCUS

DEFINITION AGNCOURT 15595023 NIH_MGC_183 Homo sapiens cDNA clone
 IMAGE:30529710 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 841)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-re@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein

cDNA Library Preparation: Invitrogen Corp

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: NDAM617 row: 1 column: 07

High quality sequence stop: 738.

Location/Qualifiers

1. .841

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:30529710"

/lab_host="DH10B-Tona (T1 and T5 phage resistant)"

/clone_lib="NIH_MGC_183"

/note="Organ: Pooled muscle (cardiac and skeletal);

Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2:

NotI; Library is oligo-dT primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.7. Library was constructed by Invitrogen."

ORIGIN

Alignment Scores:

Pred. No.: 2,02e-141

Score: 1424.00

Length: 841

Matches: 279

Percent Similarity: 99.64%
 Best Local Similarity: 99.64%
 Query Match: 72.58%
 DB: 7
 Gaps: 0
 Conservative: 0
 Mismatches: 1
 Indels: 1

US-09-736-250-1 (1-377) x CF552849 (1-841)

Qy 71 SerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeuSerCysIle 90
 |||||
 Db 3 AGTCTTTTGGATAGTTTTTTAGCTACCGTAAGGCTCATCCAAATACTTTGAGTTGATT 62
 |||||
 Qy 91 AlaLysSerCysPheLeuAlaLysThrValGluGluAspGluArgIleProVal 110
 |||||
 Db 63 GCAATCAGCTGTTTTTCTTAGCTGCCAAGACTGTTGAGGAAGATGAGAAATTCAGTA 122
 |||||
 Qy 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIleLeuArgMet 130
 |||||
 Db 123 CTAAGGATTATGGCAAGACAGCTTTCTGTGGATGTTCTCTCATCTGAAATTTTCAGAAATG 182
 |||||
 Qy 131 GluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrProLeuAspPhe 150
 |||||
 Db 183 GAGAGAATTATTTCTGGATAAGTTGAATTTGGGATCTTCACACAGCCACACCATTTGGATTTT 242
 |||||
 Qy 151 LeuHisThrPheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
 |||||
 Db 243 CTTCAATATTTTCCATGCTGAGTGTCAACTAGGCTCAGTTTACGTTTTCAGTTTGGCCC 302
 |||||
 Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
 |||||
 Db 303 AATTTAGCCCATCTCAACATTTGGCAGTCTTTACCAAGCAACTTCTTCACTGATGGCC 362
 |||||
 Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGlu 210
 |||||
 Db 363 TGCAACCAACTTCTGCAATTCAGAGGATCCATGCTTCTCTGGCATGGTTAGTCTGGAA 422
 |||||
 Qy 211 MetGluLysLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
 |||||
 Db 423 ATGGAGAAACTCATTTCTGATTGGCTTTCTTTACAATTGAACCTGCTTCAGAAAGCACAG 482
 |||||
 Qy 231 MetAspSerSerGlnLeuLysCysArgGluLeuValAlaHisHisLeuSerThrLeu 250
 |||||
 Db 483 ATGGATAGCTCCCGATTTGATCCATTGTCGGAGGCTTGTGGCACATCACCTTTCTACTCTG 542
 |||||
 Qy 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
 |||||
 Db 543 CAGTCTTCCCTGCTCTGAAATTCGGTTTATGCTTACCGTCCCTCTCAAGCACACACCTTGGTG 602
 |||||
 Qy 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
 |||||
 Db 603 ACCTGTGACAAAGAGGT-TTTCAAGATTACATCCCTCTCTGTCCAGGCCACAGACTTCTCC 661
 |||||
 Qy 291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisLeu 310
 |||||
 Db 662 AAGGACAAACAGCAAGCCAGAGTGCCAGTACAGAGTACAGAGCTTTTACCATCATCTC 721
 |||||
 Qy 311 ProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMetGluVal 330
 |||||
 Db 722 CCAGCTGCCAGTGGTGCAGAGCAGACCTCTACTAAACGCAAGTAGAGAAATGGAAGTG 781
 |||||
 Qy 331 AspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGluAsnVal 350
 |||||
 Db 782 GATGACTTCTATGATGGAATCAACAGCGCTCTATAATGAAGATAATGTCTCAGAAAAATGTG 841
 |||||

RESULT 14

CD107527

LOCUS

DEFINITION

AGNCOURT 14020471 NIH_MGC_179 Homo sapiens cDNA clone

IMAGE:30364743 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

EST.

CD107527.1

GI:30760737

CD107527 906 bp mRNA linear EST 15-MAY-2003
 AGNCOURT 14020471 NIH_MGC_179 Homo sapiens cDNA clone
 IMAGE:30364743 5', mRNA sequence.

CD107527

CD107527

CD107527.1

GI:30760737

EST.

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

Homo sapiens

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:54 ; Search time 106.061 Seconds
(without alignments)
1374.757 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGLNQLRSLFLEKAI.....LSRQGHASCPPLQPVSVW 377

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	377	100.0	377	2	AAW21965 Human cyc
2	377	100.0	377	3	AAY52185 Human cyc
3	377	100.0	377	6	ABR39934 Human pro
4	377	100.0	377	8	ADP12615 Protein e
5	296	78.5	334	7	AAE37938 Human CGD
6	276	73.2	377	8	ABM80569 Tumour-as
7	153	40.6	300	8	ADN01131 Human cel
8	131	34.7	131	3	AAQ01903 Human sec
9	34	9.0	41	4	AAO11635 Human pol
10	14	3.7	14	2	AAW21966 Human cyc
11	10	2.7	10	6	ABJ20156 MHC bindi
12	9	2.4	9	5	ABG32308 HLA-A2 as
13	9	2.4	9	6	ABJ19986 MHC bindi
14	9	2.4	462	5	AAW85684 NBP46 roo
15	9	2.4	462	5	AAU78818 Dolichos
16	8	2.1	269	7	ADH44940 Human TCH
17	8	2.1	391	5	AAU81226 Human lun
18	8	2.1	391	5	ADL06559 Human tum
19	8	2.1	416	6	ABO01333 Human pro
20	8	2.1	416	7	ADH44925 Human TCH
21	8	2.1	416	8	ADN96038 Human NOV
22	8	2.1	545	4	AAE65649 Novel pro
23	8	2.1	545	8	ADI29256 Human MAR
24	8	2.1	667	2	AAW94919 Rat phero
25	7	1.9	12	3	AAY91912 Peptide 2

26	7	1.9	12	8	ADO04715	Human int
27	7	1.9	21	8	AAW93064	Human Tan
28	7	1.9	39	8	ADO24383	Human PRO
29	7	1.9	52	2	AAW93061	Human Tan
30	7	1.9	58	3	AAE43717	Human can
31	7	1.9	63	2	AAW93058	Human Tan
32	7	1.9	68	4	AAW96280	Human rep
33	7	1.9	68	4	ABE10911	Human ova
34	7	1.9	73	4	AAW82834	Human imm
35	7	1.9	74	4	AAU43120	Propionib
36	7	1.9	74	6	ABM39639	Propionib
37	7	1.9	85	7	ADF07949	Bacterial
38	7	1.9	88	4	ABG04101	Novel hum
39	7	1.9	88	5	ABP03890	Human ORF
40	7	1.9	95	2	AAAY37852	Chlamydia
41	7	1.9	96	5	ABM80038	Human C2H
42	7	1.9	97	4	AAO01328	Human pol
43	7	1.9	98	4	AAU22330	Human car
44	7	1.9	98	7	ADE46298	Human car
45	7	1.9	98	8	ADJ07716	Human car
46	7	1.9	104	4	ABM68248	Drosophil
47	7	1.9	108	4	AAU66549	Propionib
48	7	1.9	108	6	ABM63068	Propionib
49	7	1.9	110	4	ABE42544	Peptide #
50	7	1.9	110	4	AAW36358	Peptide #
51	7	1.9	110	4	AAW76247	Human bon
52	7	1.9	110	4	AAW63432	Human bra
53	7	1.9	115	2	AAW04930	Interfero
54	7	1.9	122	8	ADQ65672	Novel hum
55	7	1.9	123	4	AAO04444	Human pol
56	7	1.9	125	4	AAU60950	Propionib
57	7	1.9	125	6	ABM57469	Propionib
58	7	1.9	136	2	AAW93063	Human Tan
59	7	1.9	139	4	ABG08538	Novel hum
60	7	1.9	146	2	AAW00014	Chimeric
61	7	1.9	146	2	AAW99491	Chimeric
62	7	1.9	146	2	AAW99495	Chimeric
63	7	1.9	146	2	AAW30899	Synthetic
64	7	1.9	146	2	AAW30895	Synthetic
65	7	1.9	146	2	AAW30900	Synthetic
66	7	1.9	146	2	AAW22902	Biologica
67	7	1.9	146	2	AAW10152	Properly
68	7	1.9	146	2	AAW26198	Obesity p
69	7	1.9	146	2	AAW26199	Obesity p
70	7	1.9	146	2	AAW26190	Obesity p
71	7	1.9	146	2	AAW18628	Obesity p
72	7	1.9	146	2	AAW18622	Obesity p
73	7	1.9	146	2	AAW18627	Obesity p
74	7	1.9	146	2	AAW32579	Anti obes
75	7	1.9	146	2	AAW32580	Anti obes
76	7	1.9	146	2	AAW34485	Obesity p
77	7	1.9	146	2	AAW34494	Obesity p
78	7	1.9	146	2	AAW34493	Obesity p
79	7	1.9	146	2	AAW62605	Preferred
80	7	1.9	146	2	AAW69688	Obesity p
81	7	1.9	146	2	AAW69692	Obesity p
82	7	1.9	146	2	AAW69693	Obesity p
83	7	1.9	146	2	AAW51002	Anti-obes
84	7	1.9	146	2	AAW51003	Anti-obes
85	7	1.9	146	2	AAW50998	Anti-obes
86	7	1.9	146	2	AAW71301	Obesity p
87	7	1.9	146	2	AAW71310	Obesity p
88	7	1.9	146	2	AAW71835	Obesity p
89	7	1.9	146	2	AAW71844	Obesity p
90	7	1.9	146	2	AAW53336	Obesity p
91	7	1.9	146	2	AAW53335	Obesity p
92	7	1.9	146	2	AAW53331	Obesity p
93	7	1.9	148	2	AAW71848	Obesity p
94	7	1.9	150	4	ABE17457	Human ner
95	7	1.9	157	3	AAW70930	Human zil
96	7	1.9	157	3	AAW70934	Human zil
97	7	1.9	157	3	AAW70932	Human zil
98	7	1.9	157	3	AAW70929	Human zil

99	7	1.9	157	3	AA95301	Aay95301 Human int	172	7	1.9	193	7	ADH52125	Novel hum
100	7	1.9	157	7	ADH89073	Adh89073 Human zil	173	7	1.9	193	7	ADH49980	Novel hum
101	7	1.9	157	7	ADH89076	Adh89076 Human zil	174	7	1.9	193	7	Adi25490	Novel hum
102	7	1.9	157	7	ADH89071	Adh89071 Human zil	175	7	1.9	193	7	ADH90283	Novel hum
103	7	1.9	157	7	ADH89070	Adh89070 Human zil	176	7	1.9	193	7	Adi25660	Novel hum
104	7	1.9	163	3	AA97069	Aay97069 Human IL-	177	7	1.9	193	7	ADH97834	Novel hum
105	7	1.9	167	2	AAW93060	Aay93060 Human Tan	178	7	1.9	193	7	Adi03682	Novel hum
106	7	1.9	167	3	AA96932	Aay96932 Human IL-	179	7	1.9	193	7	Adi12039	Human PRO
107	7	1.9	167	3	AA96939	Aay96939 Human IL-	180	7	1.9	193	7	ADH90113	Novel hum
108	7	1.9	176	4	AA848081	Abh48081 Human ext	181	7	1.9	193	7	ADH98514	Novel hum
109	7	1.9	176	8	ADL68905	Adl66905 Human ext	182	7	1.9	193	7	Adi11189	Human PRO
110	7	1.9	178	2	AAW93057	Aau93057 Human Tan	183	7	1.9	193	7	Adi11699	Human PRO
111	7	1.9	182	4	AAU31746	Aau31746 Novel hum	184	7	1.9	193	7	ADH98344	Novel hum
112	7	1.9	188	4	ABB66418	Abb66418 Drosophil	185	7	1.9	193	7	ADH98684	Novel hum
113	7	1.9	192	3	AA95297	Aay95297 Human int	186	7	1.9	193	7	ADH98174	Novel hum
114	7	1.9	192	8	ADN05880	Adn05880 Antipori	187	7	1.9	193	7	Adi05162	Novel hum
115	7	1.9	193	3	AA96934	Aay96934 Processed	188	7	1.9	193	7	Adi03512	Novel hum
116	7	1.9	193	4	AA887596	Aab87596 Human PRO	189	7	1.9	193	7	Adi04907	Novel hum
117	7	1.9	193	5	ABG95921	Abg95921 Human sec	190	7	1.9	193	7	ADH78361	Human PRO
118	7	1.9	193	6	ABU90946	Abu90946 Novel hum	191	7	1.9	193	7	Adi19705	Novel hum
119	7	1.9	193	6	ABO34005	Abc34005 Human sec	192	7	1.9	193	7	ADH90453	Novel hum
120	7	1.9	193	6	ABU72022	Abu72022 Novel hum	193	7	1.9	193	7	Adi03172	Novel hum
121	7	1.9	193	6	ABU71576	Abu71576 Human sec	194	7	1.9	193	7	ADH78021	Human PRO
122	7	1.9	193	6	ABU72357	Abu72357 Human PRO	195	7	1.9	193	7	ADH98004	Novel hum
123	7	1.9	193	6	ABU91030	Abu91030 Human PRO	196	7	1.9	193	7	Adi01389	Novel hum
124	7	1.9	193	6	ABO27351	Abc27351 Human sec	197	7	1.9	193	7	Adi02084	Novel hum
125	7	1.9	193	6	ABU92546	Abu92546 Human sec	198	7	1.9	193	7	Adi03342	Novel hum
126	7	1.9	193	6	ABU81216	Abu81216 Human sec	199	7	1.9	193	7	Adi11529	Human PRO
127	7	1.9	193	6	ABO53330	Abc53330 Novel hum	200	7	1.9	193	7	Adi02431	Novel hum
128	7	1.9	193	6	ABU98333	Abu98333 Novel hum	201	7	1.9	193	7	Adi11869	Human PRO
129	7	1.9	193	6	ABU89338	Abu89338 Novel hum	202	7	1.9	193	7	Adi05506	Novel hum
130	7	1.9	193	6	ABU82545	Abu82545 Novel hum	203	7	1.9	193	7	ADH79578	Novel hum
131	7	1.9	193	6	ABU96509	Abu96509 Human PRO	204	7	1.9	193	7	Adi119535	Novel hum
132	7	1.9	193	6	ABU72179	Abu72179 Human PRO	205	7	1.9	193	7	Adi05336	Novel hum
133	7	1.9	193	6	ABD17199	Abd17199 Human tra	206	7	1.9	193	7	ADH79748	Novel hum
134	7	1.9	193	6	ABO44309	Abc44309 Human sec	207	7	1.9	193	7	Adi01574	Novel hum
135	7	1.9	193	6	ADA20004	Ada20004 Novel hum	208	7	1.9	193	7	Adi01744	Novel hum
136	7	1.9	193	6	ABD17387	Abd17387 Human tra	209	7	1.9	193	7	Adi01914	Novel hum
137	7	1.9	193	6	ADA20176	Ada20176 Novel hum	210	7	1.9	193	7	ADH79918	Novel hum
138	7	1.9	193	6	ABO34237	Abc34237 Human sec	211	7	1.9	193	7	Adi04736	Novel hum
139	7	1.9	193	6	ADA00473	Ada00473 Human sec	212	7	1.9	193	7	Adi02872	Novel hum
140	7	1.9	193	7	ADB85715	Adb85715 Novel hum	213	7	1.9	193	7	ADH78191	Human PRO
141	7	1.9	193	7	ADB68394	Adb68394 Human PRO	214	7	1.9	193	7	Adi25830	Novel hum
142	7	1.9	193	7	ADB68201	Adb68201 Human PRO	215	7	1.9	193	7	Adi26000	Novel hum
143	7	1.9	193	7	ADB91018	Adb91018 Novel hum	216	7	1.9	193	7	ADK65512	Novel hum
144	7	1.9	193	7	ADC07098	Adc07098 Human PRO	217	7	1.9	193	7	ADH98854	Novel hum
145	7	1.9	193	7	ADC17277	Adc17277 Mammalian	218	7	1.9	193	7	ADH80095	Novel hum
146	7	1.9	193	7	ADC14975	Adc14975 Novel hum	219	7	1.9	193	7	ADL33825	Novel hum
147	7	1.9	193	7	ADC52470	Adc52470 Novel hum	220	7	1.9	193	8	ADC52280	Novel hum
148	7	1.9	193	7	ADD36146	Add36146 Novel hum	221	7	1.9	193	8	ADH06712	Novel hum
149	7	1.9	193	7	ADG01147	Adg01147 Novel hum	222	7	1.9	193	8	ADH06542	Novel hum
150	7	1.9	193	7	ADG08700	Adg08700 Novel hum	223	7	1.9	193	8	ADG68963	Novel hum
151	7	1.9	193	7	ADP95321	Adp95321 Novel hum	224	7	1.9	193	8	ADH27853	Novel hum
152	7	1.9	193	7	ADH24174	Adh24174 Novel hum	225	7	1.9	193	8	ADH25194	Novel hum
153	7	1.9	193	7	ADH34200	Adh34200 Novel hum	226	7	1.9	193	8	ADH33826	Human PRO
154	7	1.9	193	7	ADH30033	Adh30033 Novel hum	227	7	1.9	193	8	ADH02469	Human PRO
155	7	1.9	193	7	ADH24004	Adh24004 Novel hum	228	7	1.9	193	8	ADH08076	Novel hum
156	7	1.9	193	7	ADG85408	Adg85408 Novel hum	229	7	1.9	193	8	ADG69473	Novel hum
157	7	1.9	193	7	ADH24684	Adh24684 Novel hum	230	7	1.9	193	8	ADH39293	Novel hum
158	7	1.9	193	7	ADH37540	Adh37540 Human sec	231	7	1.9	193	8	ADG84034	Human PRO
159	7	1.9	193	7	ADH02129	Adh02129 Human PRO	232	7	1.9	193	8	ADH85578	Novel hum
160	7	1.9	193	7	ADH37710	Adh37710 Human sec	233	7	1.9	193	8	ADH06372	Novel hum
161	7	1.9	193	7	ADG85748	Adg85748 Novel hum	234	7	1.9	193	8	ADH30202	Novel hum
162	7	1.9	193	7	ADH24344	Adh24344 Novel hum	235	7	1.9	193	8	ADH24514	Novel hum
163	7	1.9	193	7	ADH38638	Adh38638 Novel hum	236	7	1.9	193	8	ADG69643	Novel hum
164	7	1.9	193	7	ADG83759	Adg83759 Human PRO	237	7	1.9	193	8	ADH07906	Novel hum
165	7	1.9	193	7	ADH29567	Adh29567 Novel hum	238	7	1.9	193	8	ADG85918	Novel hum
166	7	1.9	193	7	ADH27683	Adh27683 Novel hum	239	7	1.9	193	8	ADH39464	Novel hum
167	7	1.9	193	7	ADH37880	Adh37880 Human sec	240	7	1.9	193	8	ADH33656	Human PRO
168	7	1.9	193	7	ADH38057	Adh38057 Human sec	241	7	1.9	193	8	ADH33996	Human PRO
169	7	1.9	193	7	ADH57477	Adh57477 Novel hum	242	7	1.9	193	8	ADH01206	Human PRO
170	7	1.9	193	7	ADH53619	Adh53619 Novel hum	243	7	1.9	193	8	ADG69813	Novel hum
171	7	1.9	193	7	ADH53789	Adh53789 Novel hum	244	7	1.9	193	8	ADH02299	Human PRO

245	7	1.9	193	8	ADG69303	Agg69303	Novel hum	318	7	1.9	259	4	AB63752	Ab63752	Human pro
246	7	1.9	193	8	ADG86088	Adg86088	Novel hum	319	7	1.9	269	5	ABP66319	Abp66319	Bifidobac
247	7	1.9	193	8	ADH25024	Adh25024	Novel hum	320	7	1.9	271	6	ABU17117	Abu17117	Protein e
248	7	1.9	193	8	ADH39641	Adh39641	Novel hum	321	7	1.9	274	6	ADA34157	Ada34157	Acinetoba
249	7	1.9	193	8	ADH02639	Adh02639	Human PRO	322	7	1.9	285	3	AAG24063	Aag24063	Arabidops
250	7	1.9	193	8	ADG69133	Adg69133	Novel hum	323	7	1.9	285	5	ABP27114	Abp27114	Streptoco
251	7	1.9	193	8	ADH07736	Adh07736	Novel hum	324	7	1.9	285	6	ABU46872	Abu46872	Protein e
252	7	1.9	193	8	ADG86258	Adg86258	Novel hum	325	7	1.9	287	7	ABO64370	Ab64370	Klebsiell
253	7	1.9	193	8	ADH24854	Adh24854	Novel hum	326	7	1.9	288	3	AAG37923	Aag37923	Arabidops
254	7	1.9	193	8	ADH25902	Adh25902	Novel hum	327	7	1.9	293	4	ABG04338	Abg04338	Novel hum
255	7	1.9	193	8	ADH38468	Adh38468	Novel hum	328	7	1.9	294	3	AAG10499	Aag10499	Arabidops
256	7	1.9	193	8	ADH57307	Adh57307	Novel hum	329	7	1.9	298	3	AAG15131	Aag15131	Arabidops
257	7	1.9	193	8	ADH52294	Adh52294	Novel hum	330	7	1.9	298	8	ADJ48532	Adj48532	Oil-aggoc
258	7	1.9	193	8	ADH48660	Adh48660	Novel hum	331	7	1.9	302	4	AAE00238	Aae00238	Protein e
259	7	1.9	193	8	ADH90623	Adh90623	Novel hum	332	7	1.9	302	4	AAE00230	Aae00230	Protein e
260	7	1.9	193	8	ADH11359	Adh11359	Human PRO	333	7	1.9	302	7	ADB91919	Adb91919	Acyltrans
261	7	1.9	193	8	ADH99024	Adh99024	Novel hum	334	7	1.9	302	7	ADB91935	Adb91935	Acyltrans
262	7	1.9	193	8	ADH102254	Adh102254	Novel hum	335	7	1.9	303	8	ABM82315	Abm82315	Tumour-as
263	7	1.9	193	8	ADH90793	Adh90793	Novel hum	336	7	1.9	304	3	ABM82315	Abm82315	Tumour-as
264	7	1.9	193	8	ADJ98668	Adj98668	Novel hum	337	7	1.9	306	4	AAE00227	Aae00227	Protein e
265	7	1.9	193	8	ADJ98838	Adj98838	Novel hum	338	7	1.9	306	7	ADB91913	Adb91913	Acyltrans
266	7	1.9	193	8	ADH78997	Adh78997	Novel hum	339	7	1.9	307	3	AAG24062	Aag24062	Arabidops
267	7	1.9	193	8	ADJ99231	Adj99231	Novel hum	340	7	1.9	308	5	ABB83165	Abb83165	Human ren
268	7	1.9	193	8	ADJ99401	Adj99401	Novel hum	341	7	1.9	310	3	AAG37922	Aag37922	Arabidops
269	7	1.9	193	8	ADJ99019	Adj99019	Novel hum	342	7	1.9	317	6	ABU28032	Abu28032	Protein e
270	7	1.9	193	8	ADH79166	Adh79166	Novel hum	343	7	1.9	318	8	ADN02718	Adn02718	Human rec
271	7	1.9	193	8	ADK01027	Adk01027	Human PRO	344	7	1.9	322	6	ADA34202	Ada34202	Acinetoba
272	7	1.9	193	8	ADK14548	Adk14548	Novel hum	345	7	1.9	324	3	AAG15130	Aag15130	Arabidops
273	7	1.9	193	8	ADM80997	Adm80997	Human PRO	346	7	1.9	328	7	ABO83217	Ab83217	Pseudomon
274	7	1.9	197	3	AA95300	Aay95300	Human int	347	7	1.9	331	6	ABP70981	Abp70981	Epoxide h
275	7	1.9	198	4	AB885138	Ab885138	Human int	348	7	1.9	339	6	ABU17176	Abu17176	Protein e
276	7	1.9	203	3	AA956933	Aay956933	Human IL-	349	7	1.9	350	2	AAW64539	Aaw64539	Human epi
277	7	1.9	207	3	AA956938	Aay956938	Human IL-	350	7	1.9	350	4	AB90553	Ab90553	Human sec
278	7	1.9	208	3	AA910500	Aag10500	Arabidops	351	7	1.9	350	4	AB905589	Ab905589	Human sec
279	7	1.9	211	7	ADH86449	Adh86449	Enterococ	352	7	1.9	350	4	AB88347	Ab88347	Human mem
280	7	1.9	218	3	AA970931	Aay70931	Human zil	353	7	1.9	350	5	AB883154	Ab883154	Human pol
281	7	1.9	218	3	AA970928	Aay70928	Human zil	354	7	1.9	350	5	ABB83164	Abb83164	Human ren
282	7	1.9	218	3	AA971084	Aay71084	Human zil	355	7	1.9	350	5	ABG65467	Abg65467	Human alb
283	7	1.9	218	3	AA970927	Aay70927	Human zil	356	7	1.9	350	5	ABG65466	Abg65466	Human alb
284	7	1.9	218	3	AA970933	Aay70933	Human zil	357	7	1.9	350	8	ADL78734	Adl78734	Albumin f
285	7	1.9	218	3	AA91884	Aay91884	Primate i	358	7	1.9	350	8	ADL78733	Adl78733	Albumin f
286	7	1.9	218	3	AA91885	Aay91885	Primate i	359	7	1.9	350	8	ADR67233	Adr67233	Human bla
287	7	1.9	218	3	AA95299	Aay95299	Human int	360	7	1.9	353	3	AAG24061	Aag24061	Arabidops
288	7	1.9	218	3	AA956940	Aay956940	Human IL-	361	7	1.9	353	3	AAG15129	Aag15129	Arabidops
289	7	1.9	218	3	AA928266	Aab28266	Human int	362	7	1.9	354	6	ADA35975	Ada35975	Acinetoba
290	7	1.9	218	4	AA947186	Aab47186	IL-1 rela	363	7	1.9	356	3	AAG37921	Aag37921	Arabidops
291	7	1.9	218	4	AA968116	Aag68116	Human int	364	7	1.9	357	7	ADG30772	Adg30772	Leptospi
292	7	1.9	218	4	AB885136	Ab885136	Interleuk	365	7	1.9	363	4	ABG27581	Abg27581	Novel hum
293	7	1.9	218	7	ADH89067	Adh89067	Human zil	366	7	1.9	364	7	ADE28168	Ade28168	Human MDD
294	7	1.9	218	7	ADH89075	Adh89075	Human zil	367	7	1.9	367	6	ABU19664	Abu19664	Protein e
295	7	1.9	218	7	ADH89072	Adh89072	Human zil	368	7	1.9	368	5	ABU72346	Abu72346	Murine pr
296	7	1.9	218	7	ADH89068	Adh89068	Human zil	369	7	1.9	369	6	ABR52948	AbR52948	Protein s
297	7	1.9	218	8	ADJ88304	Adj88304	Human int	370	7	1.9	369	7	ADK62612	Adk62612	Disease t
298	7	1.9	218	8	ADJ88306	Adj88306	Human int	371	7	1.9	369	8	ADS43947	Ads43947	Bacterial
299	7	1.9	218	8	ADL15866	Adl15866	Human int	372	7	1.9	370	5	ABG69035	Abg69035	Arabidops
300	7	1.9	218	8	ADL15868	Adl15868	Human int	373	7	1.9	370	5	ABG69023	Abg69023	Arabidops
301	7	1.9	218	8	ADN05012	Adn05012	Antipsori	374	7	1.9	370	5	ABG69028	Abg69028	Arabidops
302	7	1.9	218	8	ADN41836	Adn41836	Amino aci	375	7	1.9	370	7	ABO75862	Ab75862	Pseudomon
303	7	1.9	218	8	ADO04677	Ado04677	Human int	376	7	1.9	370	7	ABO75862	Ab75862	Pseudomon
304	7	1.9	218	8	ADO04679	Ado04679	Human int	377	7	1.9	370	8	ADN73799	Adn73799	Thale cre
305	7	1.9	220	4	ADG93098	Adg93098	Human pro	378	7	1.9	375	3	AAG14462	Aag14462	Arabidops
306	7	1.9	223	4	AAU52065	Aau52065	Propionib	379	7	1.9	375	8	ADN72867	Adn72867	Thale cre
307	7	1.9	223	6	ABM48584	Abm48584	Propionib	380	7	1.9	379	3	AAG10498	Aag10498	Arabidops
308	7	1.9	228	4	ABG12860	Abg12860	Novel hum	381	7	1.9	393	5	ABN92542	Abn92542	Thale cre
309	7	1.9	228	4	ABG12075	Abg12075	Novel hum	382	7	1.9	394	4	AAG90936	Aag90936	C glutami
310	7	1.9	232	3	AA914464	Aag14464	Arabidops	383	7	1.9	396	7	ADD48782	Add48782	Rat Prote
311	7	1.9	235	6	ABU29426	Abu29426	Protein e	384	7	1.9	399	7	ADM04206	Adm04206	Human pro
312	7	1.9	238	2	AA937023	Aay37023	Chlamydia	385	7	1.9	401	4	ABG04175	Abg04175	Novel hum
313	7	1.9	242	8	ADQ37047	Adq37047	Oss49462	386	7	1.9	401	4	ABG04196	Abg04196	Novel hum
314	7	1.9	249	2	AAW97095	Aaw97095	Thermosta	387	7	1.9	403	8	ADN19466	Adn19466	Bacterial
315	7	1.9	249	4	AB62020	Ab62020	P. furios	388	7	1.9	417	4	ABG19659	Abg19659	Novel hum
316	7	1.9	249	8	ADQ26700	Adq26700	PCNA slid	389	7	1.9	420	8	ADM47996	Adm47996	Polypepti
317	7	1.9	252	7	ADC96892	Adc96892	E. faeciu	390	7	1.9	424	3	AB35801	Ab35801	Protein i

391	7	1.9	424	8	ADM48000	Adm48000 Polypepti	464	7	1.9	895	5	AAU86165	Aau86165 Mouse alp
392	7	1.9	428	4	AA879936	Ab879936 Coryneb	465	7	1.9	951	8	ADQ37103	Adq37103 Cell prol
393	7	1.9	428	4	ABG08766	Abg08766 Novel hum	466	7	1.9	952	7	ADC00492	Adc00492 Enterohae
394	7	1.9	428	5	AAE14780	Aae14780 Coryneb	467	7	1.9	966	6	ABM70145	Abm70145 Photorhab
395	7	1.9	428	5	ABB98395	Abb98395 Coryneb	468	7	1.9	973	4	ABBS8699	Abbs8699 Drosophil
396	7	1.9	436	4	AAE59872	Ab59872 Coryneb	469	7	1.9	982	4	ABG36919	Abg36919 Cell prol
397	7	1.9	437	2	AA800071	Ab800071 Carbon mo	470	7	1.9	996	5	ABB91788	Abb91788 Herbicida
398	7	1.9	437	8	ADM30767	Adm30767 Rat sonic	471	7	1.9	1026	7	ADC00868	Adc00868 Enterohae
399	7	1.9	437	8	ADO50491	Ado50491 Rat sonic	472	7	1.9	1026	7	ADC00339	Adc00339 Enterohae
400	7	1.9	439	4	AAE00240	Aae00240 Taxus cus	473	7	1.9	1045	2	AAR66221	Aar66221 Sucrose-p
401	7	1.9	439	5	ABB79398	Abb79398 Taxane sy	474	7	1.9	1045	7	ADE93716	Ade93716 Beet sucr
402	7	1.9	439	6	ABB82996	Abb82996 T. cuspid	475	7	1.9	1057	4	ABG09834	Abg09834 Novel hum
403	7	1.9	439	7	ADB91939	Adb91939 Acyltrans	476	7	1.9	1068	6	ABP78187	Abp78187 N. gonorr
404	7	1.9	446	5	ABP35708	Abp35708 Fungal ZB	477	7	1.9	1080	4	ABG14396	Abg14396 Novel hum
405	7	1.9	446	8	ADJ93495	Adj93495 RDS2. 5/2	478	7	1.9	1080	7	ADC00043	Adc00043 Enterohae
406	7	1.9	448	4	AAE00254	Aae00254 Taxus cus	479	7	1.9	1115	4	ABB71925	Abb71925 Drosophil
407	7	1.9	448	7	ADB91967	Adb91967 Acyltrans	480	7	1.9	1190	8	ADG29513	Adg29513 Bacterial
408	7	1.9	449	5	ABP69364	Abp69364 Human pol	481	7	1.9	1228	6	ABU03505	Abu03505 Angiogene
409	7	1.9	456	2	AAW35703	Aaw35703 Carnation	482	7	1.9	1228	8	ADQ39914	Adq39914 Human myo
410	7	1.9	508	2	AAW35711	Aaw35711 Chrysanth	483	7	1.9	1236	7	ADK40931	Adk40931 Novel hum
411	7	1.9	510	8	ADN21340	Adn21340 Bacterial	484	7	1.9	1236	8	ADR15652	Adr15652 Kinase 49
412	7	1.9	513	5	ABB83701	Abb83701 Human HTA	485	7	1.9	1245	4	ABG21517	Abg21517 Novel hum
413	7	1.9	513	8	ADH23368	Adh23368 Human Tip	486	7	1.9	1245	4	ABG25816	Abg25816 Novel hum
414	7	1.9	513	8	ADJ78504	Adj78504 TlFeo pro	487	7	1.9	1274	5	ABB79601	Abb79601 Human nuc
415	7	1.9	517	5	ABB97525	Abb97525 Novel hum	488	7	1.9	1405	4	ABG07888	Abg07888 Novel hum
416	7	1.9	528	2	AAR96267	Aar96267 Mutant Th	489	7	1.9	1554	7	ADD93658	Add93658 Streptoco
417	7	1.9	528	6	ADB16231	Adb16231 T. aquati	490	7	1.9	1669	4	ABG13314	Abg13314 Novel hum
418	7	1.9	540	4	ABG05292	Abg05292 Novel hum	491	7	1.9	2458	2	AAR07640	Aar07640 Deduced p
419	7	1.9	544	4	ABE61602	Ab61602 Drosophil	492	7	1.9	2458	2	AAR04031	Aar04031 Full leng
420	7	1.9	550	2	AAW94922	Aaw94922 Rat phero	493	7	1.9	3700	7	ADI23890	Adi23890 Streptomy
421	7	1.9	556	4	ABB69870	Abb69870 Drosophil	494	7	1.9	6291	7	ADI23927	Adi23927 Streptomy
422	7	1.9	560	3	AA842484	Aa842484 Human ORF	495	6	1.6	9	7	ADC99890	Adc99890 Murine IL
423	7	1.9	560	5	AAO17144	Aao17144 Human blo	496	6	1.6	10	4	AAG96875	Aag96875 Human com
424	7	1.9	560	5	AAO17145	Aao17145 Human blo	497	6	1.6	10	4	AAG96601	Aag96601 Human com
425	7	1.9	572	4	ABG03563	Abg03563 Novel hum	498	6	1.6	10	8	ADG98114	Adg98114 Apoptosis
426	7	1.9	573	8	ADS44435	Ads44435 Bacterial	499	6	1.6	12	3	AAB12275	Aab12275 Mutated N
427	7	1.9	574	4	ABE62467	Ab62467 Drosophil	500	6	1.6	12	6	ABR59086	AbR59086 Alzheimer
428	7	1.9	578	8	ADP74053	Adp74053 Candida a	501	6	1.6	12	8	ADN31709	Adn31709 Human Alz
429	7	1.9	622	5	ABP74053	Abp74053 Bacterial	502	6	1.6	13	2	AA74214	Aa74214 Internal
430	7	1.9	639	7	ADD27949	Ad27949 Arabidops	503	6	1.6	13	5	AAE24108	Aae24108 Rice CO39
431	7	1.9	639	8	ADN73509	Adn73509 Thale cre	504	6	1.6	13	7	ADM75198	Adm75198 Potential
432	7	1.9	652	4	AAU38102	Aau38102 Streptoco	505	6	1.6	13	7	ADM75463	Adm75463 Potential
433	7	1.9	663	4	AA893313	Aa893313 Human pro	506	6	1.6	13	7	ADM74934	Adm74934 Potential
434	7	1.9	663	8	ADR14479	Adr14479 Human NF-	507	6	1.6	13	7	ADM75728	Adm75728 Potential
435	7	1.9	666	8	ADS09737	Ads09737 Chinese h	508	6	1.6	14	8	ADG98131	Adg98131 Apoptosis
436	7	1.9	684	6	ABT37930	Abt37930 NOXV prot	509	6	1.6	15	4	AAB97259	Aab97259 Human spl
437	7	1.9	685	8	ADS09695	Ads09695 House mou	510	6	1.6	16	6	ABP82862	Abp82862 G protein
438	7	1.9	685	8	ADS09693	Ads09693 Hamster/N	511	6	1.6	18	2	AAW07268	Aaw07268 Amphiphil
439	7	1.9	685	8	ADS09731	Ads09731 Mammalian	512	6	1.6	18	8	ADG98128	Adg98128 Apoptosis
440	7	1.9	685	8	ADS09697	Ads09697 House mou	513	6	1.6	22	8	ADG98130	Adg98130 Apoptosis
441	7	1.9	685	8	ADS09726	Ads09726 House mou	514	6	1.6	23	2	AAW75019	Aaw75019 Human sec
442	7	1.9	685	8	ADS09651	Ads09651 House mou	515	6	1.6	23	5	ABG95481	Abg95481 Human nov
443	7	1.9	695	2	AAW94925	Aaw94925 Rat phero	516	6	1.6	23	6	ABO34675	AbO34675 Region of
444	7	1.9	704	6	ABJ37934	Abj37934 NOXV prot	517	6	1.6	23	7	ADI23336	Adi23336 Novel hum
445	7	1.9	709	5	ABG91737	Abg91737 Purine/py	518	6	1.6	23	8	ADG98148	Adg98148 Apoptosis
446	7	1.9	723	2	AAW94905	Aaw94905 Mouse phe	519	6	1.6	23	8	ADH74338	Adh74338 Human sec
447	7	1.9	730	5	ABG91661	Abg91661 Purine/py	520	6	1.6	23	8	ADR44125	Adr44125 Human OC-
448	7	1.9	739	7	ABO65357	AbO65357 Klebsiell	521	6	1.6	24	8	ADG98126	Adg98126 Apoptosis
449	7	1.9	743	6	ABJ37932	Abj37932 NOXV prot	522	6	1.6	29	2	AAR60931	Aar60931 Hs229-Vas
450	7	1.9	752	7	ABO81381	AbO81381 Pseudomon	523	6	1.6	30	2	AAW11546	Aaw11546 Human 5'
451	7	1.9	772	8	ADG26981	Adg26981 Bacterial	524	6	1.6	30	2	AAW95024	Aaw95024 Sorbitol
452	7	1.9	789	2	AAW14055	Aaw14055 Pumpkin e	525	6	1.6	30	3	AAG55291	Aag55291 Arabidops
453	7	1.9	789	8	ADM98975	Adm98975 Diterpene	526	6	1.6	31	2	AAW13992	Aaw13992 Single ch
454	7	1.9	793	2	AAW94923	Aaw94923 Rat phero	527	6	1.6	31	7	ABM74179	Abm74179 DNA clone
455	7	1.9	798	2	AAW94924	Aaw94924 Rat phero	528	6	1.6	32	2	AAW13993	Aaw13993 Single ch
456	7	1.9	798	7	ADD48569	Add48569 Rat Prote	529	6	1.6	32	2	AAW13991	Aaw13991 Single ch
457	7	1.9	804	2	AAW94914	Aaw94914 Mouse phe	530	6	1.6	32	2	AAW13990	Aaw13990 Single ch
458	7	1.9	816	8	ADS95106	Ads95106 Human the	531	6	1.6	32	2	AAW20205	Aaw20205 H. pylori
459	7	1.9	833	2	AAR96262	Aar96262 Mutant Th	532	6	1.6	32	5	AAE16407	Aae16407 pPTG26 ca
460	7	1.9	833	5	ADI92686	Adi92686 T. aquati	533	6	1.6	32	5	AAO19536	Aao19536 Substance
461	7	1.9	833	6	ADB16226	Adb16226 T. aquati	534	6	1.6	32	6	ABJ18544	Abj18544 Ganglios
462	7	1.9	852	2	AAW94904	Aaw94904 Mouse phe	535	6	1.6	32	7	ABO33895	AbO33895 Anti-GPI-
463	7	1.9	889	4	ABG23879	Abg23879 Novel hum	536	6	1.6	32	7	ABO33897	AbO33897 Anti-GPI-

537	6	1.6	34	4	AM18787	610	6	1.6	43	8	ADJ38329	Adj38329 Human cal
538	6	1.6	34	4	AB37888	611	6	1.6	43	8	ADM57746	Adm57746 Human cal
539	6	1.6	34	4	AM31295	612	6	1.6	44	8	ADS05593	AdS05593 Staphyloc
540	6	1.6	34	4	AB23146	613	6	1.6	45	4	ABG12463	Abg12463 Novel hum
541	6	1.6	34	4	AM71018	614	6	1.6	46	6	ABO14059	AbO14059 Novel hum
542	6	1.6	34	4	AM58520	615	6	1.6	46	8	ADN60756	Adn60756 Human sec
543	6	1.6	34	4	AGS52733	616	6	1.6	46	8	ADN05385	Adn05385 Antipsori
544	6	1.6	34	5	ABG40809	617	6	1.6	47	2	AAI27654	Aai27654 Human sec
545	6	1.6	34	6	ADA95130	618	6	1.6	47	8	ADG78465	Adg78465 Human sec
546	6	1.6	34	6	AAE36681	619	6	1.6	48	1	AAp82386	Aap82386 Human spl
547	6	1.6	34	7	ABW01737	620	6	1.6	48	2	AAr15041	Aar15041 Human thy
548	6	1.6	34	8	ADM97052	621	6	1.6	48	3	AAy98484	Aay98484 Thymopoie
549	6	1.6	35	3	AB56225	622	6	1.6	48	3	AAy59029	Aay59029 Peptide 1
550	6	1.6	35	4	AM13693	623	6	1.6	48	3	AAy59028	Aay59028 Peptide 1
551	6	1.6	35	4	AB32624	624	6	1.6	48	4	AB45837	Ab45837 Nucleic a
552	6	1.6	35	4	AM26093	625	6	1.6	48	4	AAU04274	Aau04274 Nuclear 1
553	6	1.6	35	4	ABB27473	626	6	1.6	49	3	AAy98483	Aay98483 Thymopoie
554	6	1.6	35	4	ABB18122	627	6	1.6	49	4	AB45836	Ab45836 Nucleic a
555	6	1.6	35	4	AM65831	628	6	1.6	49	4	AAU04273	Aau04273 Nuclear 1
556	6	1.6	35	4	AM53454	629	6	1.6	49	8	ADG98121	Adg98121 Apoptosis
557	6	1.6	35	4	ABG47477	630	6	1.6	49	8	ABO58069	AbO58069 Human gen
558	6	1.6	35	4	AM01443	631	6	1.6	50	2	AAr15042	Aar15042 Rat thymo
559	6	1.6	35	5	ABG35465	632	6	1.6	50	4	AAU58238	Aau58238 Propionib
560	6	1.6	35	5	ADG98111	633	6	1.6	50	6	ABM54757	Abm54757 Propionib
561	6	1.6	37	3	AG63541	634	6	1.6	51	7	ADB49311	Adb49311 WW domain
562	6	1.6	37	4	AM76961	635	6	1.6	52	5	ABP01606	Abp01606 Human ORF
563	6	1.6	38	2	AM88826	636	6	1.6	53	4	AAU56530	Aau56530 Propionib
564	6	1.6	38	3	AB34255	637	6	1.6	53	4	AAU53101	Aau53101 Propionib
565	6	1.6	38	3	AG11009	638	6	1.6	53	4	ABG19128	Abg19128 Novel hum
566	6	1.6	38	3	AB55177	639	6	1.6	53	6	ABM49620	Abm49620 Propionib
567	6	1.6	38	4	AB50768	640	6	1.6	53	6	ABM53049	Abm53049 Propionib
568	6	1.6	38	6	ABO45025	641	6	1.6	54	3	AAg57041	Aag57041 Arabidops
569	6	1.6	38	7	ABO26505	642	6	1.6	54	5	ABP05824	Abp05824 Human ORF
570	6	1.6	38	8	ABO54386	643	6	1.6	55	5	ABP00846	Abp00846 Human ORF
571	6	1.6	39	3	AG15094	644	6	1.6	56	4	ABB17368	Abb17368 Human ner
572	6	1.6	39	4	AM31153	645	6	1.6	57	3	ABY87302	AbY87302 Human sig
573	6	1.6	39	4	AM25509	646	6	1.6	57	5	ABG77449	Abg77449 Selected
574	6	1.6	40	4	AM15982	647	6	1.6	57	5	ABJ11351	AbJ11351 Yeast sel
575	6	1.6	40	4	AB34977	648	6	1.6	57	7	ADE11835	Adel11835 Human sec
576	6	1.6	40	4	AM28482	649	6	1.6	58	3	AAy76213	Aay76213 Human sec
577	6	1.6	40	4	ABB29799	650	6	1.6	58	3	AAg57040	Aag57040 Arabidops
578	6	1.6	40	4	AB220385	651	6	1.6	58	4	AM90572	Am90572 Human imm
579	6	1.6	40	4	AM68159	652	6	1.6	59	4	AM19354	Am19354 Peptide #
580	6	1.6	40	4	AM55784	653	6	1.6	59	4	ABB38712	Abb38712 Peptide #
581	6	1.6	40	4	ABG49811	654	6	1.6	59	4	AM32178	Aam32178 Peptide #
582	6	1.6	40	4	AM03717	655	6	1.6	59	4	ABB23776	Abb23776 Protein #
583	6	1.6	40	5	ABG37689	656	6	1.6	59	4	AM71898	Am71898 Human bon
584	6	1.6	42	4	AM18300	657	6	1.6	59	4	AAU62221	Aau62221 Propionib
585	6	1.6	42	4	AM13867	658	6	1.6	59	4	AM59345	Am59345 Human bra
586	6	1.6	42	4	ABB32812	659	6	1.6	59	4	ABG53580	Abg53580 Human liv
587	6	1.6	42	4	ABB37335	660	6	1.6	59	5	ABP06509	Abp06509 Human ORF
588	6	1.6	42	4	AM26274	661	6	1.6	59	5	ABG41711	Abg41711 Human pep
589	6	1.6	42	4	AM30785	662	6	1.6	59	6	ABM58740	Abm58740 Propionib
590	6	1.6	42	4	ABB32081	663	6	1.6	59	7	ADF78992	Adf78992 KIX2-ERTb
591	6	1.6	42	4	ABB27642	664	6	1.6	60	2	AAy36383	Aay36383 Fragment
592	6	1.6	42	4	ABB18294	665	6	1.6	60	4	AAU43876	Aau43876 Propionib
593	6	1.6	42	4	ABB22622	666	6	1.6	60	6	ABM40395	Abm40395 Propionib
594	6	1.6	42	4	AM65998	667	6	1.6	60	6	ADA11842	Ada11842 Human mov
595	6	1.6	42	4	AM70463	668	6	1.6	61	4	AAU48735	Aau48735 Propionib
596	6	1.6	42	4	AM53619	669	6	1.6	61	5	ABP02276	Abp02276 Human ORF
597	6	1.6	42	4	ABG47664	670	6	1.6	61	5	ABP05669	Abp05669 Human ORF
598	6	1.6	42	4	ABG52150	671	6	1.6	61	6	ABM45254	Abm45254 Propionib
599	6	1.6	42	4	AM01610	672	6	1.6	61	8	ADM48215	Adm48215 Streptoco
600	6	1.6	42	5	ABG35646	673	6	1.6	62	5	ABP03086	Abp03086 Human ORF
601	6	1.6	42	5	ABG40101	674	6	1.6	62	5	ABP07062	Abp07062 Human ORF
602	6	1.6	42	6	ABJ26678	675	6	1.6	62	5	ABP32215	Abp32215 Human ORF
603	6	1.6	43	2	AAr33554	676	6	1.6	63	4	AAO11880	Aao11880 Human pol
604	6	1.6	43	2	AAr49199	677	6	1.6	63	4	ABG23791	Abg23791 Novel hum
605	6	1.6	43	2	AAW63146	678	6	1.6	63	4	AAAB29530	AaAB29530 Human CR2
606	6	1.6	43	2	AAW80716	679	6	1.6	63	6	ADA49714	Ada49714 Death dom
607	6	1.6	43	3	AB10577	680	6	1.6	63	7	ADF05235	Adf05235 Bacterial
608	6	1.6	43	4	AB69635	681	6	1.6	64	3	ABG36768	Abg36768 Arabidops
609	6	1.6	43	5	AAE24790	682	6	1.6	64	3	AAG12929	Aag12929 Arabidops

683	6	1.6	64	4	AAW15161	Aam15161 Peptide #	756	6	1.6	71	4	AAW77286	Aam77286 Human bon
684	6	1.6	64	4	AAW20020	Aam20020 Peptide #	757	6	1.6	71	4	AAU55114	AAU55114 Propionib
685	6	1.6	64	4	ABB40124	Abb40124 Peptide #	758	6	1.6	71	4	ABG24180	Novel hum
686	6	1.6	64	4	ABB34154	Abb34154 Peptide #	759	6	1.6	71	5	ABG46301	Human pep
687	6	1.6	64	4	AAW33763	Aam33763 Peptide #	760	6	1.6	71	5	ADH32281	Novel yea
688	6	1.6	64	4	AAW27618	Aam27618 Peptide #	761	6	1.6	71	6	ABM51633	Propionib
689	6	1.6	64	4	ABB28986	Abb28986 Peptide #	762	6	1.6	72	4	AAW75744	Human col
690	6	1.6	64	4	ABB24591	Abb24591 Peptide #	763	6	1.6	72	4	AAW83615	Human col
691	6	1.6	64	4	ABB19598	Abb19598 Protein #	764	6	1.6	72	4	AAO05618	Human pol
692	6	1.6	64	4	AAW73568	Aam73568 Human bon	765	6	1.6	72	4	AAU40872	Propionib
693	6	1.6	64	4	AAW67326	Aam67326 Human bon	766	6	1.6	72	6	ABM37391	Propionib
694	6	1.6	64	4	AAW60885	Aam60885 Human bra	767	6	1.6	72	8	ABO53816	Human gen
695	6	1.6	64	4	AAW54946	Aam54946 Human bra	768	6	1.6	73	4	ABO3783	Human mus
696	6	1.6	64	4	ABG55297	Abb55297 Human liv	769	6	1.6	73	4	AAO00950	Human pol
697	6	1.6	64	4	ABG48988	Abb48988 Human liv	770	6	1.6	73	4	AAU59828	Propionib
698	6	1.6	64	4	AAW02899	Aam02899 Peptide #	771	6	1.6	73	4	AAU45926	Propionib
699	6	1.6	64	5	ABG43434	Abb43434 Human pep	772	6	1.6	73	5	ABP05551	Human ORF
700	6	1.6	64	5	ABG36969	Abb36969 Human pep	773	6	1.6	73	6	ABM42445	Propionib
701	6	1.6	64	5	AAE15374	Aae15374 Aspergill	774	6	1.6	73	6	ABM56347	Propionib
702	6	1.6	65	2	AAE55789	Aae55789 Cell deat	775	6	1.6	73	6	ABU13077	Novel hum
703	6	1.6	65	4	AAW18374	Aam18374 Peptide #	776	6	1.6	73	8	ADJ29103	Novel hum
704	6	1.6	65	4	AAW65246	Aag65246 D melanog	777	6	1.6	74	4	ABG29302	Novel hum
705	6	1.6	65	4	ABW60552	Abb60552 Drosophil	778	6	1.6	74	5	AAU76252	A. thalia
706	6	1.6	65	4	AAW86392	Aam86392 Human imm	779	6	1.6	75	1	AAW82326	Protein M
707	6	1.6	65	4	AAW70535	Aam70535 Human bon	780	6	1.6	75	1	AAW82326	Protein M
708	6	1.6	65	4	AAW05971	Aam05971 Peptide #	781	6	1.6	75	6	AAU63518	Propionib
709	6	1.6	65	5	AAE19839	Aae19839 Drosophil	782	6	1.6	75	6	ABM60037	Propionib
710	6	1.6	66	3	AAW02508	Aag02508 Human sec	783	6	1.6	76	4	AAU66632	Propionib
711	6	1.6	66	4	ABG19494	Abb19494 Novel hum	784	6	1.6	76	4	AAU59146	Propionib
712	6	1.6	66	4	AAU21051	Aau21051 Human nov	785	6	1.6	76	5	ABP39442	Staphyloc
713	6	1.6	67	4	AAW62161	Aag62161 Human gen	786	6	1.6	76	6	ABM55665	Propionib
714	6	1.6	67	4	AAW662190	Aag662190 Human gen	787	6	1.6	76	6	ABM63151	Propionib
715	6	1.6	67	4	ABG00022	Abb00022 Novel hum	788	6	1.6	76	8	ADS05270	Staphyloc
716	6	1.6	67	4	ABG02469	Abb02469 Novel hum	789	6	1.6	77	2	AAW44726	Amino aci
717	6	1.6	67	5	ABG63507	Abb63507 Human alb	790	6	1.6	77	3	AAW44019	Human can
718	6	1.6	67	5	ABG63508	Abb63508 Human alb	791	6	1.6	77	4	AAW90947	Human imm
719	6	1.6	67	8	ADL76773	Adl76773 Albumin f	792	6	1.6	78	3	AAW90947	Human imm
720	6	1.6	67	8	ADL76772	Adl76772 Albumin f	793	6	1.6	78	4	AAU60256	Propionib
721	6	1.6	68	3	AAW00812	Aag00812 Human sec	794	6	1.6	78	5	ABP10742	Human ORF
722	6	1.6	68	4	AAU44892	Aau44892 Propionib	795	6	1.6	78	5	ABG69653	Human sec
723	6	1.6	68	6	ABW41411	Bmw41411 Propionib	796	6	1.6	78	6	ABM56775	Propionib
724	6	1.6	68	6	ABU00285	Abu00285 Human nov	797	6	1.6	80	4	AAU59725	Propionib
725	6	1.6	69	2	AAW88724	Aaw88724 Secreted	798	6	1.6	80	5	ABP00826	Human ORF
726	6	1.6	69	3	AAW58275	Aag58275 Arabidops	799	6	1.6	80	6	ABM56244	Propionib
727	6	1.6	69	3	AAW51554	Aag51554 Arabidops	800	6	1.6	80	7	ADC38698	Human sec
728	6	1.6	69	3	AAW09754	Aag09754 Arabidops	801	6	1.6	80	8	ADP24388	PRO poly
729	6	1.6	69	3	AAW36534	Aag36534 Arabidops	802	6	1.6	81	3	AAW57063	Human pro
730	6	1.6	69	3	AAW51525	Aag51525 Arabidops	803	6	1.6	81	4	AAW84895	Human imm
731	6	1.6	69	4	ABW50491	Abb50491 Human col	804	6	1.6	81	5	AAU80868	Human CAR
732	6	1.6	69	4	ABB12233	Abb12233 Human sec	805	6	1.6	81	5	ABU81727	Human ova
733	6	1.6	69	4	AAW52092	Aaw52092 Propionib	806	6	1.6	81	6	ADA56818	Human cas
734	6	1.6	69	5	ABP07927	Abp07927 Human ORF	807	6	1.6	81	6	ADA40667	Human sec
735	6	1.6	69	6	ABW48611	Abb48611 Propionib	808	6	1.6	81	6	ABR47685	Human sec
736	6	1.6	69	6	ABO44748	Abb44748 Novel hum	809	6	1.6	81	7	ADE11762	Human sec
737	6	1.6	69	7	ABO26228	Abb26228 Human pro	810	6	1.6	81	8	ADP30166	Human sec
738	6	1.6	70	2	AAW85910	Aay85910 S. pneumo	811	6	1.6	82	3	AAW76139	Human sec
739	6	1.6	70	2	AAW35938	Aay35938 Extended	812	6	1.6	82	4	AAO08254	Human pol
740	6	1.6	70	2	AAW28573	Aay28573 Secreted	813	6	1.6	82	8	ADS07055	Staphyloc
741	6	1.6	70	4	AAU39046	Aau39046 Human sec	814	6	1.6	83	3	AAW36533	Arabidops
742	6	1.6	70	4	AAU53345	Aau53345 Propionib	815	6	1.6	83	7	ADP05432	Bacterial
743	6	1.6	70	4	AAU56487	Aau56487 Propionib	816	6	1.6	85	3	AAW03573	Human sec
744	6	1.6	70	5	ABP41876	Abp41876 Human ova	817	6	1.6	85	5	ABP31152	Human ORF
745	6	1.6	70	5	ABW55755	Abb55755 Human pol	818	6	1.6	85	8	ADG22709	Cyanophag
746	6	1.6	70	6	ABU00959	Abu00959 S. pneumo	819	6	1.6	86	4	AAW99872	Human exc
747	6	1.6	70	6	ABW49864	Abb49864 Propionib	820	6	1.6	86	4	AAW86227	Human imm
748	6	1.6	70	6	ABW3006	Abb3006 Propionib	821	6	1.6	86	4	AAW43671	Human bla
749	6	1.6	70	7	AAO27232	Aao27232 Protein s	822	6	1.6	86	5	ABW79369	Human ova
750	6	1.6	70	7	ADP19246	Adp19246 Human sec	823	6	1.6	86	8	ADF71630	Human bla
751	6	1.6	70	8	ADP19246	Adp19246 Human sec	824	6	1.6	87	3	AAW34201	Gene 37 h
752	6	1.6	71	4	AAW92805	Aam92805 Human dig	825	6	1.6	87	3	AAW34202	Human sec
753	6	1.6	71	4	AAW37438	Aam37438 Peptide #	826	6	1.6	87	4	AAU55966	Propionib
754	6	1.6	71	4	AAW86403	Aam86403 Human imm	827	6	1.6	87	5	ABP64128	Human ORF
755	6	1.6	71	4	AAW86403	Aam86403 Human imm	828	6	1.6	87	6	ABM52485	Propionib

829	6	1.6	87	8	ADK51430	Adk51430 Murine an	902	6	1.6	104	4	AAU33672	Pseudomon
830	6	1.6	87	8	ADK51392	Adk51392 Murine an	903	6	1.6	104	5	AAM53044	Human zin
831	6	1.6	87	8	ABM82237	ABM82237 Tumour-as	904	6	1.6	104	6	ABU41310	Protein e
832	6	1.6	87	8	ADR40102	Adr40102 Human PKH	905	6	1.6	104	6	ABU39900	Protein e
833	6	1.6	87	8	ADR73444	Adr73444 Human bla	906	6	1.6	104	6	ABU15559	Protein e
834	6	1.6	88	4	AAU29334	Aau29334 Human dig	907	6	1.6	104	6	ABM71048	Staphyloc
835	6	1.6	88	4	AAU20030	Aau20030 Human liv	908	6	1.6	104	7	ADP78991	KLK2-EHTb
836	6	1.6	88	5	ABP23239	Abp29239 Streptococ	909	6	1.6	104	7	ADM05243	Human pro
837	6	1.6	88	5	ABP40891	Abp40891 Human liv	910	6	1.6	104	8	ADG78417	Human sec
838	6	1.6	88	7	ADJ15009	Adj15009 Human liv	911	6	1.6	105	4	AAM15243	Peptide #
839	6	1.6	88	8	ADK46404	Adk46404 Streptococ	912	6	1.6	105	4	ABB34233	Peptide #
840	6	1.6	88	8	ADR95467	Adr95467 Novel S.	913	6	1.6	105	4	AAM27704	Peptide #
841	6	1.6	89	4	ABK62542	Abk62542 B. melite	914	6	1.6	105	4	ABB29071	Peptide #
842	6	1.6	89	7	ADC96552	Adc96552 E. faeciu	915	6	1.6	105	4	AAM67412	Human bon
843	6	1.6	90	2	AAU37903	Aay37903 Amino aci	916	6	1.6	105	4	AAM55027	Human bra
844	6	1.6	90	5	ABU10594	Abu10594 cDNA enco	917	6	1.6	105	4	ABG49071	Human liv
845	6	1.6	90	5	ADH32283	Adh32283 Novel yea	918	6	1.6	105	4	AAM02986	Peptide #
846	6	1.6	91	5	ABP10026	Abp10026 Human ORF	919	6	1.6	105	4	ABG49071	Human liv
847	6	1.6	91	5	ABP31979	Abp31979 Human ATP	920	6	1.6	105	7	ADH86628	Enterococ
848	6	1.6	91	6	ABU18519	Abu18519 Protein e	921	6	1.6	105	8	ADK48360	Streptococ
849	6	1.6	91	8	ABO60466	AbO60466 Human gen	922	6	1.6	107	2	AAR28434	Sequence
850	6	1.6	92	4	ABE17549	AbE17549 Human gen	923	6	1.6	107	2	AAR52043	Heavy cha
851	6	1.6	92	5	ABE97780	AbE97780 Human sec	924	6	1.6	108	5	ABR41195	Human DIT
852	6	1.6	93	3	AAE51662	Aae51662 Human sec	925	6	1.6	108	7	ABO72605	Pseudomon
853	6	1.6	93	4	ABE69620	AbE69620 Drosophil	926	6	1.6	108	7	ABO72605	Pseudomon
854	6	1.6	94	5	AAE25420	Aae25420 Human Nod	927	6	1.6	109	4	ABG19307	Novel hum
855	6	1.6	94	5	ABP60145	AbP60145 Human tri	928	6	1.6	110	4	AAM18435	Peptide #
856	6	1.6	94	5	ABG69875	AbG69875 Human sec	929	6	1.6	110	4	ABB37475	Peptide #
857	6	1.6	94	5	ABJ04739	AbJ04739 Nod2 casp	930	6	1.6	110	4	AAM30909	Peptide #
858	6	1.6	94	6	ABP75798	AbP75798 Human sec	931	6	1.6	110	4	ABB32224	Peptide #
859	6	1.6	95	2	AAW88599	Aaw88599 Secreted	932	6	1.6	110	4	AAM70596	Human bon
860	6	1.6	95	3	AAE65258	Aay65258 Human S'	933	6	1.6	110	4	AAO08741	Human pol
861	6	1.6	95	4	ABE50366	AbE50366 Human sec	934	6	1.6	110	4	AAU51131	Propionib
862	6	1.6	95	4	AAU56542	Aau56542 Propionib	935	6	1.6	110	4	ABG52276	Human liv
863	6	1.6	95	5	ABP62916	AbP62916 Human pol	936	6	1.6	110	4	AAO60603	Peptide #
864	6	1.6	95	6	ABM53061	ABm53061 Propionib	937	6	1.6	110	5	ABP02171	Human ORF
865	6	1.6	95	6	ABO44623	ABO44623 Novel hum	938	6	1.6	110	5	ABG40267	Human pep
866	6	1.6	96	1	ABO26103	ABO26103 Human pro	939	6	1.6	110	6	ABM47650	Propionib
867	6	1.6	96	4	AAU27452	Aau27452 Novel bon	940	6	1.6	110	6	ABM51697	Propionib
868	6	1.6	96	4	AAO01860	Aao01860 Human pol	941	6	1.6	110	6	ABR58493	Human sec
869	6	1.6	96	6	ADJ11174	AdJ11174 Alloicoc	942	6	1.6	110	8	ADG23652	Bacterial
870	6	1.6	96	7	ADD36274	AdD36274 D melanog	943	6	1.6	111	2	AAR98496	MAB 2E3 h
871	6	1.6	96	8	ADQ08897	AdQ08897 Drosophil	944	6	1.6	111	2	AAR98494	MAB 2F2 h
872	6	1.6	97	4	AAU22281	Aau22281 Human car	945	6	1.6	111	2	AAW42453	Mouse ant
873	6	1.6	97	6	ABU01567	AbU01567 S. pneumo	946	6	1.6	111	2	AAW42455	Mouse ant
874	6	1.6	97	7	ADE46249	Ade46249 Human car	947	6	1.6	111	3	AAG33847	Arabidops
875	6	1.6	97	8	ADJ07667	AdJ07667 Human car	948	6	1.6	111	7	ADC08105	Rice prot
876	6	1.6	98	2	AAV49211	Aav49211 MAB 1A7 l	949	6	1.6	112	2	AAR26003	H-chain v
877	6	1.6	98	4	ABG28593	ABG28593 Novel hum	950	6	1.6	112	2	AAV35943	Extended
878	6	1.6	98	5	AAU11263	Aau11263 Partial h	951	6	1.6	112	5	ABP09703	Human ORF
879	6	1.6	98	6	ADA14771	Ada14771 Mouse art	952	6	1.6	112	5	ABU51491	Helicobac
880	6	1.6	98	7	ADC35313	AdC35313 Prior art	953	6	1.6	113	3	ABY16745	Bacteriop
881	6	1.6	98	7	ADF05177	AdF05177 Bacterial	954	6	1.6	112	7	ABO33836	Human ant
882	6	1.6	99	7	ADG88727	AdG88727 Ribosomal	955	6	1.6	112	7	ABO33834	Human ant
883	6	1.6	99	7	ADD36236	AdD36236 Frog orth	956	6	1.6	112	8	ADC33367	Human nov
884	6	1.6	99	8	ADQ08859	AdQ08859 Xenopus l	957	6	1.6	112	8	ADP19251	Human sec
885	6	1.6	100	4	ABU53241	AbU53241 Human tes	958	6	1.6	113	2	AAR21268	Murine VH
886	6	1.6	100	5	ABP35338	ABP35338 Human ORF	959	6	1.6	113	3	AAV74309	Neisseria
887	6	1.6	100	6	ADA35444	Ada35444 Acinetoba	960	6	1.6	113	3	AAV70080	Mouse aor
888	6	1.6	101	4	AAU93191	Aau93191 Human pol	961	6	1.6	113	3	AGI16278	Arabidops
889	6	1.6	101	4	AAU66900	Aau66900 Propionib	962	6	1.6	113	6	ABR58492	Human sec
890	6	1.6	101	4	ABG29446	ABG29446 Novel hum	963	6	1.6	113	6	ABU00147	Human nov
891	6	1.6	101	6	ABM63419	ABm63419 Propionib	964	6	1.6	114	3	AAH52552	Helicobac
892	6	1.6	101	8	ADL30534	ADL30534 Human pro	965	6	1.6	114	3	AAG58274	Arabidops
893	6	1.6	102	3	AAQ00612	Aaq00612 Human sec	966	6	1.6	114	4	AAE11175	Clostridi
894	6	1.6	102	4	AAH95310	AAH95310 Human pro	967	6	1.6	114	5	AAU02563	Anti-adip
895	6	1.6	103	4	AAH88410	AAH88410 Human mem	968	6	1.6	114	5	AAE17793	Escherich
896	6	1.6	103	5	ABR40424	ABr40424 Human sec	969	6	1.6	114	8	ADK17087	Nanoarcha
897	6	1.6	103	5	ABR40500	ABr40500 Human sec	970	6	1.6	115	2	AAW04595	Anti-DNA
898	6	1.6	103	6	ABO14011	ABO14011 Novel hum	971	6	1.6	115	4	ABG06719	Novel hum
899	6	1.6	103	7	ADF07339	AdF07339 Bacterial	972	6	1.6	115	5	ABP07259	Human ORF
900	6	1.6	103	8	ADN60708	Adn60708 Human sec	973	6	1.6	115	5	AAE29298	S. aureus
901	6	1.6	104	2	AAV27606	Aay27606 Human sec	974	6	1.6	115	7	ADF58686	Human pol

975 1.6 115 8 ADF77174
 976 1.6 116 2 AAR07322
 977 1.6 116 2 AAR28287
 978 1.6 116 2 AAR40951
 979 1.6 116 2 AAW14490
 980 1.6 116 2 AAR99877
 981 1.6 116 4 AAU07513
 982 1.6 116 5 ABP02834
 983 1.6 116 5 ABB79733
 984 1.6 116 6 ABO27162
 985 1.6 116 8 ADQ91072
 986 1.6 116 8 ADS12312
 987 1.6 117 3 AAB16448
 988 1.6 117 3 AAG38294
 989 1.6 117 4 AAB63651
 990 1.6 117 4 AAM94298
 991 1.6 117 5 ABB90352
 992 1.6 117 5 ABB90184
 993 1.6 117 6 ABJ18566
 994 1.6 117 7 ABR82773
 995 1.6 117 7 ABR82883
 996 1.6 117 7 ADC88400
 997 1.6 117 7 ADD41650
 998 1.6 117 8 ADG25836
 999 1.6 117 8 ADQ81963
 1000 1.6 118 2 AAY00292

ALIGNMENTS

RESULT 1
 AAW21965
 ID AAW21965 standard; protein; 377 AA.
 XX AC AAW21965;
 XX DT 02-DEC-1997 (first entry)
 XX DE Human cyclin I.
 XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
 XX OS Homo sapiens.
 XX FN WO9712973-A1.
 XX PD 10-APR-1997.
 XX PF 07-OCT-1996; 96WO-JP002905.
 XX PR 05-OCT-1995; 95JP-00284663.
 XX PA (SUME) SUMITOMO ELECTRIC IND CO.
 XX PI Nakamura T;
 XX DR WPI; 1997-226217/20.
 XX DR N-PSDB; AAT73937.
 XX PT Human cyclin I protein and related (anti:sense) DNA - used for neuron
 XX PT labelling method and cancer cell detection.
 XX PS Claim 1; Fig 1; 45pp; Japanese.

This sequence is human cyclin I. Antisense polynucleotides are useful for as probes and can be labelled and used for detection of neurones by hybridisation with mRNA for cyclin I (contained in the neurones and arising by the expression of the cyclin I gene in these cells). The gene can be used for detection of cancer cells by detecting the expression of the cyclin I gene in these cells. Also antibodies specific for the fragments of the protein (especially AAW21966) can be used for detection

SQ Sequence 377 AA;
 Query Match 100.0%; Score 377; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKFPGLNORLSFLLEKAITREAAQWKNVVRKMPNQNVSPQRDEVIQWLAKLYQFN 60
 Db 1 MKFPGLNORLSFLLEKAITREAAQWKNVVRKMPNQNVSPQRDEVIQWLAKLYQFN 60
 Qy 61 LYETETALASSILDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSEFC 120
 Db 61 LYETETALASSILDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSEFC 120
 Qy 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180
 Db 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180
 Qy 181 LTKQLLHCMA CNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
 Db 181 LTKQLLHCMA CNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCR 240
 Qy 241 ELVAHHLSTLQSSILPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFSKDASKPEVPV 300
 Db 241 ELVAHHLSTLQSSILPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFSKDASKPEVPV 300
 Qy 301 RGTAAAFVHHLPAASGCKQTSTKRVKVEEMVEDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 Db 301 RGTAAAFVHHLPAASGCKQTSTKRVKVEEMVEDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 Qy 361 QEGHASPCLPPLQPVSVVM 377
 Db 361 QEGHASPCLPPLQPVSVVM 377

RESULT 2

AAW2185
 ID AAY52185 standard; protein; 377 AA.
 XX AC AAY52185;
 XX DT 09-FEB-2000 (first entry)
 XX DE Human cyclin I amino acid sequence.
 XX KW Cyclin-dependent kinase 2; CDK2; hsReg; hsReg*-1; hsReg*-2; cyclin I;
 XX KW ERF; cell cycle; proliferation; cancer; hyperproliferative disorder;
 XX KW atherosclerosis; tumour.
 XX OS Homo sapiens.
 XX FN WO9925829-A2.
 XX PD 27-MAY-1999.
 XX PF 12-NOV-1998; 98WO-US024095.
 XX PR 13-NOV-1997; 97US-00969106.
 XX PA (CURA-) CURAGEN CORP.
 XX PI Yang M, Nandabalan K, Schulz VP;
 XX DR WPI; 2000-061923/05.
 XX DR N-PSDB; AAZ37836.
 XX PT New complexes of the cyclin-dependent kinase 2 protein with its
 XX PT interacting proteins, used to treat, e.g. atherosclerosis.
 XX PS Example; Fig 2; 90pp; English.
 XX CC This is the human Cyclin I amino acid sequence. Cyclin I is expressed at
 XX CC almost constant levels throughout the cell cycle, and is implicated in

controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hReg, hReg*-1 and hReg*-2 (AAV52185-V52188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition. Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or atherosclerosis-associated disease by contacting cells or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 377; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60

Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180

Qy 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKAQMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKAQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360

Qy 361 QEGHASPCCPLQPVSV 377
Db 361 QEGHASPCCPLQPVSV 377

RESULT 3
ABR39934
ID ABR39934 standard; protein; 377 AA.
XX AC ABR39934;
XX AC ABR39934;
DT 11-AUG-2003 (first entry)
XX Human prostate selective polypeptide Pr325.
XX Prostate; molecular marker; cancer; cytostatic; gene therapy; human.
XX Homo sapiens.
XX WO2003014298-A2.
FN
XX

PD 20-FEB-2003.
XX 02-AUG-2002; 2002WO-US024431.
XX 03-AUG-2001; 2001US-0309470P.
XX 30-OCT-2001; 2001US-0330747P.
XX (ORIG-) ORIGENE TECHNOLOGIES INC.
PA Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
PI WPI: 2003-256562/25.
XX N-PSDB; ACC47339.
DR New polynucleotide, useful for preparing a composition for treating
XX prostate disease, e.g., cancer.
XX Claim 5; Page 147-149; 212pp; English.
XX The invention relates to prostate selective polynucleotides and
XX polypeptides. The polynucleotides are expressed in prostate and are
XX useful as molecular markers, as drug targets, and for detecting,
XX monitoring, preventing or treating diseases and conditions related to
XX prostate, such as prostate cancers. The present sequence represents a
XX prostate specific polypeptide

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 377; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
Db 1 MKFPGPLENQLSFLLEKAITREAQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60

Qy 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180

Qy 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKAQMDSSQLIHCR 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKAQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIKRLYNEDNVSENVSGVCGTDLR 360

Qy 361 QEGHASPCCPLQPVSV 377
Db 361 QEGHASPCCPLQPVSV 377

RESULT 4
ADP12615
ID ADP12615 standard; protein; 377 AA.
XX AC ADP12615;
XX AC ADP12615;
DT 12-AUG-2004 (first entry)
XX Protein encoded by mRNA of the invention #225.
XX transplacent rejection; immune system; rheumatoid arthritis; lupus;
XX inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
KW

XX OS Homo sapiens.
XX PN WO2004042346-A2.
XX PD 21-MAY-2004.
XX PF 24-APR-2003; 2003WO-US012946.
XX PR 24-APR-2002; 2002US-00131831.
XX PR 20-DEC-2002; 2002US-00325899.
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX PI Rosenberg S;
XX PI WPI; 2004-400724/37.
XX DR Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX PT the genes.
XX PS Claim 65; SEQ ID NO 2624; 1762pp; English.
XX CC The present invention relates to diagnosing or monitoring transplant
XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX CC comprises detecting the expression level of one or more genes. The
XX CC methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX CC islet, lung, bone marrow or stem cell transplant rejection,
XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
XX CC individual. The method is also useful in assessing the immune status of
XX CC an individual. The methods are also useful in diagnosing and monitoring
XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX CC viral, bacterial or fungal infection. The present sequence represents a
XX CC protein that is encoded by the mRNA of the invention.
XX SQ Sequence 377 AA;
Query Match 100.0%; Score 377; DB 8; Length 377;
Best Local Similarity, 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKFPGLENQRLSFLEKAITREAQMKVYVRKMPNSQNVSPQRDEVIQWLAKLYQFN 60
DB 1 MKFPGLENQRLSFLEKAITREAQMKVYVRKMPNSQNVSPQRDEVIQWLAKLYQFN 60
QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120
DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIATVSTRPOLLPSLPKSQHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIATVSTRPOLLPSLPKSQHLAV 180
QY 181 LTKQLLHMCACNQLQFQGMALAMVLSLEKLIPOWLSLTIQLLOKQWDSQLTHCR 240
DB 181 LTKQLLHMCACNQLQFQGMALAMVLSLEKLIPOWLSLTIQLLOKQWDSQLTHCR 240
QY 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDPFSDKNSKPEVPV 300
DB 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDPFSDKNSKPEVPV 300
QY 301 RGTAAFYHLLPAAGCKQTSTKRKVEEVEDDFDVGIKRLYNENNVENGVSGVGTDLR 360
DB 301 RGTAAFYHLLPAAGCKQTSTKRKVEEVEDDFDVGIKRLYNENNVENGVSGVGTDLR 360
QY 361 QEGHASPCLPQPVSV 377
DB 361 QEGHASPCLPQPVSV 377

RESULT 5

AAE37938
ID AAE37938 standard; protein; 334 AA.

XX
AC AAE37938;

DT 06-NOV-2003 (first entry)

DE Human CGDD-27 protein.

XX Human; cell growth, differentiation and death protein; CGDD; leukaemia;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
KW protozoacide; nootropic.

XX Homo sapiens.

OS WO2003050253-A2.

XX 19-JUN-2003.

XX 04-DEC-2002; 2002WO-US039133.

XX 07-DEC-2001; 2001US-0340747P.

XX 20-DEC-2001; 2001US-0342761P.

XX 15-JAN-2002; 2002US-0349705P.

XX 06-FEB-2002; 2002US-0354764P.

XX 12-FEB-2002; 2002US-0356216P.

XX (INCY-) INCYTE GENOMICS INC.

XX Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
PI Burriil JD, Blake JJ, Ho A, Zheng W;

XX WPI; 2003-532903/50.

XX N-PSDB; AAD57247.

XX New CGDD polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with an abnormal expression or activity of CGDD,
PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer,
PT and/or infections.

XX Claim 1; Page 250; 299pp; English.

XX The present invention relates to novel cell growth, differentiation and
PS death (CGDD) proteins and polynucleotides encoding them. The sequences of
XX the invention are useful in diagnosing, preventing and treating disorders
CC associated with an abnormal expression or activity of CGDD such as
CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
CC disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
CC create humanised animals or transgenic animals to model human diseases.
CC The invention is also used in gene therapy. The present sequence is human
CC CGDD-27 protein

SO	Sequence 334 AA;	
Query Match	78.5%; Score 296; DB 7; Length 334;	
Best Local Similarity	100.0%; Pred. No. 1.1e-283;	
Matches 296; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	82 AHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDSEFCGSSSEILRMERIIIDKLNWD 141	
DB	39 AHPKYLSCIAISCFPLAAKTVEEDERIPVLKVLARDSEFCGSSSEILRMERIIIDKLNWD 98	
QY	142 LHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAVLKQLHMCACNQLLQFRGSM 201	
DB	99 LHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAVLKQLHMCACNQLLQFRGSM 158	
QY	202 LALAMVSLMEKLIIPDWLSLTIELLQKQAMDSQSLIHCRELVANHLSTLQSSPLNSVYV 261	
DB	159 LALAMVSLMEKLIIPDWLSLTIELLQKQAMDSQSLIHCRELVANHLSTLQSSPLNSVYV 218	
QY	262 YRPLKHTLVATCDKGVFRLHPSSVPGDPFSKNSKPEVPVRCGTAAFYHHLPAASGCKQTST 321	
DB	219 YRPLKHTLVATCDKGVFRLHPSSVPGDPFSKNSKPEVPVRCGTAAFYHHLPAASGCKQTST 278	
QY	322 KRKVEEMEVDVDFYDGIKELYNEDNVSENVGVCCTDLRSRQCHASPCPPLQPVSM 377	
DB	279 KRKVEEMEVDVDFYDGIKELYNEDNVSENVGVCCTDLRSRQCHASPCPPLQPVSM 334	
RESULT 6		
ABM80569		
ID	ABM80569 standard; protein; 377 AA.	
XX	ABM80569;	
AC		
XX	18-NOV-2004 (first entry)	
DT		
XX	Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.	
DE		
XX	Tumour-associated antigenic target; TAT; human; overexpression; cancer;	
KW	tumour; diagnosis; cell proliferative disorder; breast cancer;	
KW	colorectal cancer; lung cancer; ovarian cancer; liver cancer;	
KW	central nervous system cancer; bladder cancer; pancreatic cancer;	
KW	cervical cancer; melanoma; leukaemia; hybridisation probe;	
KW	chromosome identification; chromosome mapping; gene mapping;	
KW	gene therapy; cytostatic.	
XX		
OS	Homo sapiens.	
XX		
PN	WO2004030615-A2.	
XX		
PD	15-APR-2004.	
XX		
PF	29-SEP-2003; 2003WO-US028547.	
XX		
PR	02-OCT-2002; 2002US-0414971P.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Wu TD, Zhang Z, Zhou Y;	
XX		
DR	WPI; 2004-347921/32.	
DR	N-PSDB; ACN38124.	
XX		
PT	New tumor-associated antigenic target polypeptides and nucleic acids,	
PT	useful in preparing a medicament for treating or detecting a	
PT	proliferative disorder, e.g. breast, lung, colorectal, ovarian or	
PT	prostate cancer or tumor.	
XX		
PS	Claim 12; SEQ ID NO 1450; 7273pp; English.	
XX		
CC	The invention relates to human tumour-associated antigenic target (TAT)	
CC	polypeptides, and their related nucleic acids. The TAT polypeptides are	
CC	overexpressed in cancer tissues compared to normal tissues, and may thus	
CC	serve as effective targets for the diagnosis and treatment of cancer in	
CC		
CC	mammals. The invention also relates to nucleic acid and polypeptide	
CC	sequences at least 80% identical to the TAT nucleic acids and	
CC	polypeptides; expression vectors and host cells comprising a TAT nucleic	
CC	acid; an antibody specific for a TAT polypeptide; a peptide or organic	
CC	molecule which binds to a TAT polypeptide; fusion proteins comprising a	
CC	TAT polypeptide; and methods and compositions for the treatment or	
CC	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,	
CC	antibodies, antigonists, binding molecules and compositions are useful	
CC	for diagnosing or treating a cell proliferative disorder associated with	
CC	increased TAT expression, particularly cancers such as breast cancer,	
CC	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder	
CC	cancer, pancreatic cancer, cervical cancer, cancers of the central	
CC	nervous system, melanoma and leukaemia. TAT nucleic acids may further be	
CC	used as hybridisation probes, in chromosome and gene mapping, in	
CC	chromosome identification and in gene therapy. The present sequence	
CC	represents a TAT polypeptide of the invention	
XX		
SQ	Sequence 377 AA;	
Query Match	73.2%; Score 276; DB 8; Length 377;	
Best Local Similarity	99.7%; Pred. No. 7.4e-264;	
Matches 376; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 MKFPGPLENORLSFLLKAITREAQMKVNVKMPSONVSPSORDEVIOWLAKLYQFN 60	
DB	1 MKFPGPLENORLSFLLKAITREAQMKVNVKMPSONVSPSORDEVIOWLAKLYQFN 60	
QY	61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120	
DB	61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPC 120	
QY	121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180	
DB	121 GCSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIAVSTRPQLLFSLPKLSPSOHLAV 180	
QY	181 LTKQLLHMCACNQLLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLQKQAMDSQSLIHCR 240	
DB	181 LTKQLLHMCACNQLLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLQKQAMDSQSLIHCR 240	
QY	241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDPFSKNSKPEVPV 300	
DB	241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDPFSKNSKPEVPV 300	
QY	301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDVDFYDGIKELYNEDNVSENVGVCCTDLRSR 360	
DB	301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDVDFYDGIKELYNEDNVSENVGVCCTDLRSR 360	
QY	361 QEGHASPCPPLQPVSM 377	
DB	361 QEGHASPCPPLQPVSM 377	
RESULT 7		
ADN01131		
ID	ADN01131 standard; protein; 300 AA.	
XX		
AC	ADN01131;	
XX		
DT	01-JUL-2004 (first entry)	
XX		
DE	Human cell growth, differentiation, and death-associated protein #15.	
XX		
KW	human; cell growth; cell differentiation; cell death; CGDD;	
KW	cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;	
KW	cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;	
KW	developmental disorder; Cushing's syndrome; hypothyroidism;	
KW	neurological disorder; epilepsy; stroke; Alzheimer's disease;	
KW	Pick's disease; Huntington's disease; Parkinson's disease;	
KW	multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;	
KW	allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;	
KW	reproductive disorder; infertility; endometriosis; uterine fibroid.	
XX		
OS	Homo sapiens.	

KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
XX OS Homo sapiens.
XX WO200164835-A2.
XX
XX PD 07-SEP-2001.
XX
XX PF 26-FEB-2001; 2001WO-US004927.
XX
XX PR 28-FEB-2000; 2000US-00515126.
XX PR 18-MAY-2000; 2000US-00577409.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT;
XX WPI; 2001-514838/56.
XX DR N-PSDB; AAI91566.
XX
XX PT Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX PS Claim 20; SEQ ID NO 2527; 1399pp + Sequence Listing; English.
XX
XX CC The invention relates to human polynucleotides (AAI79941-AAI93841) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIFO at ffp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 41 AA;

Query Match 9.0%; Score 34; DB 4; Length 41;
Best Local Similarity 100.0%; Pred. No. 2.1e-25;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENQLSFLLEKAITREAOQWKVNRKM 34
DB 8 MKFPGPLENQLSFLLEKAITREAOQWKVNRKM 41

RESULT 10
AAW21966
ID AAW21966 standard; protein; 14 AA.
XX
XX AC AAW21966;
XX
XX DT 02-DEC-1997 (first entry)
XX
XX DE Human cyclin I peptide fragment.
XX
XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX
XX OS Homo sapiens.
XX
XX PN WO9712973-A1.
XX
XX PD 10-APR-1997.
XX
XX PF 07-OCT-1996; 96WO-JP002905.
XX

PR 05-OCT-1995; 95JP-00284663.
FA (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX PI Nakamura T;
XX
XX DR WPI; 1997-226217/20.
XX
XX PT Human cyclin I protein and related (anti:sense) DNA - used for neuron
XX labelling method and cancer cell detection.
XX
XX PS Claim 7; Page 30; 45pp; Japanese.
XX
XX CC This peptide is a fragment of human cyclin I which can be specifically
XX recognised by antibodies of the invention. The antibodies are used to
XX detect the presence of cyclin I. Antisense cyclin I polynucleotides are
XX useful for as probes and can be labelled and used for detection of
XX neurones by hybridisation with mRNA for cyclin I (contained in the
XX neurones and arising by the expression of the cyclin I gene in these
XX cells). The gene can be used for detection of cancer cells by detecting
XX the expression of the cyclin I gene in these cells
XX
XX SQ Sequence 14 AA;

Query Match 3.7%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 343 EDNVSENVGSGVCGT 356
DB 1 EDNVSENVGSGVCGT 14

RESULT 11
ABJ20156
ID ABJ20156 standard; peptide; 10 AA.
XX
XX AC ABJ20156;
XX
XX DT 10-APR-2003 (first entry)
XX
XX DE MHC binding peptide SEQ ID No 321.
XX
XX KW Antirheumatic; antiallergic; antiarthritic; nootropic; neuroprotective;
XX antiinflammatory; major histocompatibility complex; MHC;
XX autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
XX rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
XX inflammation; gene therapy; MHC binding peptide.
XX
XX OS Synthetic.
XX
XX PN WO200294981-A2.
XX
XX PD 28-NOV-2002.
XX
XX PF 16-MAY-2002; 2002WO-IL000383.
XX
XX PR 16-MAY-2001; 2001US-0290958P.
XX PR 29-MAY-2001; 2001US-00865548.
XX
XX PA (TECR) TECHNION RES & DEV FOUND LTD.
XX
XX PI Barnea E, Beer I, Ziv T, Admon A, Dassau L, Buchsbaum S;
XX
XX DR WPI; 2003-210043/20.
XX
XX PT Identifying peptides that are capable of binding to major
XX histocompatibility complex (MHC) molecules of a particular haplotype by
XX analyzing peptides bound to the soluble and secreted form of the MHC
XX molecules of the particular haplotype.
XX
XX PS Claim 58; Page 225; 238pp; English.
XX

CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The
 CC method is useful for identifying peptides for treating an autoimmune
 CC disease, such as T or B cell and/or allergic disease or condition,
 CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
 CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
 CC sequences of the invention may be used in a gene therapy application.
 CC This sequence represents a peptide relating to the method for identifying
 CC MHC binding peptides of the invention

XX
 SQ Sequence 10 AA;
 Query Match 2.7%; Score 10; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.03; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

Qy 71 SLDRFLATV 80
 Db 1 SLDRFLATV 10
 |||||

RESULT 12
 ABG32308
 ID ABG32308 standard; peptide; 9 AA.

XX AC ABG32308;

XX DT 05-NOV-2002 (first entry)

XX DE HLA-A2 associated immunogenic peptide from human Cyclin protein.

XX KW Human; immunogen; epitope; HLA-A1; human leukocyte antigen; CTL;
 KW cytotoxic T lymphocyte; cytotoxic; cancer; colorectal carcinoma;
 KW ovarian carcinoma; lung carcinoma; prostate carcinoma; vaccine; tumour;
 KW HLA-2; passive immunotherapy; cyclin.

XX OS Homo sapiens.

XX FN WO200246416-A2.

XX PD 13-JUN-2002.

XX PF 04-DEC-2001; 2001WO-US047290.

XX PR 04-DEC-2000; 2000US-0251022P.

XX PR 20-DEC-2000; 2000US-0256824P.

XX PA (ARGO-) ARGONEX INC.

XX PI Ramakrishna V, Ross M, Philip R;

XX DR WPI; 2002-619021/66.

XX PT New immunogen useful as a vaccine for inducing cytotoxic T-lymphocyte,
 XX and for diagnosing, preventing or treating cancer e.g. ovarian carcinoma.

XX PS Claim 1; Page 50; 60pp; English.

XX
 CC The invention relates to an immunogen comprising an isolated polypeptide
 CC whose amino acid sequence comprises an epitopic peptide, does not include
 CC MAGE 4 or MFG-E8 proteins, or consists of MAGE D protein or its
 CC immunologically active fragment. Also included are a polynucleotide
 CC encoding the immunogen or its complement, a vector comprising the
 CC polynucleotide, a mammalian cell comprising the vector and expressing the
 CC polynucleotide, a vaccine composition comprising the immunogen and an
 CC antibody specific for the immunogen. The immunogen is useful for inducing
 CC a cytotoxic T lymphocyte (CTL) in vitro that is specific for a tumour
 CC cell expressing human leukocyte antigen (HLA)-A1 or A2. The immunogen is
 CC useful for inducing a CTL response when administered to a subject. A
 CC mammalian cell that can express the immunogen, is useful for inducing a

CC CTL response in vitro that is specific for a tumour cell expressing HLA-1
 CC or HLA-2. The immunogen or cell is useful for inducing CTL for treating a
 CC subject with cancer (carcinoma, preferably colorectal carcinoma, ovarian
 CC carcinoma, lung carcinoma and prostate carcinoma). The immunogen is also
 CC useful for screening and diagnostic agents, for gene screening in
 CC patients afflicted with cancer, for screening a sample for the presence
 CC of CTLs that specifically recognise the corresponding epitopes, as a
 CC diagnostic tool to evaluate the efficacy of the immunotherapeutic
 CC treatments, to prepare class I MHC (major histocompatibility class)
 CC tetramers which are utilised in conjunction with flow cytometry to
 CC quantitate the frequency of peptide-specific CTL that are present in a
 CC samples of lymphocytes from an individual, and for stimulating the
 CC production of antibodies for use in passive immunotherapy, for use as
 CC diagnostic reagents, and for use as reagents in other processes such as
 CC affinity chromatography. The present sequence is an immunogenic epitope
 CC of the invention derived from human cyclin

SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRFLATV 80
 Db 1 LLDRFLATV 9
 |||||

RESULT 13

ABJ19986

ID ABJ19986 standard; peptide; 9 AA.

XX AC ABJ19986;

XX DT 10-APR-2003 (first entry)

XX DE MHC binding peptide SEQ ID No 151.

XX KW Antirheumatic; anti-allergic; antiarthritic; nootropic; neuroprotective;
 KW anti-inflammatory; major histocompatibility complex; MHC;
 KW autoimmune disease; T cell; B cell; allergic disease; multiple sclerosis;
 KW rheumatoid arthritis; neurodegenerative disorder; Alzheimer's disease;
 KW inflammation; gene therapy; MHC binding peptide.

XX OS Synthetic.

XX FN WO200294981-A2.

XX PD 28-NOV-2002.

XX PF 16-MAY-2002; 2002WO-IL000383.

XX PR 16-MAY-2001; 2001US-0290958P.

XX PR 29-MAY-2001; 2001US-00865548.

XX PA (TECR) TECHNION RES & DEV FOUND LTD.

XX PI Barnea E, Beer I, Ziv T, Admon A, Dassaou L, Buchsbaum S;

XX DR WPI; 2003-210043/20.

XX
 CC Identifying peptides that are capable of binding to major
 CC histocompatibility complex (MHC) molecules of a particular haplotype by
 CC analysing peptides bound to the soluble and secreted form of the MHC
 CC molecules of the particular haplotype.

XX FS Claim 37; Page 183; 238pp; English.

XX
 CC The invention relates to a novel method for identifying peptides
 CC originating from a particular cell type, which are capable of binding to
 CC major histocompatibility complex (MHC) molecules of a particular
 CC haplotype. The method comprises analysing peptides bound to the soluble
 CC and secreted form of the MHC molecules of the particular haplotype. The

CC method is useful for identifying peptides for treating an autoimmune
CC disease, such as T or B cell and/or allergic disease or condition,
CC rheumatoid arthritis, or multiple sclerosis, neurodegenerative disorders,
CC e.g. Alzheimer's disease, or diseases associated with inflammation. The
CC sequences of the invention may be used in a gene therapy application.
CC This sequence represents a peptide relating to the method for identifying
CC MHC binding peptides of the invention

XX SQ Sequence 9 AA;

Query Match 2.4%; Score 9; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRFLATV 80
| | | | | | | |
Db 1 LLDRFLATV 9

RESULT 14
AAW85684
ID AAW85684 standard; protein; 462 AA.

XX AC AAW85684;

XX DT 19-JUL-1999 (first entry)

XX DE NBP46 root lectin.

XX KW NBP46; lectin; Rhizobium; leguminous plant; transgenic plant; nitrogen;
XX KW nitrogen fixation; fertilizer.

XX OS Dolichos biflorus.

XX EH Key Location/Qualifiers

FT Region 52..73
/label= Conserved region
/note= "Conserved among various plant and animal
FT pyrases"

FT Region 128..144
/label= Conserved region
/note= "Conserved among various plant and animal
FT pyrases"

FT Modified-site 139
/note= "Potential N-glycosylation site"

FT Region 153..175
/label= Conserved region
/note= "Conserved among various plant and animal
FT pyrases"

FT Region 160..180
/label= Conserved region
/note= "Conserved among various plant and animal
FT pyrases"

FT Modified-site 276
/note= "Potential N-glycosylation site"

XX WO9907223-A1.

XX PD 18-FEB-1999.

XX PF 05-AUG-1998; 98WO-US016261.

XX PR 06-AUG-1997; 97US-00907226.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Etzler ME, Murphy JB;

XX DR WPI; 1999-167136/14.

XX DR N-PSDB; AAX08522.

XX PT New polynucleotides encoding Nod factor binding lectins - useful for
PT production of transgenic plants which are able to fix nitrogen.

XX PS Claim 7; Page 43; 57pp; English.

XX CC The NBP46 root lectin is instrumental in recognising and binding to
CC nitrogen fixing rhizobial bacteria via a lectin-carbohydrate interaction.
CC The production of transgenic plants comprising an expression cassette
CC expressing the NBP46 root lectin is advantageous since it would mean that
CC non-leguminous plants could fix nitrogen from the atmosphere, lessening
CC the need for the addition of nitrogen containing fertilizer to soil. This
CC would lead to higher crop yields where soil has been overplanted and
CC replenishment of the depleted soil with usable nitrogen. Alternatively,
CC expression of NBP46 can be used to modulate oligosaccharide signalling in
CC the plant. The nucleic acid sequences can be used to inhibit expression
CC of an endogenous gene and also to suppress endogenous NBP46 gene
XX expression

XX SQ Sequence 462 AA;

Query Match 2.4%; Score 9; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 LLFSLPKLS 173
| | | | | | | |

Db 20 LLFSLPKLS 28

RESULT 15

AAU78818
ID AAU78818 standard; protein; 462 AA.

XX AC AAU78818;

XX DT 18-JUN-2002 (first entry)

XX DE Dolichos biflorus lectin/nucleotide phosphohydrolase, LNP.

XX KW Lectin/nucleotide phosphohydrolase; LNP; mycorrhizal infection;
XX KW carbohydrate binding protein; nucleotide dephosphorylation;
XX KW oligosaccharide signalling; nutrient uptake; plant growth;
XX KW plant development; antisense technology.

XX OS Dolichos biflorus.

XX EH Key Location/Qualifiers

FT Peptide 1..48
/label= Signal_peptide

FT Protein 49..462
/label= Mature LNP

FT /note= "Lectin/nucleotide phosphohydrolase"

XX WO200220725-A2.

XX PD 14-MAR-2002.

XX PF 06-SEP-2001; 2001WO-US028165.

XX PR 06-SEP-2000; 2000US-00657631.

XX PA (REGC) UNIV CALIFORNIA.

XX PI Etzler ME, Roberts NJ;

XX DR WPI; 2002-304376/34.

XX DR N-PSDB; ABK11098.

XX PT Modulating mycorrhizal infection, useful for improving plant growth, by
PT transforming plant cell with a sequence encoding lectin/nucleotide
PT phosphohydrolase.

XX PS Claim 1; Page 31; 37pp; English.

XX PT The invention describes a method of modulating mycorrhizal infection by

CC introducing into a plant an expression cassette comprising a plant
CC promoter operably linked to a heterologous LNP (lectin/nucleotide
CC phosphohydrolase) polynucleotide, or its complement. The LNP's described
CC in the invention are involved in binding a variety of carbohydrates,
CC catalysing the dephosphorylation of nucleotide di- and tri-phosphates and
CC are suspected to be involved in oligosaccharide signalling, important for
CC the interaction of mycorrhizal fungi and plants. The method is useful to
CC increase mycorrhizal infection (by increasing expression of the
CC polynucleotide), resulting in increased uptake of nutrients by plants and
CC better growth/development, but antisense (or other methods of)
CC suppression of LNP expression is also contemplated. This is the amino
CC acid sequence of the Dolichos biflorus lectin/nucleotide phosphohydrolase
CC (LNP) that can be used to modulate mycorrhizal infection in plants
XX
SQ Sequence 462 AA;

Query Match 2.4%; Score 9; DB 5; Length 462;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 LLFSLPKLS 173
| | | | | | | | | |
Db 20 LLFSLPKLS 28

Search completed: February 11, 2005, 03:16:03
Job time : 162.061 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:39 ; Search time 32.7826 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGPLENQRSLFLEKAI.....LSRQEGHASPCPLQPVSM 377

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA.*

- 1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	377	2	US-08-969-106-6
2	377	100.0	377	3	US-09-054-492B-1
3	377	100.0	377	4	US-09-338-125-6
4	254	67.4	254	4	US-09-796-149B-4
5	131	34.7	131	4	US-09-513-999C-5984
6	14	3.7	14	3	US-09-054-492B-5
7	9	2.4	462	4	US-09-129-112-2
8	8	2.1	127	4	US-09-270-767-57798
9	8	2.1	170	4	US-09-270-767-39916
10	8	2.1	170	4	US-09-270-767-55133
11	7	1.9	21	3	US-09-128-155-12
12	7	1.9	52	3	US-09-128-155-8
13	7	1.9	63	3	US-09-128-155-4
14	7	1.9	70	4	US-09-270-767-34602
15	7	1.9	70	4	US-09-270-767-49819
16	7	1.9	78	4	US-09-248-796A-25813
17	7	1.9	85	4	US-09-543-681A-8234
18	7	1.9	136	3	US-09-128-155-11
19	7	1.9	146	2	US-08-788-943A-6
20	7	1.9	146	2	US-08-788-943A-10
21	7	1.9	146	2	US-08-788-943A-11
22	7	1.9	146	2	US-08-823-104-6
23	7	1.9	146	2	US-08-823-104-15
24	7	1.9	146	3	US-08-674-774-6
25	7	1.9	146	3	US-08-674-774-10
26	7	1.9	146	3	US-08-674-774-11
27	7	1.9	146	5	PCT-US96-00952-4
28	7	1.9	146	5	PCT-US96-00952-8
29	7	1.9	146	5	PCT-US96-00952-9
30	7	1.9	146	2	US-08-823-104-17
31	7	1.9	167	3	US-09-128-155-7
32	7	1.9	178	3	US-09-128-155-2
33	7	1.9	211	4	US-09-134-000C-4334
34	7	1.9	218	3	US-09-233-625-2
35	7	1.9	218	4	US-09-398-412B-2
36	7	1.9	218	4	US-09-398-412B-4
37	7	1.9	231	4	US-09-248-796A-15072
38	7	1.9	235	4	US-09-248-796A-15284
39	7	1.9	243	3	US-09-446-504-1
40	7	1.9	243	3	US-09-712-266-1
41	7	1.9	252	4	US-09-107-532A-6519
42	7	1.9	264	4	US-09-248-796A-15036
43	7	1.9	272	4	US-09-949-016-8863
44	7	1.9	274	4	US-09-328-352-5444
45	7	1.9	287	4	US-09-489-039A-10887
46	7	1.9	302	3	US-09-457-046B-8
47	7	1.9	302	3	US-09-457-046B-24
48	7	1.9	302	4	US-09-866-570B-8
49	7	1.9	302	4	US-09-866-570B-24
50	7	1.9	306	3	US-09-457-046B-2
51	7	1.9	306	4	US-09-866-570B-2
52	7	1.9	322	4	US-09-328-352-5489
53	7	1.9	328	4	US-09-252-991A-31963
54	7	1.9	350	4	US-09-800-729-91
55	7	1.9	350	4	US-09-800-729-127
56	7	1.9	354	4	US-09-328-352-7262
57	7	1.9	370	4	US-09-252-991A-24608
58	7	1.9	428	4	US-09-789-599A-2
59	7	1.9	437	3	US-08-757-230A-2
60	7	1.9	437	3	US-08-757-230A-9
61	7	1.9	437	4	US-08-700-393-2
62	7	1.9	437	5	PCT-US95-02315-2
63	7	1.9	439	3	US-09-457-046B-28
64	7	1.9	439	4	US-09-866-570B-28
65	7	1.9	441	4	US-09-949-016-10792
66	7	1.9	446	4	US-09-538-092-781
67	7	1.9	448	3	US-09-457-046B-56
68	7	1.9	448	4	US-09-866-570B-56
69	7	1.9	464	2	US-08-477-451-18
70	7	1.9	500	4	US-09-142-108C-4
71	7	1.9	508	4	US-09-142-108C-17
72	7	1.9	528	2	US-08-484-956-90
73	7	1.9	528	2	US-08-757-653-90
74	7	1.9	528	3	US-08-520-946-90
75	7	1.9	528	4	US-09-655-378A-90
76	7	1.9	560	4	US-09-949-016-6458
77	7	1.9	560	4	US-09-912-559-3
78	7	1.9	560	4	US-09-912-559-4
79	7	1.9	621	4	US-09-902-540-9744
80	7	1.9	626	4	US-09-248-796A-14855
81	7	1.9	739	4	US-09-489-039A-11874
82	7	1.9	752	4	US-09-252-991A-30127
83	7	1.9	789	3	US-08-727-308-1
84	7	1.9	833	2	US-08-484-956-85
85	7	1.9	833	2	US-08-757-653-85
86	7	1.9	833	3	US-08-520-946-85
87	7	1.9	833	4	US-08-758-282B-40
88	7	1.9	833	4	US-09-655-378A-85
89	7	1.9	833	4	US-09-577-304A-40
90	7	1.9	1045	2	US-08-553-436A-6
91	7	1.9	1045	4	US-09-394-272-7
92	7	1.9	1228	4	US-09-949-016-6805
93	7	1.9	1236	4	US-09-949-016-10398
94	6	1.6	13	1	US-08-324-301-5
95	6	1.6	14	1	US-08-182-967-23
96	6	1.6	23	4	US-09-149-476-621
97	6	1.6	23	4	US-09-618-304B-8
98	6	1.6	30	3	US-09-136-251-7
99	6	1.6	30	4	US-09-634-496-7
100	6	1.6	30	4	US-09-635-145A-7

Sequence 8, Appli
Sequence 9, Appli
Sequence 17, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 4334, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 4, Appli
Sequence 15072, A
Sequence 15284, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 6519, Ap
Sequence 15036, A
Sequence 8463, Ap
Sequence 5444, Ap
Sequence 10887, A
Sequence 8, Appli
Sequence 24, Appli
Sequence 8, Appli
Sequence 24, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 5489, Ap
Sequence 31963, A
Sequence 91, Appli
Sequence 127, App
Sequence 127, App
Sequence 24608, A
Sequence 2, Appli
Sequence 2, Appli
Sequence 9, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 28, Appli
Sequence 28, Appli
Sequence 10792, A
Sequence 781, App
Sequence 56, Appli
Sequence 56, Appli
Sequence 18, Appli
Sequence 4, Appli
Sequence 17, Appli
Sequence 90, Appli
Sequence 90, Appli
Sequence 90, Appli
Sequence 6458, Ap
Sequence 4, Appli
Sequence 4, Appli
Sequence 9744, Ap
Sequence 14855, A
Sequence 11874, A
Sequence 30127, A
Sequence 1, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 85, Appli
Sequence 40, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 6805, Ap
Sequence 10398, A
Sequence 23, Appli
Sequence 621, App
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli

101	6	1.6	31	2	US-08-526-583-15	Sequence 15, Appl	174	4	US-09-543-681A-7624	Sequence 7624, Ap
102	6	1.6	32	2	US-08-526-583-13	Sequence 13, Appl	175	4	US-09-902-540-11774	Sequence 11774, A
103	6	1.6	32	2	US-08-526-583-14	Sequence 14, Appl	176	4	US-09-134-000C-4513	Sequence 4513, Ap
104	6	1.6	32	2	US-08-526-583-16	Sequence 16, Appl	177	4	US-09-583-110-4875	Sequence 4875, Ap
105	6	1.6	38	4	US-09-203-258-721	Sequence 721, Appl	178	1	US-08-122-546-12	Sequence 12, Appl
106	6	1.6	40	4	US-09-902-540-15209	Sequence 15209, A	179	1	US-07-942-245-14	Sequence 14, Appl
107	6	1.6	43	1	US-07-745-206A-30	Sequence 30, Appl	180	6	US-08-764-938-12	Sequence 12, Appl
108	6	1.6	43	1	US-08-455-543A-57	Sequence 57, Appl	181	6	US-09-131-052-12	Sequence 12, Appl
109	6	1.6	43	2	US-08-223-305C-57	Sequence 57, Appl	182	6	US-09-131-053A-12	Sequence 12, Appl
110	6	1.6	43	2	US-08-311-363-30	Sequence 30, Appl	183	6	US-09-248-796A-24843	Sequence 24843, A
111	6	1.6	48	2	US-08-460-890A-49	Sequence 49, Appl	184	6	US-09-252-991A-21351	Sequence 21351, A
112	6	1.6	48	3	US-08-167-641C-49	Sequence 49, Appl	185	6	US-08-467-420A-15	Sequence 15, Appl
113	6	1.6	48	3	US-08-460-971A-49	Sequence 49, Appl	186	6	US-08-470-110A-15	Sequence 15, Appl
114	6	1.6	48	3	US-08-462-040-49	Sequence 49, Appl	187	6	US-08-940-371-15	Sequence 15, Appl
115	6	1.6	49	2	US-08-460-890A-48	Sequence 48, Appl	188	6	US-08-637-647-15	Sequence 15, Appl
116	6	1.6	49	3	US-08-167-641C-48	Sequence 48, Appl	189	6	US-09-270-767-39367	Sequence 39367, A
117	6	1.6	49	3	US-08-460-971A-48	Sequence 48, Appl	190	6	US-09-270-767-54584	Sequence 54584, A
118	6	1.6	49	3	US-08-462-040-48	Sequence 48, Appl	191	6	US-09-902-540-13065	Sequence 13065, A
119	6	1.6	50	4	US-09-621-976-7723	Sequence 7723, Ap	192	6	US-08-795-868-18	Sequence 18, Appl
120	6	1.6	51	3	US-08-630-916A-117	Sequence 117, Appl	193	6	US-09-303-069-18	Sequence 18, Appl
121	6	1.6	52	3	US-09-330-330-12	Sequence 12, Appl	194	6	US-09-134-250-18	Sequence 18, Appl
122	6	1.6	52	3	US-09-621-976-5568	Sequence 5568, Ap	195	6	US-09-726-219A-218	Sequence 218, App
123	6	1.6	58	4	US-09-270-767-35469	Sequence 35469, A	196	6	US-09-865-483-8	Sequence 8, Appli
124	6	1.6	58	4	US-09-270-767-50686	Sequence 50686, A	197	6	US-08-881-037-22	Sequence 22, Appl
125	6	1.6	58	4	US-09-248-796A-23846	Sequence 23846, A	198	6	US-08-122-546-8	Sequence 8, Appli
126	6	1.6	61	4	US-09-583-110-4730	Sequence 4730, Ap	199	6	US-08-764-938-8	Sequence 18, Appl
127	6	1.6	61	4	US-09-270-767-43046	Sequence 43046, A	200	6	US-08-308-494A-21	Sequence 21, Appl
128	6	1.6	61	4	US-09-270-767-58375	Sequence 58375, A	201	6	US-09-131-052-8	Sequence 8, Appli
129	6	1.6	61	4	US-09-248-796A-21236	Sequence 21236, A	202	6	US-08-397-411-4	Sequence 4, Appli
130	6	1.6	61	4	US-09-248-796A-25070	Sequence 25070, A	203	6	US-09-131-053A-8	Sequence 8, Appli
131	6	1.6	63	4	US-08-828-683A-28	Sequence 28, Appl	204	6	US-09-232-290-36	Sequence 36, Appl
132	6	1.6	63	4	US-09-543-681A-5520	Sequence 5520, Ap	205	6	US-09-615-192A-400	Sequence 400, App
133	6	1.6	64	4	US-09-248-796A-27960	Sequence 27960, A	206	6	US-09-732-210-653	Sequence 653, App
134	6	1.6	65	1	US-08-123-343A-2	Sequence 2, Appli	207	6	US-07-634-278-60	Sequence 60, Appl
135	6	1.6	66	4	US-09-513-999C-6589	Sequence 6589, Ap	208	6	US-08-477-728-60	Sequence 60, Appl
136	6	1.6	68	4	US-09-621-976-5772	Sequence 5772, Ap	209	6	US-08-474-040-60	Sequence 60, Appl
137	6	1.6	68	4	US-09-248-796A-22651	Sequence 22651, A	210	6	US-08-487-200-60	Sequence 60, Appl
138	6	1.6	68	4	US-09-513-999C-4893	Sequence 4893, Ap	211	6	US-08-667-769A-15	Sequence 15, Appl
139	6	1.6	69	4	US-09-205-258-439	Sequence 439, Ap	212	6	US-08-752-844-16	Sequence 16, Appl
140	6	1.6	70	3	US-08-851-843A-200	Sequence 200, App	213	6	US-08-591-196-16	Sequence 16, Appl
141	6	1.6	70	3	US-08-974-549A-319	Sequence 319, App	214	6	US-08-484-537-60	Sequence 60, Appl
142	6	1.6	70	3	US-08-854-050-200	Sequence 200, App	215	6	US-09-293-533-16	Sequence 16, Appl
143	6	1.6	70	3	US-09-430-323-200	Sequence 200, App	216	6	US-09-252-991A-24595	Sequence 24595, A
144	6	1.6	70	3	US-09-402-181B-319	Sequence 319, App	217	6	PCT-US95-17082A-15	Sequence 15, Appl
145	6	1.6	76	3	US-09-721-456-319	Sequence 319, App	218	6	US-08-652-558-8	Sequence 8, Appli
146	6	1.6	76	3	US-09-134-001C-4287	Sequence 4287, Ap	219	6	US-08-652-558-38	Sequence 38, Appl
147	6	1.6	77	4	US-09-248-796A-27483	Sequence 27483, A	220	6	US-09-254-189-5	Sequence 5, Appli
148	6	1.6	78	4	US-09-270-767-42639	Sequence 42639, A	221	6	US-08-881-037-67	Sequence 67, Appl
149	6	1.6	84	4	US-09-543-681A-5717	Sequence 5717, Ap	222	6	US-09-732-210-733	Sequence 733, App
150	6	1.6	85	4	US-09-513-999C-7654	Sequence 7654, Ap	223	6	US-09-461-325-355	Sequence 355, App
151	6	1.6	86	4	US-09-621-976-7127	Sequence 7127, Ap	224	6	US-09-198-452A-1225	Sequence 1225, Ap
152	6	1.6	88	4	US-09-583-110-2919	Sequence 2919, Ap	225	6	US-10-012-542-355	Sequence 355, App
153	6	1.6	88	4	US-09-107-433-4102	Sequence 4102, Ap	226	6	US-10-115-123-355	Sequence 355, App
154	6	1.6	89	4	US-09-107-532A-6179	Sequence 6179, Ap	227	6	US-09-232-290-41	Sequence 41, Appl
155	6	1.6	94	4	US-09-902-540-12396	Sequence 12396, A	228	6	US-09-328-352-5925	Sequence 5925, Ap
156	6	1.6	94	4	US-10-014-269-6	Sequence 6, Appli	229	6	US-09-248-796A-21935	Sequence 21935, A
157	6	1.6	95	4	US-09-205-258-314	Sequence 314, Ap	230	6	US-09-716-129-173	Sequence 173, App
158	6	1.6	95	4	US-09-471-276-1419	Sequence 1419, Ap	231	6	US-09-513-999C-4892	Sequence 4892, Ap
159	6	1.6	96	4	US-09-270-767-40163	Sequence 40163, A	232	6	US-09-949-016-11072	Sequence 11072, A
160	6	1.6	96	4	US-09-270-767-55379	Sequence 55379, A	233	6	US-09-248-796A-19032	Sequence 19032, A
161	6	1.6	97	3	US-08-881-037-66	Sequence 66, Appl	234	6	US-09-252-991A-23430	Sequence 23430, A
162	6	1.6	97	4	US-08-752-844-5	Sequence 5, Appli	235	6	US-09-270-767-42781	Sequence 42781, A
163	6	1.6	98	2	US-08-621-976-6523	Sequence 6523, Ap	236	6	US-09-248-796A-14793	Sequence 14793, A
164	6	1.6	98	2	US-08-591-196-5	Sequence 5, Appli	237	6	US-09-513-999C-7977	Sequence 7977, Ap
165	6	1.6	98	4	US-09-293-533-5	Sequence 5, Appli	238	6	US-09-774-639-114	Sequence 114, App
166	6	1.6	98	4	US-09-543-681A-5462	Sequence 5462, Ap	239	6	US-09-513-999C-7872	Sequence 7872, Ap
167	6	1.6	99	4	US-09-732-210-980	Sequence 980, App	240	6	US-08-621-751A-4	Sequence 4, Appli
168	6	1.6	99	4	US-09-270-767-57896	Sequence 57896, A	241	6	US-07-634-278-33	Sequence 33, Appl
169	6	1.6	100	4	US-09-328-352-6731	Sequence 6731, Ap	242	6	US-08-477-728-33	Sequence 33, Appl
170	6	1.6	100	4	US-09-248-796A-19747	Sequence 19747, A	243	6	US-08-474-040-33	Sequence 33, Appl
171	6	1.6	100	4	US-09-248-796A-20216	Sequence 20216, A	244	6	US-08-487-200-33	Sequence 33, Appl
172	6	1.6	102	4	US-09-621-976-4820	Sequence 4820, Ap	245	6	US-08-484-537-33	Sequence 33, Appl
173	6	1.6	102	4	US-09-513-999C-4693	Sequence 4693, Ap	246	6	US-09-438-185A-859	Sequence 859, App

247	6	1.6	139	4	US-09-640-211A-887	Sequence 887, App	320	6	1.6	206	4	US-09-394-142B-18	Sequence 18, Appl
248	6	1.6	141	4	US-09-248-796A-26930	Sequence 26930, A	321	6	1.6	208	4	US-09-107-532A-5399	Sequence 5399, Ap
249	6	1.6	142	4	US-09-248-796A-26917	Sequence 26917, A	322	6	1.6	210	4	US-09-710-279-708	Sequence 708, App
250	6	1.6	143	4	US-09-252-991A-21626	Sequence 21626, A	323	6	1.6	210	4	US-09-248-796A-15470	Sequence 15470, A
251	6	1.6	142	4	US-09-270-767-32362	Sequence 32362, A	324	6	1.6	210	4	US-09-949-016-7162	Sequence 7162, Ap
252	6	1.6	142	4	US-09-903-540-12459	Sequence 12459, A	325	6	1.6	212	1	US-08-353-341-1	Sequence 1, Appli
253	6	1.6	145	4	US-09-270-767-39030	Sequence 39030, A	326	6	1.6	212	4	US-09-270-767-42586	Sequence 42586, A
254	6	1.6	145	4	US-09-270-767-39030	Sequence 39030, A	327	6	1.6	212	4	US-09-270-767-41374	Sequence 41374, A
255	6	1.6	145	4	US-09-270-767-54247	Sequence 54247, A	328	6	1.6	214	4	US-09-270-767-56590	Sequence 56590, A
256	6	1.6	147	4	US-08-489-039A-12992	Sequence 12992, A	329	6	1.6	216	4	US-09-902-540-12039	Sequence 12039, A
257	6	1.6	152	2	US-08-752-844-4	Sequence 4, Appli	330	6	1.6	218	4	US-09-902-540-12039	Sequence 12039, A
258	6	1.6	152	3	US-09-591-196-4	Sequence 4, Appli	331	6	1.6	218	4	US-09-489-039A-10574	Sequence 10574, A
259	6	1.6	152	3	US-09-192-838B-4	Sequence 4, Appli	332	6	1.6	219	4	US-09-538-092-499	Sequence 499, App
260	6	1.6	152	4	US-09-293-533-4	Sequence 4, Appli	333	6	1.6	220	4	US-09-949-016-11039	Sequence 11039, A
261	6	1.6	152	4	US-09-324-131-4	Sequence 4, Appli	334	6	1.6	221	4	US-09-270-767-60149	Sequence 60149, A
262	6	1.6	152	4	US-09-732-210-872	Sequence 872, App	335	6	1.6	222	1	US-08-336-257A-5	Sequence 5, Appli
263	6	1.6	154	4	US-09-732-210-871	Sequence 871, App	336	6	1.6	222	2	US-08-190-199A-67	Sequence 67, Appl
264	6	1.6	154	4	US-09-732-210-873	Sequence 873, App	337	6	1.6	222	4	US-09-270-767-40120	Sequence 40120, A
265	6	1.6	157	4	US-09-270-767-33063	Sequence 33063, A	338	6	1.6	222	4	US-09-270-767-55336	Sequence 55336, A
266	6	1.6	157	4	US-09-270-767-48280	Sequence 48280, A	339	6	1.6	222	4	US-09-949-016-5983	Sequence 5983, Ap
267	6	1.6	158	2	US-08-414-938A-2	Sequence 2, Appli	340	6	1.6	222	6	5386025-2	Patent No. 5386025
268	6	1.6	159	4	US-09-270-767-38167	Sequence 38167, A	341	6	1.6	222	6	5386025-2	Patent No. 5386025
269	6	1.6	159	4	US-09-270-767-53384	Sequence 53384, A	342	6	1.6	222	6	5386025-2	Patent No. 5386025
270	6	1.6	160	4	US-09-394-142B-10	Sequence 10, Appl	343	6	1.6	224	3	US-08-871-572B-13	Sequence 13, Appl
271	6	1.6	160	4	US-09-903-540-13231	Sequence 13231, A	344	6	1.6	224	3	US-09-134-001C-4608	Sequence 4608, Ap
272	6	1.6	161	4	US-09-252-991A-23037	Sequence 23037, A	345	6	1.6	224	4	US-09-482-273-174	Sequence 174, App
273	6	1.6	165	4	US-09-583-110-5057	Sequence 5057, Ap	346	6	1.6	225	1	US-08-462-169B-22	Sequence 22, Appl
274	6	1.6	166	4	US-09-252-991A-19472	Sequence 19472, A	347	6	1.6	225	3	US-08-951-822-25	Sequence 25, Appl
275	6	1.6	167	4	US-09-270-767-46834	Sequence 46834, A	348	6	1.6	225	3	US-09-103-079-22	Sequence 22, Appl
276	6	1.6	168	4	US-09-198-452A-72	Sequence 72, Appl	349	6	1.6	225	3	US-08-705-245-3	Sequence 3, Appli
277	6	1.6	168	4	US-09-903-540-12311	Sequence 12311, A	350	6	1.6	225	3	US-08-705-245-10	Sequence 10, Appl
278	6	1.6	169	4	US-09-107-433-2609	Sequence 2609, Ap	351	6	1.6	225	3	US-09-368-951-25	Sequence 25, Appl
279	6	1.6	170	4	US-09-502-540-12331	Sequence 12331, A	352	6	1.6	225	4	US-09-425-021-22	Sequence 22, Appl
280	6	1.6	173	4	US-09-585-228-2	Sequence 228-2	353	6	1.6	225	4	US-09-229-947-25	Sequence 25, Appl
281	6	1.6	173	4	US-09-252-991A-23656	Sequence 23656, A	354	6	1.6	225	4	US-09-564-829-16	Sequence 16, Appl
282	6	1.6	174	4	US-09-270-767-44914	Sequence 44914, A	355	6	1.6	225	4	US-09-490-714-10	Sequence 3, Appli
283	6	1.6	174	4	US-09-673-395A-304	Sequence 304, App	356	6	1.6	225	4	US-09-462-159B-2	Sequence 2, Appli
284	6	1.6	174	4	US-09-270-767-36870	Sequence 36870, A	357	6	1.6	225	4	US-09-949-016-10966	Sequence 10966, A
285	6	1.6	176	4	US-09-270-767-52087	Sequence 52087, A	358	6	1.6	226	3	US-09-134-001C-5486	Sequence 5486, Ap
286	6	1.6	176	4	US-09-270-767-39416	Sequence 39416, A	359	6	1.6	228	4	US-09-543-681A-5259	Sequence 5259, Ap
287	6	1.6	176	4	US-09-270-767-54633	Sequence 54633, A	360	6	1.6	229	4	US-09-583-110-4946	Sequence 4946, Ap
288	6	1.6	176	4	US-09-248-796A-19842	Sequence 19842, A	361	6	1.6	230	4	US-09-602-787A-472	Sequence 472, App
289	6	1.6	177	3	US-08-748-506-21	Sequence 21, Appl	362	6	1.6	231	4	US-09-248-796A-15033	Sequence 15033, A
290	6	1.6	177	3	US-09-082-920-3	Sequence 3, Appli	363	6	1.6	231	2	US-08-190-199A-61	Sequence 61, Appl
291	6	1.6	177	4	US-09-543-681A-5159	Sequence 5159, Ap	364	6	1.6	235	4	US-09-580-235-2	Sequence 2, Appli
292	6	1.6	177	4	US-09-603-472A-62	Sequence 62, Appl	365	6	1.6	235	4	US-09-580-235-6	Sequence 6, Appli
293	6	1.6	181	4	US-09-489-039A-9684	Sequence 9684, Ap	366	6	1.6	235	4	US-09-580-181-2	Sequence 2, Appli
294	6	1.6	182	4	US-09-270-767-41975	Sequence 41975, A	367	6	1.6	235	4	US-09-580-181-6	Sequence 6, Appli
295	6	1.6	183	4	US-09-248-796A-19228	Sequence 19228, A	368	6	1.6	235	4	US-09-102-530-2	Sequence 2, Appli
296	6	1.6	184	4	US-09-252-991A-29270	Sequence 29270, A	369	6	1.6	235	4	US-09-102-530-6	Sequence 6, Appli
297	6	1.6	187	3	US-09-134-001C-4780	Sequence 4780, Ap	370	6	1.6	235	4	US-09-107-433-4367	Sequence 4367, Ap
298	6	1.6	188	4	US-09-543-681A-8022	Sequence 8022, Ap	371	6	1.6	235	4	US-09-107-433-4367	Sequence 4367, Ap
299	6	1.6	189	2	US-08-464-517-21	Sequence 21, Appl	372	6	1.6	236	2	US-08-464-517-22	Sequence 22, Appl
300	6	1.6	189	2	US-08-246-361A-21	Sequence 21, Appl	373	6	1.6	236	2	US-08-246-361A-22	Sequence 22, Appl
301	6	1.6	189	3	US-08-463-772-21	Sequence 21, Appl	374	6	1.6	236	3	US-08-463-772-22	Sequence 22, Appl
302	6	1.6	189	5	PCT-US93-05000-21	Sequence 21, Appl	375	6	1.6	236	3	US-09-634-137-32	Sequence 32, Appl
303	6	1.6	190	4	US-09-543-681A-8168	Sequence 8168, Ap	376	6	1.6	236	4	US-09-248-796A-23590	Sequence 23590, A
304	6	1.6	191	4	US-09-640-211A-1080	Sequence 1080, Ap	377	6	1.6	236	5	PCT-US93-05000-22	Sequence 22, Appl
305	6	1.6	193	4	US-09-792-024-103	Sequence 103, App	378	6	1.6	237	2	US-08-576-626A-56	Sequence 56, Appl
306	6	1.6	195	4	US-09-270-767-44051	Sequence 44051, A	379	6	1.6	237	3	US-09-320-878-11	Sequence 11, Appl
307	6	1.6	196	4	US-09-328-352-5445	Sequence 5445, Ap	380	6	1.6	237	3	US-09-105-537-18	Sequence 18, Appl
308	6	1.6	196	4	US-09-583-110-4152	Sequence 4152, Ap	381	6	1.6	237	4	US-09-657-440-11	Sequence 11, Appl
309	6	1.6	197	4	US-09-252-991A-28165	Sequence 28165, A	382	6	1.6	239	2	US-08-860-174A-2	Sequence 2, Appli
310	6	1.6	200	4	US-09-252-991A-29135	Sequence 29135, A	383	6	1.6	239	4	US-09-949-016-9708	Sequence 9708, Ap
311	6	1.6	200	4	US-09-540-236-3005	Sequence 3005, Ap	384	6	1.6	239	6	5455030-13	Patent No. 5455030
312	6	1.6	201	1	US-08-240-124-4	Sequence 4, Appli	385	6	1.6	239	6	5455030-13	Patent No. 5455030
313	6	1.6	201	2	US-08-453-943-4	Sequence 4, Appli	386	6	1.6	240	4	US-09-270-767-40675	Sequence 40675, A
314	6	1.6	201	2	US-09-057-121-4	Sequence 4, Appli	387	6	1.6	240	4	US-09-270-767-55891	Sequence 55891, A
315	6	1.6	201	3	US-09-358-734-4	Sequence 4, Appli	388	6	1.6	241	4	US-09-554-765-13	Sequence 13, Appl
316	6	1.6	201	4	US-09-615-192A-391	Sequence 391, App	389	6	1.6	241	4	US-09-248-796A-21751	Sequence 21751, A
317	6	1.6	201	4	US-09-214-631-8	Sequence 8, Appli	390	6	1.6	241	4	US-10-101-464A-698	Sequence 698, App
318	6	1.6	203	4	US-09-134-000C-5644	Sequence 5644, Ap	391	6	1.6	241	4	US-09-736-219A-187	Sequence 187, App
319	6	1.6	204	4	US-09-328-352-6580	Sequence 6580, Ap	392	6	1.6	242	6	5455030-15	Patent No. 5455030
320	6	1.6	204	4	US-09-302-540-15674	Sequence 15674, A	393	6	1.6	242	6	5455030-15	Patent No. 5455030

333	6	1.6	246	4	US-09-270-767-39204	Sequence 39204, A	466	1.6	302	4	US-09-107-433-4911	Sequence 4911, Ap
334	6	1.6	246	4	US-09-270-767-54421	Sequence 54421, A	467	1.6	302	4	US-09-949-1016-10213	Sequence 10213, A
335	6	1.6	247	1	US-08-353-341-2	Sequence 2, Appli	468	1.6	303	4	US-09-198-452A-904	Sequence 904, App
336	6	1.6	247	3	US-08-858-207A-300	Sequence 300, App	469	1.6	303	4	US-09-107-532A-5585	Sequence 5585, Ap
337	6	1.6	247	4	US-09-252-991A-32400	Sequence 32400, A	470	1.6	303	4	US-09-543-681A-7946	Sequence 7946, Ap
338	6	1.6	247	4	US-09-583-110-3069	Sequence 3069, Ap	471	1.6	305	4	US-09-674-529B-14	Sequence 14, Appli
339	6	1.6	248	4	US-09-270-767-38407	Sequence 38407, A	472	1.6	306	4	US-09-328-352-8079	Sequence 8079, Ap
340	6	1.6	248	4	US-09-270-767-53624	Sequence 53624, A	473	1.6	309	2	US-08-464-517-4	Sequence 4, Appli
401	6	1.6	249	4	US-09-673-395A-586	Sequence 586, App	474	1.6	309	3	US-08-463-772-4	Sequence 4, Appli
402	6	1.6	249	4	US-09-796-149B-3	Sequence 3, Appli	475	1.6	309	4	US-09-655-908-12	Sequence 12, Appli
403	6	1.6	249	4	US-09-796-149B-7	Sequence 7, Appli	476	1.6	309	4	US-09-710-279-936	Sequence 936, App
404	6	1.6	251	4	US-09-489-039A-5020	Sequence 9020, Ap	477	1.6	310	4	US-09-438-185A-841	Sequence 841, App
405	6	1.6	251	4	US-09-107-433-4204	Sequence 4204, Ap	478	1.6	311	4	US-09-252-991A-16719	Sequence 16719, A
406	6	1.6	253	4	US-09-796-149B-8	Sequence 8, Appli	479	1.6	311	4	US-09-270-767-44261	Sequence 44261, A
407	6	1.6	253	4	US-09-902-540-9969	Sequence 9969, Ap	480	1.6	314	4	US-09-270-767-46010	Sequence 46010, A
408	6	1.6	254	3	US-09-449-437A-4	Sequence 4, Appli	481	1.6	315	1	US-08-253-155A-34	Sequence 34, Appli
409	6	1.6	254	3	US-09-449-437A-6	Sequence 6, Appli	482	1.6	317	4	US-09-270-767-40937	Sequence 40937, A
410	6	1.6	254	3	US-09-195-106-2	Sequence 2, Appli	483	1.6	317	4	US-09-270-767-56153	Sequence 56153, A
411	6	1.6	256	4	US-09-489-039A-8086	Sequence 8086, Ap	484	1.6	318	4	US-09-902-540-10733	Sequence 10733, A
412	6	1.6	256	4	US-09-270-767-39978	Sequence 39978, A	485	1.6	320	3	US-09-134-001C-4439	Sequence 4439, Ap
413	6	1.6	256	4	US-09-270-767-55195	Sequence 55195, A	486	1.6	325	4	US-09-651-200-20	Sequence 20, Appli
414	6	1.6	257	4	US-09-252-991A-26120	Sequence 26120, A	487	1.6	327	3	US-08-748-506-14	Sequence 14, Appli
415	6	1.6	258	3	US-09-134-001C-4806	Sequence 4806, Ap	488	1.6	327	3	US-08-748-506-22	Sequence 22, Appli
416	6	1.6	260	4	US-09-270-767-33511	Sequence 33511, A	489	1.6	327	3	US-08-748-506-23	Sequence 23, Appli
417	6	1.6	260	4	US-09-902-540-14188	Sequence 14188, A	490	1.6	327	3	US-08-748-506-24	Sequence 24, Appli
418	6	1.6	262	4	US-09-252-991A-18779	Sequence 18779, A	491	1.6	328	4	US-09-489-039A-9306	Sequence 9306, Ap
419	6	1.6	262	4	US-09-270-767-43745	Sequence 43745, A	492	1.6	331	4	US-09-328-352-6400	Sequence 6400, Ap
420	6	1.6	262	4	US-09-809-920-13	Sequence 13, Appli	493	1.6	332	4	US-09-949-016-10159	Sequence 10159, A
421	6	1.6	263	2	US-08-752-844-66	Sequence 66, Appli	494	1.6	332	4	US-09-902-540-12515	Sequence 12515, A
422	6	1.6	263	4	US-09-293-533-66	Sequence 66, Appli	495	1.6	333	4	US-09-543-681A-6874	Sequence 6874, Ap
423	6	1.6	264	4	US-09-710-279-388	Sequence 388, App	496	1.6	336	4	US-09-543-681A-5330	Sequence 5330, Ap
424	6	1.6	266	2	US-07-857-224B-43	Sequence 43, Appli	497	1.6	336	4	US-09-540-16045	Sequence 16045, A
425	6	1.6	266	2	US-07-857-224B-44	Sequence 44, Appli	498	1.6	337	4	US-09-252-991A-18558	Sequence 18558, A
426	6	1.6	266	4	US-09-328-352-4705	Sequence 4705, Ap	499	1.6	337	4	US-09-705-534-2	Sequence 2, Appli
427	6	1.6	269	3	US-09-134-001C-4919	Sequence 4919, Ap	500	1.6	337	4	US-09-949-016-6825	Sequence 6825, Ap
428	6	1.6	269	4	US-09-252-991A-30515	Sequence 30515, A	501	1.6	338	3	US-08-961-536-2	Sequence 2, Appli
429	6	1.6	270	4	US-09-540-236-2797	Sequence 2797, Ap	502	1.6	338	4	US-09-583-110-4275	Sequence 4275, Ap
430	6	1.6	271	4	US-09-252-991A-24319	Sequence 24319, A	503	1.6	338	4	US-09-432-682-2	Sequence 2, Appli
431	6	1.6	272	4	US-08-756-416-39	Sequence 39, Appli	504	1.6	342	4	US-09-489-039A-12340	Sequence 12340, A
432	6	1.6	272	4	US-09-270-767-59048	Sequence 59048, A	505	1.6	344	3	US-09-393-554-3	Sequence 3, Appli
433	6	1.6	272	4	US-09-726-219A-183	Sequence 183, App	506	1.6	345	4	US-09-248-796A-25189	Sequence 25189, A
434	6	1.6	272	4	US-09-949-016-6331	Sequence 6331, Ap	507	1.6	346	4	US-09-107-433-4305	Sequence 4305, Ap
435	6	1.6	272	4	US-09-949-016-10996	Sequence 10996, A	508	1.6	349	4	US-09-398-858-22	Sequence 22, Appli
436	6	1.6	275	4	US-09-252-991A-29459	Sequence 29459, A	509	1.6	351	4	US-08-311-731A-28	Sequence 28, Appli
437	6	1.6	275	4	US-09-270-767-57677	Sequence 57677, A	510	1.6	351	4	US-09-902-540-13214	Sequence 13214, A
438	6	1.6	275	4	US-09-270-767-61549	Sequence 61549, A	511	1.6	353	4	US-09-949-016-7157	Sequence 7157, Ap
439	6	1.6	280	4	US-09-252-991A-31168	Sequence 31168, A	512	1.6	357	4	US-09-489-039A-13443	Sequence 13443, A
440	6	1.6	281	4	US-09-583-110-2802	Sequence 2802, Ap	513	1.6	360	4	US-09-328-352-7879	Sequence 7879, Ap
441	6	1.6	281	4	US-09-902-540-16177	Sequence 16177, A	514	1.6	360	4	US-09-602-787A-150	Sequence 150, App
442	6	1.6	282	1	US-08-324-301-15	Sequence 15, Appli	515	1.6	361	4	US-09-252-991A-25005	Sequence 25005, A
443	6	1.6	282	4	US-09-270-767-41601	Sequence 41601, A	516	1.6	362	4	US-09-248-796A-20105	Sequence 20105, A
444	6	1.6	284	4	US-09-248-796A-19213	Sequence 19213, A	517	1.6	363	1	US-08-530-950-6	Sequence 6, Appli
445	6	1.6	286	4	US-09-328-352-6975	Sequence 6975, Ap	518	1.6	363	3	US-08-888-429A-6	Sequence 6, Appli
446	6	1.6	287	4	US-09-107-433-4368	Sequence 4368, Ap	519	1.6	363	3	US-09-149-879-6	Sequence 6, Appli
447	6	1.6	289	2	US-08-246-361A-4	Sequence 4, Appli	520	1.6	363	4	US-09-057-009-6	Sequence 6, Appli
448	6	1.6	289	4	US-09-328-352-6027	Sequence 6027, Ap	521	1.6	363	4	US-09-593-653-6	Sequence 6, Appli
449	6	1.6	289	4	US-09-919-497-54	Sequence 54, Appli	522	1.6	363	4	US-09-142-108C-25	Sequence 25, Appli
450	6	1.6	289	4	US-09-949-016-6127	Sequence 6127, Ap	523	1.6	369	4	US-09-252-991A-18905	Sequence 18905, A
451	6	1.6	289	5	PCT-US93-05000-4	Sequence 4, Appli	524	1.6	369	4	US-09-252-991A-28650	Sequence 28650, A
452	6	1.6	291	4	US-09-328-352-4678	Sequence 4678, Ap	525	1.6	369	4	US-09-902-540-10817	Sequence 10817, A
453	6	1.6	292	3	US-08-858-207A-391	Sequence 391, App	526	1.6	370	2	US-08-341-538A-2	Sequence 2, Appli
454	6	1.6	292	4	US-09-543-681A-6495	Sequence 6495, Ap	527	1.6	370	2	US-08-725-518-2	Sequence 2, Appli
455	6	1.6	292	4	US-09-583-110-3607	Sequence 3607, Ap	528	1.6	371	4	US-09-636-215-708	Sequence 708, App
456	6	1.6	293	4	US-09-252-991A-23471	Sequence 23471, A	529	1.6	371	4	US-09-685-166A-708	Sequence 708, App
457	6	1.6	293	4	US-09-270-767-46006	Sequence 46006, A	530	1.6	371	4	US-09-679-426-708	Sequence 708, App
458	6	1.6	295	4	US-09-949-016-6449	Sequence 6449, Ap	531	1.6	371	4	US-09-759-143-708	Sequence 708, App
459	6	1.6	298	4	US-09-270-767-41588	Sequence 41588, A	532	1.6	371	4	US-09-651-236-708	Sequence 708, App
460	6	1.6	299	4	US-09-134-000C-4703	Sequence 4703, Ap	533	1.6	372	3	US-08-120-601B-7	Sequence 7, Appli
461	6	1.6	299	4	US-09-902-540-9930	Sequence 9930, Ap	534	1.6	372	4	US-09-252-991A-21179	Sequence 21179, A
462	6	1.6	301	4	US-09-252-991A-26242	Sequence 26242, A	535	1.6	373	4	US-09-252-991A-20254	Sequence 20254, A
463	6	1.6	302	4	US-09-482-273-105	Sequence 105, App	536	1.6	374	4	US-09-543-681A-7631	Sequence 7631, Ap
464	6	1.6	302	4	US-09-252-991A-24353	Sequence 24353, A	537	1.6	374	4	US-09-489-039A-10660	Sequence 10660, A
465	6	1.6	302	4	US-08-426-630-40	Sequence 40, Appli	538	1.6	376	4	US-09-248-796A-14887	Sequence 14887, A

539	6	1.6	378	4	US-09-248-796A-15663	Sequence 15663, A	612	1.6	420	4	US-09-168-595-142	Sequence 142, App
540	6	1.6	379	4	US-09-949-016-8020	Sequence 8020, App	613	1.6	420	4	US-09-684-855-120	Sequence 120, App
541	6	1.6	379	4	US-09-252-991A-19597	Sequence 19597, A	614	1.6	420	4	US-09-543-681A-6289	Sequence 6289, App
542	6	1.6	384	4	US-09-902-540-10126	Sequence 10126, A	615	1.6	420	4	US-09-488-265B-19	Sequence 19, Appl
543	6	1.6	388	4	US-09-489-039A-9580	Sequence 9580, A	616	1.6	423	4	US-09-252-991A-26714	Sequence 15, Appl
544	6	1.6	389	4	US-09-949-016-7723	Sequence 7723, App	617	1.6	423	4	US-09-976-594-19	Sequence 19, Appl
545	6	1.6	392	4	US-08-861-774E-24	Sequence 24, Appl	618	1.6	423	4	US-09-919-039-19	Sequence 19, Appl
546	6	1.6	393	1	US-08-530-950-8	Sequence 8, Appl	619	1.6	423	4	US-09-248-796A-20238	Sequence 20238, A
547	6	1.6	393	3	US-08-888-429A-8	Sequence 8, Appl	620	1.6	424	3	US-09-087-134-8	Sequence 8, Appl
548	6	1.6	393	3	US-09-149-879-8	Sequence 8, Appl	621	1.6	424	4	US-09-252-991A-16822	Sequence 16822, A
549	6	1.6	393	4	US-08-178-257-13	Sequence 13, Appl	622	1.6	424	4	US-09-252-991A-32935	Sequence 32935, A
550	6	1.6	393	4	US-09-057-009-8	Sequence 8, Appl	623	1.6	424	4	US-09-198-452A-45	Sequence 45, Appl
551	6	1.6	393	4	US-09-593-653-8	Sequence 8, Appl	624	1.6	424	4	US-09-538-092-881	Sequence 881, App
552	6	1.6	393	6	5229279-6	Patent No. 5229279	625	1.6	425	2	US-08-732-028-2	Sequence 2, Appl
553	6	1.6	393	6	5512669-6	Patent No. 5512669	626	1.6	425	3	US-09-096-776B-8	Sequence 8, Appl
554	6	1.6	393	6	5229279-6	Patent No. 5229279	627	1.6	425	3	US-09-183-228-2	Sequence 2, Appl
555	6	1.6	393	6	5512669-6	Patent No. 5512669	628	1.6	425	3	US-09-923-922-8	Sequence 8, Appl
556	6	1.6	394	2	US-08-646-590B-40	Sequence 40, Appl	629	1.6	425	4	US-09-949-016-6670	Sequence 6670, App
557	6	1.6	394	3	US-09-412-184-40	Sequence 40, Appl	630	1.6	426	4	US-09-902-540-11847	Sequence 11847, A
558	6	1.6	394	4	US-09-134-000C-4332	Sequence 4332, App	631	1.6	426	4	US-09-902-540-14448	Sequence 14448, A
559	6	1.6	394	4	US-09-949-016-9565	Sequence 9565, App	632	1.6	430	4	US-09-252-991A-23726	Sequence 23726, A
560	6	1.6	396	1	US-08-769-309A-15	Sequence 15, Appl	633	1.6	433	4	US-08-840-767-6	Sequence 6, Appl
561	6	1.6	396	3	US-08-994-570-15	Sequence 15, Appl	634	1.6	436	3	US-09-150-213-4	Sequence 4, Appl
562	6	1.6	399	1	US-08-530-950-10	Sequence 10, Appl	635	1.6	437	1	US-08-176-427B-8	Sequence 8, Appl
563	6	1.6	399	2	US-08-874-186-32	Sequence 32, Appl	636	1.6	437	2	US-08-356-060A-11	Sequence 11, Appl
564	6	1.6	399	3	US-08-888-429A-10	Sequence 10, Appl	637	1.6	437	3	US-08-946-329A-20	Sequence 20, Appl
565	6	1.6	399	3	US-09-149-879-10	Sequence 10, Appl	638	1.6	437	3	US-08-567-357A-20	Sequence 20, Appl
566	6	1.6	399	4	US-09-057-009-10	Sequence 10, Appl	639	1.6	437	3	US-08-460-900C-11	Sequence 11, Appl
567	6	1.6	399	4	US-09-593-653-10	Sequence 10, Appl	640	1.6	437	3	US-08-729-743A-20	Sequence 20, Appl
568	6	1.6	399	4	US-09-538-092-1129	Sequence 1129, App	641	1.6	437	3	US-08-674-509B-11	Sequence 11, Appl
569	6	1.6	400	4	US-09-252-991A-27093	Sequence 27093, A	642	1.6	437	3	US-08-954-698-11	Sequence 11, Appl
570	6	1.6	400	4	US-09-949-016-7917	Sequence 7917, App	643	1.6	437	3	US-09-057-860A-6	Sequence 6, Appl
571	6	1.6	401	4	US-09-252-991A-27198	Sequence 27198, A	644	1.6	437	3	US-08-349-498-20	Sequence 20, Appl
572	6	1.6	401	4	US-09-489-039A-13241	Sequence 13241, A	645	1.6	437	3	US-09-293-505-14	Sequence 14, Appl
573	6	1.6	403	4	US-09-489-039A-11021	Sequence 11021, A	646	1.6	437	3	US-08-957-874-11	Sequence 11, Appl
574	6	1.6	405	4	US-09-270-767-33493	Sequence 33493, A	647	1.6	437	4	US-09-325-256-20	Sequence 20, Appl
575	6	1.6	405	4	US-09-949-016-10726	Sequence 10726, A	648	1.6	437	4	US-09-639-695-11	Sequence 11, Appl
576	6	1.6	406	4	US-09-248-796A-16432	Sequence 16432, A	649	1.6	437	4	US-09-448-188-11	Sequence 11, Appl
577	6	1.6	407	4	US-09-252-991A-25732	Sequence 25732, A	650	1.6	437	4	US-08-954-128-11	Sequence 11, Appl
578	6	1.6	407	4	US-09-543-681A-7929	Sequence 7929, App	651	1.6	437	4	US-09-704-917-13	Sequence 13, Appl
579	6	1.6	407	4	US-09-583-110-5234	Sequence 5234, App	652	1.6	437	4	US-08-954-740-11	Sequence 11, Appl
580	6	1.6	408	4	US-09-489-039A-9583	Sequence 9583, App	653	1.6	437	4	US-09-151-999-13	Sequence 13, Appl
581	6	1.6	408	4	US-09-949-016-9941	Sequence 9941, App	654	1.6	437	4	US-09-736-476-11	Sequence 11, Appl
582	6	1.6	409	3	US-09-258-754-449	Sequence 449, App	655	1.6	437	4	US-09-060-939A-14	Sequence 14, Appl
583	6	1.6	409	4	US-09-676-475A-449	Sequence 449, App	656	1.6	437	4	US-09-021-660A-37	Sequence 37, Appl
584	6	1.6	410	1	US-08-091-519-13	Sequence 13, Appl	657	1.6	437	4	US-09-418-221-13	Sequence 13, Appl
585	6	1.6	410	1	US-08-442-043A-13	Sequence 13, Appl	658	1.6	437	5	PCT-US95-15463-20	Sequence 20, Appl
586	6	1.6	410	3	US-09-258-754-450	Sequence 450, App	659	1.6	437	5	PCT-US95-15923-20	Sequence 20, Appl
587	6	1.6	410	3	US-09-258-754-451	Sequence 451, App	660	1.6	439	3	US-08-448-722A-5	Sequence 5, Appl
588	6	1.6	410	3	US-09-258-754-452	Sequence 452, App	661	1.6	439	3	US-08-189-309B-5	Sequence 5, Appl
589	6	1.6	410	3	US-09-173-151A-27	Sequence 27, Appl	662	1.6	439	4	US-09-270-767-36825	Sequence 36825, A
590	6	1.6	410	4	US-09-461-908-13	Sequence 13, Appl	663	1.6	439	4	US-09-270-767-52042	Sequence 52042, A
591	6	1.6	410	4	US-08-441-893A-13	Sequence 13, Appl	664	1.6	440	4	US-09-631-603-22	Sequence 22, Appl
592	6	1.6	410	4	US-09-684-855-143	Sequence 143, App	665	1.6	440	4	US-09-826-509-567	Sequence 567, App
593	6	1.6	410	4	US-09-676-475A-450	Sequence 451, App	666	1.6	441	4	US-09-489-039A-12079	Sequence 12079, A
594	6	1.6	410	4	US-09-676-475A-451	Sequence 451, App	667	1.6	443	3	US-08-993-359-30	Sequence 30, Appl
595	6	1.6	410	4	US-09-676-475A-452	Sequence 452, App	668	1.6	443	4	US-09-273-871A-5	Sequence 5, Appl
596	6	1.6	410	5	PCT-US91-03478-13	Sequence 13, Appl	669	1.6	443	4	US-09-482-558A-30	Sequence 30, Appl
597	6	1.6	412	4	US-09-489-039A-9118	Sequence 9118, App	670	1.6	443	4	US-10-083-452-5	Sequence 5, Appl
598	6	1.6	414	4	US-09-252-991A-29160	Sequence 29160, A	671	1.6	444	3	US-09-119-788-2	Sequence 2, Appl
599	6	1.6	416	3	US-09-416-050A-4	Sequence 4, Appl	672	1.6	444	4	US-09-426-290-2	Sequence 2, Appl
600	6	1.6	416	3	US-09-664-800-4	Sequence 4, Appl	673	1.6	444	4	US-09-252-991A-17767	Sequence 17767, A
601	6	1.6	416	3	US-09-665-309-4	Sequence 4, Appl	674	1.6	444	4	US-09-826-509-551	Sequence 551, App
602	6	1.6	416	3	US-09-661-569-4	Sequence 4, Appl	675	1.6	445	4	US-09-949-016-6083	Sequence 6083, App
603	6	1.6	416	4	US-09-252-991A-16734	Sequence 16734, A	676	1.6	446	4	US-09-252-991A-21834	Sequence 21834, A
604	6	1.6	416	4	US-09-252-991A-32660	Sequence 32660, A	677	1.6	447	4	US-09-252-991A-32755	Sequence 32755, A
605	6	1.6	418	1	US-07-816-283-10	Sequence 10, Appl	678	1.6	447	4	US-09-394-142B-24	Sequence 24, Appl
606	6	1.6	418	1	US-08-417-103-10	Sequence 10, Appl	679	1.6	447	4	US-09-949-016-6560	Sequence 6560, App
607	6	1.6	418	4	US-09-826-509-573	Sequence 573, App	680	1.6	448	4	US-09-916-229A-2	Sequence 2, Appl
608	6	1.6	419	4	US-09-252-991A-26976	Sequence 26976, A	681	1.6	450	4	US-09-540-236-2654	Sequence 2654, App
609	6	1.6	419	4	US-09-543-681A-4862	Sequence 4862, App	682	1.6	450	4	US-09-248-796A-20538	Sequence 20538, A
610	6	1.6	419	4	US-09-107-433-3656	Sequence 3656, App	683	1.6	451	4	US-09-134-000C-6421	Sequence 6421, App
611	6	1.6	420	2	US-08-592-126-142	Sequence 142, App	684	1.6	451	4	US-09-949-016-7630	Sequence 7630, App

685	1	1.6	453	1	US-08-769-309A-14	Sequence 14, Appl	758	1	US-08-245-500A-3	Sequence 3, Appl
686	3	1.6	453	3	US-08-994-570-14	Sequence 14, Appl	759	1	US-08-390-546-3	Sequence 3, Appl
687	4	1.6	458	4	US-09-252-991A-25185	Sequence 25185, A	760	1	US-08-390-479A-3	Sequence 3, Appl
688	4	1.6	459	4	US-09-328-352-8095	Sequence 8095, Ap	761	1	US-08-557-393-3	Sequence 3, Appl
689	4	1.6	459	4	US-09-902-540-16639	Sequence 16639, A	762	1	US-08-390-516C-3	Sequence 3, Appl
690	1	1.6	461	1	US-08-186-222-2	Sequence 2, Appl	763	1	US-08-390-517A-3	Sequence 3, Appl
691	4	1.6	463	4	US-09-907-794A-285	Sequence 285, App	764	1	US-08-390-515A-3	Sequence 3, Appl
692	4	1.6	463	4	US-09-905-125A-285	Sequence 285, App	765	1	US-08-801-718-3	Sequence 3, Appl
693	4	1.6	463	4	US-09-902-775A-285	Sequence 285, App	766	1	US-09-170-159A-3	Sequence 3, Appl
694	4	1.6	463	4	US-09-905-700A-285	Sequence 285, App	767	1	US-09-480-718-44	Sequence 44, Appl
695	4	1.6	463	4	US-09-903-603A-285	Sequence 285, App	768	1	US-09-949-016-8486	Sequence 8486, Ap
696	4	1.6	463	4	US-09-904-920A-285	Sequence 285, App	769	1	US-10-237-551-204	Sequence 204, App
697	4	1.6	463	4	US-09-904-964A-285	Sequence 285, App	770	1	US-09-949-016-7790	Sequence 7790, Ap
698	4	1.6	463	4	US-09-905-381A-285	Sequence 285, App	771	1	US-09-902-540-14215	Sequence 14215, A
699	4	1.6	463	4	US-09-906-618-285	Sequence 285, App	772	1	US-09-710-279-1558	Sequence 1558, A
700	4	1.6	466	4	US-09-252-991A-32781	Sequence 32781, A	773	1	US-09-134-000C-4863	Sequence 4863, Ap
701	3	1.6	467	3	US-08-701-582D-2	Sequence 2, Appl	774	1	US-09-252-991A-27888	Sequence 27888, A
702	3	1.6	467	3	US-08-701-582D-4	Sequence 4, Appl	775	1	US-09-988-863A-2	Sequence 2, Appl
703	3	1.6	467	3	US-09-082-039A-2	Sequence 2, Appl	776	1	US-09-130-337A-25	Sequence 25, Appl
704	3	1.6	467	3	US-09-082-039A-15	Sequence 15, Appl	777	1	US-09-107-532A-5470	Sequence 5470, Ap
705	3	1.6	467	3	US-08-840-767-42	Sequence 42, Appl	778	1	US-09-252-991A-18691	Sequence 18691, A
706	3	1.6	467	3	US-08-840-767-50	Sequence 50, Appl	779	1	US-09-142-108C-2	Sequence 2, Appl
707	3	1.6	467	3	US-09-096-776B-7	Sequence 7, Appl	780	1	US-09-142-108C-6	Sequence 6, Appl
708	3	1.6	467	3	US-09-087-134-2	Sequence 2, Appl	781	1	US-09-252-991A-32774	Sequence 32774, A
709	3	1.6	467	3	US-09-087-134-5	Sequence 5, Appl	782	1	US-09-134-000C-51277	Sequence 5127, Ap
710	3	1.6	467	3	US-09-552-138-2	Sequence 2, Appl	783	1	US-09-142-108C-15	Sequence 15, Appl
711	3	1.6	467	3	US-09-552-138-15	Sequence 15, Appl	784	1	US-09-902-540-16127	Sequence 15127, A
712	4	1.6	467	4	US-08-580-031A-15	Sequence 15, Appl	785	1	US-09-142-108C-21	Sequence 21, Appl
713	4	1.6	467	4	US-09-523-922-7	Sequence 7, Appl	786	1	US-09-693-746-10	Sequence 10, Appl
714	4	1.6	468	4	US-09-248-796A-17308	Sequence 17308, A	787	1	US-09-328-352-5423	Sequence 5423, Ap
715	3	1.6	470	3	US-09-134-001C-4610	Sequence 4610, Ap	788	1	US-09-693-746-12	Sequence 12, Appl
716	4	1.6	471	4	US-09-270-767-60488	Sequence 60488, A	789	1	US-08-853-659A-35	Sequence 35, Appl
717	3	1.6	472	3	US-08-492-459-22	Sequence 22, Appl	790	1	US-08-852-401-3	Sequence 3, Appl
718	3	1.6	472	3	US-08-423-752-22	Sequence 22, Appl	791	1	US-09-107-532A-6562	Sequence 6562, Ap
719	3	1.6	472	3	US-08-716-873-36	Sequence 36, Appl	792	1	US-09-949-016-7125	Sequence 7125, Ap
720	3	1.6	472	3	US-09-368-431-36	Sequence 36, Appl	793	1	US-09-949-016-7126	Sequence 7126, Ap
721	3	1.6	472	3	US-09-414-006-22	Sequence 22, Appl	794	1	US-09-949-016-7127	Sequence 7127, Ap
722	4	1.6	472	4	US-09-447-223-22	Sequence 22, Appl	795	1	US-09-949-016-7128	Sequence 7128, Ap
723	4	1.6	472	4	US-09-328-352-6296	Sequence 6296, Ap	796	1	US-09-949-016-7129	Sequence 7129, Ap
724	4	1.6	472	4	US-09-951-217-36	Sequence 36, Appl	797	1	US-09-252-991A-26641	Sequence 26641, A
725	4	1.6	474	4	US-09-489-039A-14147	Sequence 14147, A	798	1	US-09-310-174B-13	Sequence 13, Appl
726	4	1.6	476	4	US-09-142-108C-23	Sequence 23, Appl	799	1	US-09-620-461-13	Sequence 13, Appl
727	3	1.6	477	3	US-09-113-309-3	Sequence 3, Appl	800	1	US-09-949-016-8028	Sequence 8028, Ap
728	3	1.6	477	3	US-09-521-109-3	Sequence 3, Appl	801	1	US-09-949-016-8343	Sequence 8343, Ap
729	3	1.6	477	3	US-08-840-767-2	Sequence 2, Appl	802	1	US-09-328-352-7300	Sequence 7300, Ap
730	3	1.6	477	3	US-09-562-332-3	Sequence 3, Appl	803	1	US-09-134-001C-4091	Sequence 4091, Ap
731	4	1.6	478	4	US-09-770-916-2	Sequence 2, Appl	804	1	US-10-037-667-1	Sequence 1, Appl
732	4	1.6	478	4	US-09-902-540-14070	Sequence 14070, A	805	1	US-09-710-279-3134	Sequence 3134, Ap
733	1	1.6	479	1	US-08-278-635B-2	Sequence 2, Appl	806	1	US-09-248-796A-15935	Sequence 15935, A
734	3	1.6	479	3	US-08-464-258B-2	Sequence 2, Appl	807	1	US-09-252-991A-21132	Sequence 21132, A
735	3	1.6	479	3	US-08-471-961-2	Sequence 2, Appl	808	1	US-09-252-991A-18055	Sequence 18055, A
736	4	1.6	479	4	US-09-345-109C-2	Sequence 2, Appl	809	1	US-09-543-681A-7663	Sequence 7663, Ap
737	4	1.6	480	4	US-09-543-681A-4680	Sequence 4680, Ap	810	1	US-09-270-767-42391	Sequence 42391, A
738	4	1.6	480	4	US-09-248-796A-15701	Sequence 15701, A	811	1	US-09-252-991A-15984	Sequence 15984, A
739	4	1.6	480	4	US-09-949-016-8233	Sequence 8233, Ap	812	1	US-09-248-796A-17366	Sequence 17366, A
740	4	1.6	481	4	US-09-252-991A-27157	Sequence 27157, A	813	1	US-08-309-341-2	Sequence 2, Appl
741	4	1.6	482	4	US-09-248-796A-18796	Sequence 18796, A	814	1	US-08-309-341-4	Sequence 4, Appl
742	3	1.6	485	3	US-08-930-894-2	Sequence 2, Appl	815	1	US-08-608-267-2	Sequence 2, Appl
743	4	1.6	485	4	US-09-248-796A-18473	Sequence 18473, A	816	1	US-08-608-267-4	Sequence 4, Appl
744	4	1.6	485	4	US-09-949-016-7633	Sequence 7633, Ap	817	1	US-08-608-452-2	Sequence 2, Appl
745	4	1.6	490	4	US-09-461-325-250	Sequence 250, App	818	1	US-08-608-452-4	Sequence 4, Appl
746	4	1.6	490	4	US-09-461-325-518	Sequence 518, App	819	1	US-08-608-224-2	Sequence 2, Appl
747	4	1.6	490	4	US-09-252-991A-30355	Sequence 30355, A	820	1	US-08-608-224-4	Sequence 4, Appl
748	4	1.6	490	4	US-10-012-542-250	Sequence 250, App	821	1	US-08-967-149-2	Sequence 2, Appl
749	4	1.6	490	4	US-10-012-542-518	Sequence 518, App	822	1	US-08-967-149-4	Sequence 4, Appl
750	4	1.6	490	4	US-09-270-767-40737	Sequence 40737, A	823	1	US-09-538-092-278	Sequence 278, App
751	4	1.6	490	4	US-09-270-767-55953	Sequence 55953, A	824	1	US-09-364-206-47	Sequence 47, Appl
752	4	1.6	490	4	US-10-115-123-518	Sequence 250, App	825	1	US-09-252-991A-29263	Sequence 29263, A
753	4	1.6	490	4	US-10-115-123-518	Sequence 518, App	826	1	US-09-252-991A-22037	Sequence 22037, A
754	4	1.6	490	4	US-10-053-510-19	Sequence 19, Appl	827	1	US-09-543-681A-6918	Sequence 6918, Ap
755	1	1.6	491	1	US-07-903-103-2	Sequence 2, Appl	828	1	US-09-270-767-39217	Sequence 39217, A
756	1	1.6	491	1	US-08-044-619A-2	Sequence 2, Appl	829	1	US-09-270-767-54434	Sequence 54434, A
757	1	1.6	491	1	US-08-283-911-2	Sequence 2, Appl	830	1	US-09-815-923-14	Sequence 14, Appl

831	6	1.6	601	2	US-08-795-868-16	Sequence 16, Appl	904	4	US-09-854-845-45	Sequence 45, Appl
832	6	1.6	602	3	US-09-303-069-16	Sequence 16, Appl	905	4	US-09-835-145A-2	Sequence 2, Appl
833	6	1.6	603	3	US-09-134-250-16	Sequence 16, Appl	906	4	US-09-489-039A-11310	Sequence 11310, A
834	6	1.6	604	4	US-09-107-532A-3809	Sequence 3809, Ap	907	4	US-09-854-845-43	Sequence 43, Appl
835	6	1.6	605	4	US-09-902-540-12446	Sequence 12446, A	908	4	US-09-362-336A-14	Sequence 14, Appl
836	6	1.6	606	4	US-09-543-681A-5181	Sequence 5181, Ap	909	4	US-09-252-911A-21696	Sequence 21696, A
837	6	1.6	607	4	US-08-207-954-5	Sequence 5, Appl	910	4	US-09-688-188B-24	Sequence 24, Appl
838	6	1.6	608	3	US-09-134-001C-2994	Sequence 2994, Ap	911	4	US-09-231-417D-24	Sequence 24, Appl
839	6	1.6	609	4	US-09-252-991A-20596	Sequence 20596, A	912	4	US-09-949-016-7201	Sequence 7201, Ap
840	6	1.6	610	4	US-09-328-352-5752	Sequence 5752, Ap	913	4	US-09-949-016-7202	Sequence 7202, Ap
841	6	1.6	611	3	US-08-968-563-13	Sequence 13, Appl	914	4	US-09-252-991A-29893	Sequence 29893, A
842	6	1.6	612	3	US-08-969-683A-13	Sequence 13, Appl	915	4	US-08-942-686-2	Sequence 2, Appl
843	6	1.6	613	3	US-09-297-928-9	Sequence 9, Appl	916	4	US-08-444-818-70	Sequence 70, Appl
844	6	1.6	614	4	US-09-275-252A-4	Sequence 2, Appl	917	4	US-09-854-845-49	Sequence 49, Appl
845	6	1.6	615	4	US-09-331-568A-2	Sequence 2, Appl	918	4	US-08-789-078-1	Sequence 1, Appl
846	6	1.6	616	4	US-09-331-568A-26	Sequence 26, Appl	919	4	US-08-752-633-1	Sequence 1, Appl
847	6	1.6	617	1	US-08-653-740-7	Sequence 7, Appl	920	4	US-08-476-062A-45	Sequence 45, Appl
848	6	1.6	618	2	US-09-073-594-7	Sequence 7, Appl	921	4	US-07-728-215-31	Sequence 31, Appl
849	6	1.6	619	3	US-09-275-925-7	Sequence 7, Appl	922	4	US-08-938-085A-31	Sequence 31, Appl
850	6	1.6	620	3	US-09-252-991A-21205	Sequence 21205, A	923	4	US-09-252-991A-26777	Sequence 26777, A
851	6	1.6	621	4	US-09-949-016-6530	Sequence 6530, Ap	924	4	US-10-072-844-31	Sequence 31, Appl
852	6	1.6	622	4	US-09-252-991A-31696	Sequence 31696, A	925	4	US-10-072-844-31	Sequence 31, Appl
853	6	1.6	623	4	US-10-101-464A-927	Sequence 927, App	926	4	US-10-072-844-31	Sequence 31, Appl
854	6	1.6	624	4	US-09-538-092-226	Sequence 226, App	927	4	US-10-219-631A-31	Sequence 31, Appl
855	6	1.6	625	4	US-09-360-545-59	Sequence 69, Appl	928	5	PCT-US95-04886-1	Sequence 1, Appl
856	6	1.6	626	4	US-09-949-016-7565	Sequence 7565, Ap	929	5	PCT-US95-01314-45	Sequence 45, Appl
857	6	1.6	627	4	US-09-653-274-13	Sequence 13, Appl	930	4	US-09-543-681A-4291	Sequence 4291, Ap
858	6	1.6	628	4	US-10-461-791-13	Sequence 13, Appl	931	4	US-09-854-845-47	Sequence 47, Appl
859	6	1.6	629	4	US-09-489-039A-10943	Sequence 10943, A	932	4	US-09-252-991A-32892	Sequence 32892, A
860	6	1.6	630	3	US-09-328-501-1	Sequence 1, Appl	933	4	US-09-738-946-8	Sequence 8, Appl
861	6	1.6	631	4	US-09-777-710A-1	Sequence 1, Appl	934	4	US-09-688-188B-23	Sequence 23, Appl
862	6	1.6	632	1	US-08-769-309A-17	Sequence 17, Appl	935	4	US-09-231-417D-23	Sequence 23, Appl
863	6	1.6	633	3	US-08-650-766-6	Sequence 6, Appl	936	4	US-09-688-188B-151	Sequence 151, App
864	6	1.6	634	3	US-08-922-635-5	Sequence 5, Appl	937	4	US-09-231-417D-151	Sequence 151, App
865	6	1.6	635	3	US-08-994-570-17	Sequence 17, Appl	938	3	US-09-134-001C-4917	Sequence 4917, Ap
866	6	1.6	636	4	US-09-252-991A-19760	Sequence 19760, A	939	4	US-09-252-991A-21975	Sequence 21975, A
867	6	1.6	637	4	US-09-389-487-6	Sequence 6, Appl	940	4	US-09-248-796A-18375	Sequence 18375, A
868	6	1.6	638	4	US-09-252-991A-27682	Sequence 27682, A	941	4	US-09-489-039A-12742	Sequence 12742, A
869	6	1.6	639	3	US-09-134-001C-5039	Sequence 5039, A	942	4	US-09-583-110-3214	Sequence 3214, Ap
870	6	1.6	640	4	US-09-538-092-442	Sequence 442, App	943	4	US-09-107-433-4642	Sequence 4642, Ap
871	6	1.6	641	4	US-09-270-767-45005	Sequence 45005, A	944	4	US-09-489-039A-11547	Sequence 11547, A
872	6	1.6	642	3	US-09-328-501-15	Sequence 15, Appl	945	2	US-08-785-310A-8	Sequence 8, Appl
873	6	1.6	643	4	US-09-777-710A-15	Sequence 15, Appl	946	2	US-08-816-693A-53	Sequence 53, Appl
874	6	1.6	644	3	US-09-121-321-16	Sequence 16, Appl	947	3	US-08-885-291-53	Sequence 53, Appl
875	6	1.6	645	3	US-08-933-803A-16	Sequence 16, Appl	948	3	US-09-496-672-53	Sequence 53, Appl
876	6	1.6	646	3	US-08-630-172-10	Sequence 10, Appl	949	4	US-09-489-039A-8184	Sequence 8184, Ap
877	6	1.6	647	3	US-09-375-419-10	Sequence 10, Appl	950	4	US-09-248-796A-19161	Sequence 19161, A
878	6	1.6	648	4	US-09-248-796A-16453	Sequence 16453, A	951	4	US-08-684-932A-38	Sequence 38, Appl
879	6	1.6	649	4	US-09-252-991A-29396	Sequence 29396, A	952	4	US-09-489-039A-13920	Sequence 13920, A
880	6	1.6	650	4	US-09-380-403A-2	Sequence 2, Appl	953	4	US-09-618-304B-2	Sequence 2, Appl
881	6	1.6	651	2	US-08-380-403A-5	Sequence 5, Appl	954	4	US-09-438-185A-29	Sequence 29, Appl
882	6	1.6	652	2	US-08-895-628-5	Sequence 5, Appl	955	4	US-09-854-845-29	Sequence 29, Appl
883	6	1.6	653	2	US-08-895-628-5	Sequence 5, Appl	956	4	US-09-854-845-29	Sequence 29, Appl
884	6	1.6	654	2	US-08-895-628-5	Sequence 5, Appl	957	4	US-09-489-039A-13252	Sequence 13252, A
885	6	1.6	655	4	US-08-895-628-5	Sequence 5, Appl	958	4	US-09-489-039A-13252	Sequence 13252, A
886	6	1.6	656	4	US-08-895-628-5	Sequence 5, Appl	959	4	US-09-854-845-27	Sequence 27, Appl
887	6	1.6	657	4	US-08-895-628-5	Sequence 5, Appl	960	4	US-09-538-092-932	Sequence 932, App
888	6	1.6	658	4	US-09-248-796A-26144	Sequence 26144, A	961	4	US-09-949-016-8846	Sequence 8846, Ap
889	6	1.6	659	4	US-09-949-016-7806	Sequence 7806, Ap	962	4	US-09-949-016-8847	Sequence 8847, Ap
890	6	1.6	660	3	US-09-489-039A-13463	Sequence 13463, A	963	4	US-09-949-016-8275	Sequence 8275, Ap
891	6	1.6	661	3	US-08-968-563-18	Sequence 18, Appl	964	4	US-09-949-016-8276	Sequence 8276, Ap
892	6	1.6	662	3	US-08-968-563-18	Sequence 18, Appl	965	4	US-09-538-092-206	Sequence 206, App
893	6	1.6	663	3	US-09-297-928-15	Sequence 15, Appl	966	4	US-09-949-016-7553	Sequence 7553, Ap
894	6	1.6	664	4	US-09-902-540-15419	Sequence 15419, A	967	4	US-08-620-694A-2	Sequence 2, Appl
895	6	1.6	665	4	US-09-417-197-75	Sequence 75, Appl	968	4	US-09-022-255-2	Sequence 2, Appl
896	6	1.6	666	4	US-09-417-197-75	Sequence 75, Appl	969	4	US-09-022-255-2	Sequence 2, Appl
897	6	1.6	667	4	US-09-417-197-75	Sequence 75, Appl	970	4	US-09-022-255-2	Sequence 2, Appl
898	6	1.6	668	4	US-09-417-197-75	Sequence 75, Appl	971	4	US-09-022-255-2	Sequence 2, Appl
899	6	1.6	669	4	US-09-417-197-75	Sequence 75, Appl	972	4	US-09-022-255-2	Sequence 2, Appl
900	6	1.6	670	4	US-09-417-197-75	Sequence 75, Appl	973	4	US-09-022-255-2	Sequence 2, Appl
901	6	1.6	671	4	US-09-417-197-75	Sequence 75, Appl	974	4	US-09-022-255-2	Sequence 2, Appl
902	6	1.6	672	4	US-09-417-197-75	Sequence 75, Appl	975	4	US-09-022-255-2	Sequence 2, Appl
903	6	1.6	673	4	US-09-417-197-75	Sequence 75, Appl	976	4	US-09-022-255-2	Sequence 2, Appl

977 6 1.6 867 4 US-09-248-796A-19207
978 6 1.6 870 4 US-09-602-787A-578
979 6 1.6 870 4 US-09-854-845-31
980 6 1.6 871 4 US-09-328-352-7076
981 6 1.6 874 4 US-09-543-681A-6958
982 6 1.6 883 4 US-09-252-991A-16929
983 6 1.6 901 4 US-09-714-767A-4
984 6 1.6 901 4 US-09-538-092-826
985 6 1.6 916 4 US-09-949-016-8291
986 6 1.6 916 4 US-09-949-016-8292
987 6 1.6 919 4 US-09-949-016-7873
988 6 1.6 943 4 US-09-583-110-4794
989 6 1.6 945 4 US-09-107-433-3340
990 6 1.6 959 4 US-09-543-681A-6879
991 6 1.6 965 4 US-09-538-092-650
992 6 1.6 966 4 US-09-606-312-2
993 6 1.6 983 4 US-09-252-991A-21667
994 6 1.6 995 4 US-09-252-991A-22297
995 6 1.6 995 4 US-09-252-991A-32802
996 6 1.6 997 1 US-08-232-540-1
997 6 1.6 997 1 US-08-428-949A-1
998 6 1.6 997 1 US-08-428-948A-1
999 6 1.6 997 2 US-08-428-946-1
1000 6 1.6 997 4 US-09-198-452A-602

ALIGNMENTS

RESULT 1
US-08-969-106-6

; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US-08-969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6

Query Match 100.0%; Score 377; DB 2; Length 377;

Sequence 19207, A
Sequence 578, App
Sequence 31, Appl
Sequence 7076, Ap
Sequence 6958, Ap
Sequence 16929, A
Sequence 4, Appl
Sequence 826, App
Sequence 8291, Ap
Sequence 8292, Ap
Sequence 7873, Ap
Sequence 4794, Ap
Sequence 3340, Ap
Sequence 6879, Ap
Sequence 650, App
Sequence 2, Appl
Sequence 21667, A
Sequence 22297, A
Sequence 32802, A
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 602, App

Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKFPGPLENORLSFLEKAITREAOQWKVNRKMPNSQNVSPSQRDVIOWLAKLKYQFN 60
Db 1 MKFPGPLENORLSFLEKAITREAOQWKVNRKMPNSQNVSPSQRDVIOWLAKLKYQFN 60
Qy 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIRIPVLKVLARDSFC 120
Db 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEIRIPVLKVLARDSFC 120
Qy 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFAHAVSTRPQLLPSLPSQHLAV 180
Db 121 GCSSEILRMERIILDKLNDLHTATPLDFLHIFAHAVSTRPQLLPSLPSQHLAV 180
Qy 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHC 240
Db 181 LTKQLLHMACNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHC 240
Qy 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFKDNKSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGDFKDNKSKPEVPV 300
Qy 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVSENVSVCCTDL 360
Db 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMVEDDFYDGIKRLYNEDNVSENVSVCCTDL 360
Qy 361 QEGHASPCLPQVSV 377
Db 361 QEGHASPCLPQVSV 377

RESULT 2

US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match 100.0%; Score 377; DB 3; Length 377;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQRSLFLEKAITREAAQMKVNVVRKMPNSQNVSPSQRDEVIQWLAKLKYQFN 60
Db 1 MKFPGPLENQRSLFLEKAITREAAQMKVNVVRKMPNSQNVSPSQRDEVIQWLAKLKYQFN 60

Qy 61 LYPTTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Db 61 LYPTTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAVSTRPOLLFSLPKLSPSQHLAV 180
Db 121 GCSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAVSTRPOLLFSLPKLSPSQHLAV 180

Qy 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHCR 240
Db 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSNVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSNVSGVCGTDLR 360

Qy 361 QEGHASPCLPPLQPVSV 377
Db 361 QEGHASPCLPPLQPVSV 377

RESULT 3

US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid

STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-338-125-6

Query Match 100.0%; Score 377; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPGPLENQRSLFLEKAITREAAQMKVNVVRKMPNSQNVSPSQRDEVIQWLAKLKYQFN 60
Db 1 MKFPGPLENQRSLFLEKAITREAAQMKVNVVRKMPNSQNVSPSQRDEVIQWLAKLKYQFN 60

Qy 61 LYPTTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120
Db 61 LYPTTFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEDEDERIPVLKVLARDSFC 120

Qy 121 GCSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAVSTRPOLLFSLPKLSPSQHLAV 180
Db 121 GCSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAVSTRPOLLFSLPKLSPSQHLAV 180

Qy 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHCR 240
Db 181 LTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWLSITIELLOKAQMDSSQLIHCR 240

Qy 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
Db 241 ELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300

Qy 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSNVSGVCGTDLR 360
Db 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDVDFDGIKRLYNEDNVSNVSGVCGTDLR 360

Qy 361 QEGHASPCLPPLQPVSV 377
Db 361 QEGHASPCLPPLQPVSV 377

RESULT 4

US-09-796-149B-4
; Sequence 4, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCES: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-4

Query Match 67.4%; Score 254; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 4.5e-242;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 VSPSQRDEVIQWLAKLKYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
Db 1 VSPSQRDEVIQWLAKLKYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60

Qy 100 KTVVEEDERIPVLKVLARDSFCGSSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAV 159
Db 61 KTVVEEDERIPVLKVLARDSFCGSSSEILRMERIITLDKLNWDLHTATPLDFLHIFHAJAV 120

Qy 160 STRPQLLFSPLPKLSPSQHLAVLTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWL 219
Db 121 STRPQLLFSPLPKLSPSQHLAVLTKQLLHCMAQNQLQFRGSMALAMVLSLEMEKLIIPDWL 180

Qy 220 SLTIELLOKAQMDSSQLIHCRBELVAHHLSTLQSSLPVNSVYVYRPLKHTLVTCDKGVFRL 279

Db 181 SLTIELLQKQWSSQLHCHRELVAHLSTLQSSLLPLNSVYVRPLKHTLVTCCKGVRL 240
Qy 280 HPSSVPGPDFSKDN 293
Db 241 HPSSVPGPDFSKDN 254

RESULT 5

US-09-513-999C-5984
; Sequence 5984, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59-US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5984
; LENGTH: 131
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5984

Query Match 34.7%; Score 131; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 4.3e-121;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 130 MERIILDKLNDIATATPLDPLHIFHAIVSTRPQLLSPLSPSOHLAVITKQLHCM 189
Db 1 MERIILDKLNDIATATPLDPLHIFHAIVSTRPQLLSPLSPSOHLAVITKQLHCM 60
Qy 190 ACNQLQPRGSMALAMVLSLEMEKLPDWLSLTIELLQKQWSSQLHCHRELVAHLST 249
Db 61 ACNQLQPRGSMALAMVLSLEMEKLPDWLSLTIELLQKQWSSQLHCHRELVAHLST 120
Qy 250 LQSSLPNSVY 260
Db 121 LQSSLPNSVY 131

RESULT 6

US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-5

Query Match 3.7%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 343 EDNVSENVGSVCGT 356
Db 1 EDNVSENVGSVCGT 14

RESULT 7

US-09-129-112-2
; Sequence 2, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (52)..(73)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (128)..(144)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (173)..(195)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyrases
US-09-129-112-2

Query Match 2.4%; Score 9; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 165 LLFSLPKLS 173
Db 20 LLFSLPKLS 28

RESULT 8

```
US-09-270-767-57798
; Sequence 57798, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 57798
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-57798

Query Match      2.1%; Score 8; DB 4; Length 127;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      180 VLTQQLH 187
Db      79 VLTQQLH 86
|||||

RESULT 9
US-09-270-767-39916
; Sequence 39916, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39916
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-39916

Query Match      2.1%; Score 8; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      219 LSLTIELL 226
Db      72 LSLTIELL 79
|||||

RESULT 10
US-09-270-767-55133
; Sequence 55133, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55133
; LENGTH: 170
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-55133

Query Match      2.1%; Score 8; DB 4; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      219 LSLTIELL 226
Db      72 LSLTIELL 79
|||||

RESULT 11
US-09-128-155-12
; Sequence 12, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-12

Query Match      1.9%; Score 7; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      66 FALASSL 72
Db      10 FALASSL 16
|||||

RESULT 12
US-09-128-155-8
; Sequence 8, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-8

Query Match      1.9%; Score 7; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      66 FALASSL 72
```

```
Db      41  FALASSL 47
|||||
RESULT 13
US-09-128-155-4
; Sequence 4, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-4

Query Match      1.9%; Score 7; DB 3; Length 63;
Best Local Similarity 100.0%; Pred.No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      66  FALASSL 72
|||||
Db      52  FALASSL 58

RESULT 14
US-09-270-767-34602
; Sequence 34602, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34602
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-34602

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11  RLSFLL 17
|||||
Db      58  RLSFLL 64

RESULT 15
US-09-270-767-49819
; Sequence 49819, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49819
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49819

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11  RLSFLL 17
|||||
Db      58  RLSFLL 64

; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 49819
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-49819

Query Match      1.9%; Score 7; DB 4; Length 70;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      11  RLSFLL 17
|||||
Db      58  RLSFLL 64

Search completed: February 11, 2005, 03:18:29
Job time : 47.7826 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:16:44 ; Search time 86.7775 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGPLENORLSFILEKAI.....LSRQGHASCPFLQPVSM 377

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1376875 seqs, 326749119 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1376875

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pcp.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pcp.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09D_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pcp.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pcp.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	
1	377	100.0	377	12	US-09-736-250-1	
2	254	67.4	254	9	US-09-796-149-4	
3	14	3.7	14	12	US-09-736-250-5	
4	9	2.4	9	10	US-09-865-548A-151	
5	9	2.4	9	14	US-10-006-177-8	
6	9	2.4	462	9	US-09-129-112-2	
7	8	2.1	83	15	US-10-425-114-42971	
8	2.1	99	15	US-10-424-599-245711	Sequence 245711, A	
9	8	2.1	216	15	US-10-424-599-196677	Sequence 196677
10	8	2.1	289	15	US-10-424-599-196680	Sequence 196680
11	8	2.1	379	16	US-10-437-963-145582	Sequence 145582
12	8	2.1	391	9	US-09-866-562-62	Sequence 62, Appl
13	8	2.1	416	15	US-10-236-392-92	Sequence 92, Appl

14	8	2.1	418	15	US-10-425-114-51949	Sequence 51949, A
15	8	2.1	514	16	US-10-767-701-44456	Sequence 44456, A
16	8	2.1	589	15	US-10-425-114-69696	Sequence 69696, A
17	8	2.1	1931	16	US-10-437-963-138321	Sequence 138321
18	7	1.9	21	13	US-10-095-407-12	Sequence 12, Appl
19	7	1.9	45	16	US-10-716-029-211	Sequence 211, Appl
20	7	1.9	50	15	US-10-424-599-219329	Sequence 219329
21	7	1.9	52	13	US-10-095-407-8	Sequence 8, Appl
22	7	1.9	56	15	US-10-424-599-161917	Sequence 161917
23	7	1.9	58	9	US-09-925-301-1162	Sequence 1162, Ap
24	7	1.9	62	14	US-10-156-761-13291	Sequence 13291, A
25	7	1.9	63	13	US-10-095-407-4	Sequence 4, Appl
26	7	1.9	68	10	US-09-764-891-4938	Sequence 4938, Ap
27	7	1.9	68	14	US-10-205-428-417	Sequence 417, Appl
28	7	1.9	71	16	US-10-437-963-157984	Sequence 157984
29	7	1.9	80	15	US-10-424-599-224197	Sequence 224197
30	7	1.9	83	16	US-10-767-701-62088	Sequence 62088, A
31	7	1.9	85	16	US-10-437-963-111076	Sequence 111076
32	7	1.9	93	15	US-10-424-599-190556	Sequence 190556
33	7	1.9	98	9	US-09-764-869-1104	Sequence 1104, Ap
34	7	1.9	98	14	US-10-091-504-1104	Sequence 1104, Ap
35	7	1.9	98	15	US-10-227-577-1104	Sequence 1104, Ap
36	7	1.9	110	9	US-09-864-761-45514	Sequence 45514, A
37	7	1.9	123	16	US-10-437-963-166119	Sequence 166119
38	7	1.9	128	15	US-10-425-114-42724	Sequence 42724, A
39	7	1.9	134	16	US-10-437-963-137857	Sequence 137857
40	7	1.9	136	13	US-10-095-407-11	Sequence 11, Appl
41	7	1.9	143	15	US-10-424-599-170638	Sequence 170638
42	7	1.9	154	15	US-10-424-599-173129	Sequence 173129
43	7	1.9	157	10	US-09-876-790-10	Sequence 10, Appl
44	7	1.9	157	14	US-10-302-554-9	Sequence 9, Appl
45	7	1.9	157	14	US-10-302-554-10	Sequence 10, Appl
46	7	1.9	157	14	US-10-302-554-12	Sequence 12, Appl
47	7	1.9	157	14	US-10-302-554-15	Sequence 15, Appl
48	7	1.9	157	17	US-10-888-779-10	Sequence 10, Appl
49	7	1.9	157	17	US-10-888-867-10	Sequence 10, Appl
50	7	1.9	157	17	US-10-888-780-10	Sequence 10, Appl
51	7	1.9	157	17	US-10-888-931-10	Sequence 10, Appl
52	7	1.9	158	16	US-10-437-963-189349	Sequence 189349
53	7	1.9	160	15	US-10-425-114-43681	Sequence 43681, A
54	7	1.9	162	15	US-10-425-114-40890	Sequence 40890, A
55	7	1.9	167	13	US-10-095-407-7	Sequence 7, Appl
56	7	1.9	176	9	US-09-965-528-25	Sequence 25, Appl
57	7	1.9	176	11	US-09-969-984-25	Sequence 25, Appl
58	7	1.9	178	13	US-10-095-407-2	Sequence 2, Appl
59	7	1.9	178	14	US-10-139-833-11	Sequence 11, Appl
60	7	1.9	178	16	US-10-767-701-59743	Sequence 59743, A
61	7	1.9	192	10	US-09-876-790-3	Sequence 3, Appl
62	7	1.9	192	14	US-10-139-833-13	Sequence 13, Appl
63	7	1.9	192	17	US-10-888-779-3	Sequence 3, Appl
64	7	1.9	192	17	US-10-888-780-3	Sequence 3, Appl
65	7	1.9	192	17	US-10-888-867-3	Sequence 3, Appl
66	7	1.9	192	17	US-10-888-931-3	Sequence 3, Appl
67	7	1.9	193	13	US-10-006-867-142	Sequence 142, App
68	7	1.9	193	13	US-10-063-547-142	Sequence 142, App
69	7	1.9	193	13	US-10-063-551-142	Sequence 142, App
70	7	1.9	193	14	US-10-063-616-142	Sequence 142, App
71	7	1.9	193	14	US-10-063-569-142	Sequence 142, App
72	7	1.9	193	14	US-10-063-513-142	Sequence 142, App
73	7	1.9	193	14	US-10-063-515-142	Sequence 142, App
74	7	1.9	193	14	US-10-063-512-142	Sequence 142, App
75	7	1.9	193	14	US-10-063-502-142	Sequence 142, App
76	7	1.9	193	14	US-10-063-549-142	Sequence 142, App
77	7	1.9	193	14	US-10-063-554-142	Sequence 142, App
78	7	1.9	193	14	US-10-063-553-142	Sequence 142, App
79	7	1.9	193	14	US-10-063-518-142	Sequence 142, App
80	7	1.9	193	14	US-10-063-598-142	Sequence 142, App
81	7	1.9	193	14	US-10-227-693-142	Sequence 142, App
82	7	1.9	193	14	US-10-063-563-142	Sequence 142, App
83	7	1.9	193	14	US-10-063-555-142	Sequence 142, App
84	7	1.9	193	14	US-10-063-594-142	Sequence 142, App
85	7	1.9	193	14	US-10-063-567-142	Sequence 142, App
86	7	1.9	193	14	US-10-063-538-142	Sequence 142, App

87	7	1.9	193	14	US-10-063-599-142	Sequence 142, App	160	7	1.9	193	14	US-10-063-649-142	Sequence 142, App
88	7	1.9	193	14	US-10-063-595-142	Sequence 142, App	161	7	1.9	193	14	US-10-063-650-142	Sequence 142, App
89	7	1.9	193	14	US-10-063-580-142	Sequence 142, App	162	7	1.9	193	14	US-10-063-652-142	Sequence 142, App
90	7	1.9	193	14	US-10-063-557-142	Sequence 142, App	163	7	1.9	193	14	US-10-063-654-142	Sequence 142, App
91	7	1.9	193	14	US-10-063-585-142	Sequence 142, App	164	7	1.9	193	14	US-10-063-659-142	Sequence 142, App
92	7	1.9	193	14	US-10-063-588-142	Sequence 142, App	165	7	1.9	193	14	US-10-063-661-142	Sequence 142, App
93	7	1.9	193	14	US-10-063-735-142	Sequence 142, App	166	7	1.9	193	14	US-10-063-528-142	Sequence 142, App
94	7	1.9	193	14	US-10-063-526-142	Sequence 142, App	167	7	1.9	193	14	US-10-063-540-142	Sequence 142, App
95	7	1.9	193	14	US-10-063-586-142	Sequence 142, App	168	7	1.9	193	14	US-10-063-568-142	Sequence 142, App
96	7	1.9	193	14	US-10-063-546-142	Sequence 142, App	169	7	1.9	193	14	US-10-063-570-142	Sequence 142, App
97	7	1.9	193	14	US-10-063-564-142	Sequence 142, App	170	7	1.9	193	14	US-10-063-582-142	Sequence 142, App
98	7	1.9	193	14	US-10-063-662-142	Sequence 142, App	171	7	1.9	193	14	US-10-063-587-142	Sequence 142, App
99	7	1.9	193	14	US-10-063-510-142	Sequence 142, App	172	7	1.9	193	14	US-10-063-592-142	Sequence 142, App
100	7	1.9	193	14	US-10-063-669-142	Sequence 142, App	173	7	1.9	193	14	US-10-063-597-142	Sequence 142, App
101	7	1.9	193	14	US-10-063-670-142	Sequence 142, App	174	7	1.9	193	14	US-10-063-602-142	Sequence 142, App
102	7	1.9	193	14	US-10-063-671-142	Sequence 142, App	175	7	1.9	193	14	US-10-063-606-142	Sequence 142, App
103	7	1.9	193	14	US-10-063-674-142	Sequence 142, App	176	7	1.9	193	14	US-10-063-608-142	Sequence 142, App
104	7	1.9	193	14	US-10-063-675-142	Sequence 142, App	177	7	1.9	193	14	US-10-063-611-142	Sequence 142, App
105	7	1.9	193	14	US-10-063-676-142	Sequence 142, App	178	7	1.9	193	14	US-10-063-614-142	Sequence 142, App
106	7	1.9	193	14	US-10-063-686-142	Sequence 142, App	179	7	1.9	193	14	US-10-063-639-142	Sequence 142, App
107	7	1.9	193	14	US-10-063-689-142	Sequence 142, App	180	7	1.9	193	14	US-10-063-643-142	Sequence 142, App
108	7	1.9	193	14	US-10-063-692-142	Sequence 142, App	181	7	1.9	193	14	US-10-063-646-142	Sequence 142, App
109	7	1.9	193	14	US-10-063-693-142	Sequence 142, App	182	7	1.9	193	14	US-10-063-651-142	Sequence 142, App
110	7	1.9	193	14	US-10-063-694-142	Sequence 142, App	183	7	1.9	193	14	US-10-063-653-142	Sequence 142, App
111	7	1.9	193	14	US-10-063-698-142	Sequence 142, App	184	7	1.9	193	14	US-10-063-660-142	Sequence 142, App
112	7	1.9	193	14	US-10-063-699-142	Sequence 142, App	185	7	1.9	193	14	US-10-063-665-142	Sequence 142, App
113	7	1.9	193	14	US-10-063-702-142	Sequence 142, App	186	7	1.9	193	14	US-10-063-584-142	Sequence 142, App
114	7	1.9	193	14	US-10-063-705-142	Sequence 142, App	187	7	1.9	193	14	US-10-063-536-142	Sequence 142, App
115	7	1.9	193	14	US-10-063-707-142	Sequence 142, App	1						

233	7	1.9	218	15	US-10-694-978-4	Sequence 4, Appli	306	7	1.9	437	15	US-10-414-267-6	Sequence 6, Appli
234	7	1.9	218	16	US-10-679-201-6	Sequence 6, Appli	307	7	1.9	439	9	US-09-866-570A-28	Sequence 28, Appli
235	7	1.9	218	17	US-10-888-779-8	Sequence 8, Appli	308	7	1.9	439	9	US-09-866-570A-28	Sequence 28, Appli
236	7	1.9	218	17	US-10-888-867-8	Sequence 8, Appli	309	7	1.9	439	14	US-10-166-984-88	Sequence 12, Appli
237	7	1.9	218	17	US-10-888-780-8	Sequence 8, Appli	310	7	1.9	439	15	US-10-167-603C-12	Sequence 12, Appli
238	7	1.9	218	17	US-10-888-331-8	Sequence 8, Appli	311	7	1.9	439	15	US-10-166-984-28	Sequence 28, Appli
239	7	1.9	238	16	US-10-437-963-171439	Sequence 171439, A	312	7	1.9	446	15	US-10-166-984-28	Sequence 28, Appli
240	7	1.9	235	15	US-10-282-122A-57350	Sequence 57350, A	313	7	1.9	446	9	US-09-866-570A-56	Sequence 56, Appli
241	7	1.9	239	14	US-10-156-761-9042	Sequence 9042, Ap	314	7	1.9	448	9	US-09-866-570A-56	Sequence 56, Appli
242	7	1.9	244	15	US-10-424-599-237463	Sequence 237463, A	315	7	1.9	448	14	US-10-166-984-56	Sequence 56, Appli
243	7	1.9	245	15	US-10-424-599-180015	Sequence 180015, A	316	7	1.9	448	15	US-10-166-984-56	Sequence 56, Appli
244	7	1.9	249	9	US-09-971-309-1	Sequence 1, Appli	317	7	1.9	451	15	US-10-166-984-56	Sequence 56, Appli
245	7	1.9	249	16	US-10-702-400-68	Sequence 68, Appli	318	7	1.9	467	15	US-10-424-599-225383	Sequence 225383, A
246	7	1.9	249	16	US-10-828-924-60	Sequence 60, Appli	319	7	1.9	510	15	US-10-369-493-3993	Sequence 3993, Ap
247	7	1.9	256	14	US-10-156-761-13846	Sequence 13846, A	320	7	1.9	511	15	US-10-424-599-253543	Sequence 253543, A
248	7	1.9	260	16	US-10-437-963-133492	Sequence 133492, A	321	7	1.9	511	14	US-10-424-599-253543	Sequence 10, Appli
249	7	1.9	266	15	US-10-434-599-173128	Sequence 173128, A	322	7	1.9	518	10	US-10-134-102-10	Sequence 90, Appli
250	7	1.9	271	15	US-10-282-122A-45041	Sequence 45041, A	323	7	1.9	528	10	US-09-940-925A-90	Sequence 90, Appli
251	7	1.9	274	16	US-10-437-963-173780	Sequence 173780, A	324	7	1.9	537	16	US-10-437-963-142350	Sequence 142350, A
252	7	1.9	285	15	US-10-282-122A-74796	Sequence 74796, A	325	7	1.9	559	15	US-10-425-114-68937	Sequence 68937, A
253	7	1.9	289	15	US-10-424-599-173670	Sequence 173670, A	326	7	1.9	560	9	US-09-912-559-3	Sequence 3, Appli
254	7	1.9	298	15	US-10-389-566-536	Sequence 536, App	327	7	1.9	560	9	US-09-912-559-3	Sequence 4, Appli
255	7	1.9	298	15	US-10-425-114-52930	Sequence 52930, A	328	7	1.9	560	14	US-10-172-712-32	Sequence 32, Appli
256	7	1.9	302	9	US-09-866-572A-8	Sequence 8, Appli	329	7	1.9	560	15	US-10-391-215-5	Sequence 5, Appli
257	7	1.9	302	9	US-09-866-572A-24	Sequence 24, Appli	330	7	1.9	560	15	US-10-391-215-5	Sequence 6, Appli
258	7	1.9	302	9	US-09-866-570A-8	Sequence 8, Appli	331	7	1.9	560	15	US-10-391-215-6	Sequence 7, Appli
259	7	1.9	302	9	US-09-866-570A-24	Sequence 24, Appli	332	7	1.9	560	15	US-10-391-215-7	Sequence 8, Appli
260	7	1.9	302	14	US-10-166-984-8	Sequence 8, Appli	333	7	1.9	573	15	US-10-369-493-22865	Sequence 10208, A
261	7	1.9	302	14	US-10-166-984-24	Sequence 24, Appli	334	7	1.9	578	15	US-10-369-493-22865	Sequence 10208, A
262	7	1.9	302	15	US-10-166-984-8	Sequence 8, Appli	335	7	1.9	603	15	US-10-425-114-68922	Sequence 68922, A
263	7	1.9	302	15	US-10-166-984-24	Sequence 24, Appli	336	7	1.9	610	15	US-10-425-114-58388	Sequence 58388, A
264	7	1.9	306	9	US-09-866-572A-2	Sequence 2, Appli	337	7	1.9	622	14	US-10-032-585-7890	Sequence 7890, Ap
265	7	1.9	306	9	US-09-866-570A-2	Sequence 2, Appli	338	7	1.9	628	15	US-10-425-114-66875	Sequence 66875, A
266	7	1.9	306	14	US-10-166-984-2	Sequence 2, Appli	339	7	1.9	639	15	US-10-360-937-39	Sequence 39, Appli
267	7	1.9	306	15	US-10-166-984-2	Sequence 2, Appli	340	7	1.9	651	16	US-10-437-963-182057	Sequence 182057, A
268	7	1.9	317	15	US-10-282-122A-55956	Sequence 55956, A	341	7	1.9	652	9	US-09-815-242-13698	Sequence 13698, A
269	7	1.9	322	15	US-10-425-114-37377	Sequence 37377, A	342	7	1.9	656	15	US-10-425-114-53846	Sequence 53846, A
270	7	1.9	327	15	US-10-425-114-43516	Sequence 43516, A	343	7	1.9	663	15	US-10-755-889-480	Sequence 480, App
271	7	1.9	331	14	US-10-214-473-50	Sequence 50, Appli	344	7	1.9	673	15	US-10-425-114-64380	Sequence 64380, A
272	7	1.9	331	14	US-10-214-473-50	Sequence 50, Appli	345	7	1.9	685	10	US-09-877-843-59	Sequence 59, Appli
273	7	1.9	332	16	US-10-437-963-171440	Sequence 171440, A	346	7	1.9	730	11	US-09-939-853A-40	Sequence 40, Appli
274	7	1.9	339	15	US-10-282-122A-45100	Sequence 45100, A	347	7	1.9	737	16	US-10-437-963-203756	Sequence 203756, A
275	7	1.9	350	9	US-09-800-729-91	Sequence 91, Appli	348	7	1.9	772	15	US-10-369-493-16014	Sequence 16014, A
276	7	1.9	350	9	US-09-800-729-137	Sequence 127, App	349	7	1.9	789	15	US-10-041-018-395	Sequence 395, App
277	7	1.9	350	11	US-09-284-320-6	Sequence 6, Appli	350	7	1.9	833	10	US-09-940-925A-85	Sequence 85, Appli
278	7	1.9	350	11	US-09-833-245-2215	Sequence 2215, Ap	351	7	1.9	833	10	US-09-864-636A-239	Sequence 239, App
279	7	1.9	350	11	US-09-833-245-2216	Sequence 2216, Ap	352	7	1.9	833	10	US-09-941-193A-85	Sequence 85, Appli
280	7	1.9	350	15	US-10-284-237-1530	Sequence 1530, Ap	353	7	1.9	833	10	US-09-758-282-40	Sequence 40, Appli
281	7	1.9	356	16	US-10-437-963-171441	Sequence 171441, A	354	7	1.9	833	11	US-09-864-426A-239	Sequence 239, App
282	7	1.9	357	15	US-10-376-397A-44	Sequence 44, Appli	355	7	1.9	833	14	US-10-084-839-239	Sequence 239, App
283	7	1.9	367	15	US-10-282-122A-47588	Sequence 47588, A	356	7	1.9	895	14	US-10-345-092-5	Sequence 5, Appli
284	7	1.9	368	10	US-09-866-050A-670	Sequence 670, App	357	7	1.9	1008	16	US-10-437-963-181880	Sequence 181880, A
285	7	1.9	369	15	US-10-369-493-22377	Sequence 22377, A	358	7	1.9	1045	14	US-10-217-700-7	Sequence 7, Appli
286	7	1.9	370	14	US-10-021-955-78	Sequence 78, Appli	359	7	1.9	1190	15	US-10-369-493-18546	Sequence 18546, A
287	7	1.9	370	14	US-10-021-955-83	Sequence 83, Appli	360	7	1.9	1216	15	US-10-028-248A-72	Sequence 72, Appli
288	7	1.9	370	14	US-10-021-955-80	Sequence 80, Appli	361	7	1.9	1216	15	US-10-107-782-72	Sequence 72, Appli
289	7	1.9	379	14	US-10-425-114-60718	Sequence 60718, A	362	7	1.9	1228	15	US-10-021-660-129	Sequence 129, App
290	7	1.9	379	15	US-10-156-761-8561-	Sequence 8561, Ap	363	7	1.9	1228	14	US-10-211-462-101	Sequence 101, App
291	7	1.9	385	15	US-10-425-114-64567	Sequence 64567, A	364	7	1.9	1228	17	US-10-741-600-1577	Sequence 1577, Ap
292	7	1.9	391	15	US-10-425-114-68619	Sequence 68619, A	365	7	1.9	1236	15	US-10-334-143-38	Sequence 38, Appli
293	7	1.9	394	9	US-09-738-626-4690	Sequence 4690, Ap	366	7	1.9	1274	16	US-10-415-615-3	Sequence 3, Appli
294	7	1.9	399	15	US-10-108-260A-2891	Sequence 2891, Ap	367	7	1.9	1282	16	US-10-437-963-110654	Sequence 110654, A
295	7	1.9	403	15	US-10-369-493-2119	Sequence 2119, Ap	368	7	1.9	1371	16	US-10-437-963-128341	Sequence 128341, A
296	7	1.9	409	14	US-10-156-761-10839	Sequence 10839, A	369	7	1.9	1435	16	US-10-437-963-174801	Sequence 174801, A
297	7	1.9	414	14	US-10-156-761-13568	Sequence 13568, A	370	7	1.9	1554	16	US-10-383-930-38	Sequence 38, Appli
298	7	1.9	420	15	US-10-310-154-414	Sequence 414, App	371	7	1.9	1579	16	US-10-437-963-172638	Sequence 172638, A
299	7	1.9	424	15	US-09-496-444-2	Sequence 2, Appli	372	7	1.9	3700	14	US-10-329-079-4	Sequence 4, Appli
300	7	1.9	424	15	US-10-310-154-418	Sequence 418, App	373	7	1.9	6291	14	US-10-329-079-41	Sequence 41, Appli
301	7	1.9	427	15	US-10-424-599-209873	Sequence 209873, A	374	6	1.6	9	14	US-10-281-478-33	Sequence 33, Appli
302	7	1.9	428	9	US-09-789-599A-2	Sequence 2, Appli	375	6	1.6	10	10	US-09-572-404B-2795	Sequence 2795, Ap
303	7	1.9	428	9	US-09-816-079-2	Sequence 2, Appli	376	6	1.6	10	10	US-09-572-404B-3069	Sequence 3069, Ap
304	7	1.9	437	15	US-10-411-927-2	Sequence 2, Appli	377	7	1.9	12	14	US-10-225-301-5	Sequence 5, Appli
305	7	1.9	437	15	US-10-456-954-6	Sequence 6, Appli	378	6	1.6	12	15	US-10-264-309-35	Sequence 35, Appli

379	6	1.6	16	14	US-10-225-567A-1535	Sequence 1535, App	452
380	6	1.6	23	10	US-09-809-391-621	Sequence 621, App	453
381	6	1.6	23	10	US-09-882-171-621	Sequence 621, App	454
382	6	1.6	23	15	US-10-164-861-621	Sequence 621, App	455
383	6	1.6	31	15	US-10-424-599-239402	Sequence 239402, App	456
384	6	1.6	32	9	US-09-828-708-69	Sequence 69, App	457
385	6	1.6	32	9	US-09-828-708-71	Sequence 71, App	458
386	6	1.6	32	16	US-10-467-513-12	Sequence 513, App	459
387	6	1.6	34	9	US-09-864-761-38444	Sequence 38444, App	460
388	6	1.6	34	10	US-09-942-024-36	Sequence 36, App	461
389	6	1.6	34	10	US-09-942-098-36	Sequence 36, App	462
390	6	1.6	34	14	US-10-218-102-127	Sequence 127, App	463
391	6	1.6	34	15	US-10-261-161-58	Sequence 58, App	464
392	6	1.6	34	16	US-10-437-963-126146	Sequence 126146, App	465
393	6	1.6	35	9	US-09-864-761-33420	Sequence 33420, App	466
394	6	1.6	35	10	US-09-986-480-319	Sequence 319, App	467
395	6	1.6	36	16	US-10-168-804B-20	Sequence 20, App	468
396	6	1.6	37	9	US-09-864-761-48546	Sequence 48546, App	469
397	6	1.6	38	10	US-09-933-767-721	Sequence 721, App	470
398	6	1.6	38	14	US-10-004-860-721	Sequence 721, App	471
399	6	1.6	38	14	US-10-023-282-721	Sequence 721, App	472
400	6	1.6	38	14	US-10-029-386-28020	Sequence 28020, App	473
401	6	1.6	39	9	US-09-864-761-48726	Sequence 48726, App	474
402	6	1.6	39	15	US-10-236-115-1024	Sequence 1024, App	475
403	6	1.6	39	16	US-10-168-804B-21	Sequence 21, App	476
404	6	1.6	40	9	US-09-864-761-35683	Sequence 35683, App	477
405	6	1.6	40	16	US-10-767-701-49319	Sequence 49319, App	478
406	6	1.6	42	9	US-09-864-761-33592	Sequence 33592, App	479
407	6	1.6	42	9	US-09-864-761-37920	Sequence 37920, App	480
408	6	1.6	42	14	US-10-163-198-11	Sequence 11, App	481
409	6	1.6	43	15	US-10-375-253-24	Sequence 24, App	482
410	6	1.6	43	16	US-10-437-963-158129	Sequence 158129, App	483
411	6	1.6	45	16	US-10-424-599-164119	Sequence 164119, App	484
412	6	1.6	45	16	US-10-437-963-111147	Sequence 111147, App	485
413	6	1.6	46	10	US-09-974-879-226	Sequence 226, App	486
414	6	1.6	46	15	US-10-424-599-143885	Sequence 143885, App	487
415	6	1.6	46	15	US-10-424-599-22989	Sequence 22989, App	488
416	6	1.6	46	16	US-10-621-401-226	Sequence 226, App	489
417	6	1.6	46	16	US-10-437-963-127744	Sequence 127744, App	490
418	6	1.6	47	10	US-09-305-736-226	Sequence 226, App	491
419	6	1.6	47	10	US-09-818-683-226	Sequence 226, App	492
420	6	1.6	47	11	US-09-818-683-226	Sequence 226, App	493
421	6	1.6	49	14	US-10-029-386-31703	Sequence 31703, App	494
422	6	1.6	49	16	US-10-437-963-118184	Sequence 118184, App	495
423	6	1.6	51	14	US-10-185-050-117	Sequence 117, App	496
424	6	1.6	51	15	US-10-424-599-197112	Sequence 197112, App	497
425	6	1.6	51	16	US-10-767-701-53206	Sequence 53206, App	498
426	6	1.6	53	15	US-10-424-599-212230	Sequence 212230, App	499
427	6	1.6	53	16	US-10-437-963-180832	Sequence 180832, App	500
428	6	1.6	55	15	US-10-424-599-229366	Sequence 229366, App	501
429	6	1.6	55	16	US-10-767-701-45316	Sequence 45316, App	502
430	6	1.6	56	15	US-10-424-599-159749	Sequence 159749, App	503
431	6	1.6	57	10	US-09-948-783-207	Sequence 207, App	504
432	6	1.6	57	15	US-10-424-599-252463	Sequence 252463, App	505
433	6	1.6	57	16	US-10-311-1744-65	Sequence 65, App	506
434	6	1.6	57	16	US-10-311-1744-76	Sequence 76, App	507
435	6	1.6	57	16	US-10-437-963-166513	Sequence 166513, App	508
436	6	1.6	57	16	US-10-767-701-48417	Sequence 48417, App	509
437	6	1.6	58	10	US-09-892-877-206	Sequence 206, App	510
438	6	1.6	58	15	US-10-424-599-247908	Sequence 247908, App	511
439	6	1.6	58	16	US-10-437-963-109006	Sequence 109006, App	512
440	6	1.6	59	9	US-09-864-761-169663	Sequence 169663, App	513
441	6	1.6	59	16	US-10-424-599-1190812	Sequence 1190812, App	514
442	6	1.6	59	15	US-10-424-599-254089	Sequence 254089, App	515
443	6	1.6	60	14	US-10-097-065-370	Sequence 370, App	516
444	6	1.6	60	15	US-10-372-876-370	Sequence 370, App	517
445	6	1.6	60	15	US-10-424-599-174447	Sequence 174447, App	518
446	6	1.6	60	16	US-10-437-963-114678	Sequence 114678, App	519
447	6	1.6	61	16	US-10-437-963-119090	Sequence 119090, App	520
448	6	1.6	61	15	US-10-424-599-205644	Sequence 205644, App	521
449	6	1.6	61	16	US-10-767-701-59078	Sequence 59078, App	522
450	6	1.6	61	16	US-10-424-599-205644	Sequence 205644, App	523
451	6	1.6	62	11	US-09-864-408A-2376	Sequence 2376, App	524

Sequence 253050, A	1.6	62	15	US-10-424-599-253050
Sequence 12156, A	1.6	62	15	US-10-425-114-71256
Sequence 109872, A	1.6	62	16	US-10-437-963-109872
Sequence 159236, A	1.6	62	16	US-10-437-963-159236
Sequence 173614, A	1.6	62	16	US-10-437-963-173614
Sequence 221760, A	1.6	63	13	US-10-112-793-28
Sequence 193019, A	1.6	63	15	US-10-424-599-221760
Sequence 33346, A	1.6	63	16	US-10-437-963-193019
Sequence 34896, A	1.6	63	16	US-10-767-701-33346
Sequence 150897, A	1.6	64	9	US-09-864-761-34896
Sequence 320265, A	1.6	64	15	US-10-424-599-150897
Sequence 148408, A	1.6	64	15	US-10-424-599-220265
Sequence 48443, A	1.6	65	9	US-10-437-963-148408
Sequence 1, Appl	1.6	65	9	US-09-864-761-48443
Sequence 1, Appl	1.6	65	9	US-09-924-102-1
Sequence 1, Appl	1.6	65	14	US-10-203-081-1
Sequence 13535, A	1.6	65	14	US-10-156-761-13535
Sequence 133003, A	1.6	66	16	US-10-437-963-133003
Sequence 21, Appl	1.6	66	14	US-10-012-140-21
Sequence 159226, A	1.6	66	15	US-10-424-599-159226
Sequence 190626, A	1.6	66	15	US-10-424-599-190626
Sequence 234, App	1.6	67	11	US-09-833-245-254
Sequence 255, App	1.6	67	11	US-09-833-245-255
Sequence 279518, A	1.6	67	15	US-10-424-599-279518
Sequence 131974, A	1.6	67	16	US-10-437-963-131974
Sequence 32826, A	1.6	68	16	US-10-767-701-32826
Sequence 135157, A	1.6	68	16	US-10-437-963-135157
Sequence 439, App	1.6	69	10	US-09-933-767-439
Sequence 439, App	1.6	69	14	US-10-004-860-439
Sequence 439, App	1.6	69	14	US-10-023-282-439
Sequence 7334, App	1.6	69	14	US-10-106-698-7334
Sequence 149679, A	1.6	69	15	US-10-424-599-149679
Sequence 152230, A	1.6	69	15	US-10-424-599-152230
Sequence 181599, A	1.6	69	15	US-10-424-599-181599
Sequence 257426, A	1.6	69	15	US-10-424-599-257426
Sequence 106289, A	1.6	69	16	US-10-276-774-2603
Sequence 116, App	1.6	70	9	US-09-729-674-116
Sequence 200, App	1.6	70	9	US-09-843-676-200
Sequence 200, App	1.6	70	10	US-09-438-486-200
Sequence 502, App	1.6	70	11	US-09-978-360A-502
Sequence 200, App	1.6	70	14	US-10-053-758-200
Sequence 200, App	1.6	70	14	US-10-054-295-200
Sequence 200, App	1.6	70	14	US-10-054-611-200
Sequence 319, App	1.6	70	15	US-10-325-810-319
Sequence 3008, App	1.6	70	15	US-10-264-049-3008
Sequence 183183, A	1.6	70	15	US-10-424-599-183183
Sequence 261515, A	1.6	70	15	US-10-424-599-261515
Sequence 43696, A	1.6	70	16	US-10-425-114-43696
Sequence 116, App	1.6	70	16	US-10-913-553-116
Sequence 319, App	1.6	70	17	US-10-877-146-319
Sequence 1056, App	1.6	71	9	US-09-864-761-48254
Sequence 48254, A	1.6	71	9	US-09-864-761-48254
Sequence 739, App	1.6	71	14	US-10-083-357-739
Sequence 6518, App	1.6	72	14	US-10-106-698-6518
Sequence 27450, A	1.6	72	14	US-10-029-386-27450
Sequence 176892, A	1.6	72	15	US-10-424-599-176892
Sequence 213151, A	1.6	72	15	US-10-424-599-213151
Sequence 227819, A	1.6	72	15	US-10-424-599-227819
Sequence 1730, App	1.6	73	9	US-09-764-877-1730
Sequence 1730, App	1.6	73	15	US-10-242-515-1730
Sequence 212040, A	1.6	73	15	US-10-424-599-212040
Sequence 270444, A	1.6	73	15	US-10-424-599-270444
Sequence 177023, A	1.6	73	16	US-10-437-963-177023
Sequence 154932, A	1.6	74	15	US-10-424-599-154932
Sequence 165862, A	1.6	74	15	US-10-424-599-165862
Sequence 171170, A	1.6	74	15	US-10-424-599-171170
Sequence 236639, A	1.6	74	15	US-10-424-599-236639
Sequence 177318, A	1.6	74	15	US-10-424-599-177318
Sequence 274773, A	1.6	74	15	US-10-424-599-274773
Sequence 45, Appl	1.6	74	16	US-10-311-174A-45
Sequence 152170, A	1.6	74	16	US-10-437-963-152170

525	6	1.6	75	15	US-10-424-599-183618	Sequence 183618,	598	6	1.6	91	16	US-10-767-701-42778	Sequence 42778, A
526	6	1.6	75	15	US-10-424-599-225545	Sequence 225545,	599	6	1.6	91	16	US-10-767-701-59309	Sequence 59309, A
527	6	1.6	75	15	US-10-424-599-262469	Sequence 262469,	600	6	1.6	92	15	US-10-424-599-148202	Sequence 148202,
528	6	1.6	75	16	US-10-767-701-58823	Sequence 58823, A	601	6	1.6	92	15	US-10-424-599-189027	Sequence 189027,
529	6	1.6	76	15	US-10-424-599-176817	Sequence 176817,	602	6	1.6	92	16	US-10-437-963-187327	Sequence 187327,
530	6	1.6	76	15	US-10-424-599-199695	Sequence 199695,	603	6	1.6	93	15	US-10-424-599-275089	Sequence 275089,
531	6	1.6	77	9	US-09-925-301-1464	Sequence 1464, Ap	604	6	1.6	93	16	US-10-767-701-47340	Sequence 47340, A
532	6	1.6	77	15	US-10-029-020-190	Sequence 190, App	605	6	1.6	94	13	US-10-014-269-6	Sequence 6, Appli
533	6	1.6	77	15	US-10-425-114-36990	Sequence 36990, A	606	6	1.6	94	13	US-10-002-974-6	Sequence 6, Appli
534	6	1.6	77	16	US-10-437-963-118108	Sequence 118108,	607	6	1.6	94	14	US-10-314-506-6	Sequence 6, Appli
535	6	1.6	77	16	US-10-437-963-175941	Sequence 175941,	608	6	1.6	94	15	US-10-424-599-152960	Sequence 152960,
536	6	1.6	78	15	US-10-051-874-84	Sequence 84, Appl	609	6	1.6	94	16	US-10-437-963-130164	Sequence 130164,
537	6	1.6	78	15	US-10-042-865-71	Sequence 71, Appl	610	6	1.6	94	16	US-10-437-963-167269	Sequence 167269,
538	6	1.6	80	13	US-10-114-893-56	Sequence 56, Appl	611	6	1.6	94	16	US-10-466-531-141	Sequence 141, App
539	6	1.6	80	15	US-10-015-115-122	Sequence 122, App	612	6	1.6	95	10	US-09-933-767-314	Sequence 314, App
540	6	1.6	80	15	US-10-051-874-77	Sequence 77, Appl	613	6	1.6	95	14	US-10-004-860-314	Sequence 314, App
541	6	1.6	80	15	US-10-051-874-146	Sequence 146, App	614	6	1.6	95	14	US-10-023-282-314	Sequence 314, App
542	6	1.6	80	15	US-10-424-599-221452	Sequence 221452,	615	6	1.6	95	15	US-10-363-616-353	Sequence 353, App
543	6	1.6	80	16	US-10-311-1748-50	Sequence 50, Appl	616	6	1.6	95	16	US-10-437-963-175908	Sequence 175908,
544	6	1.6	80	16	US-10-437-963-114598	Sequence 114598,	617	6	1.6	95	16	US-10-767-701-39219	Sequence 39219, A
545	6	1.6	80	16	US-10-437-963-174243	Sequence 174243,	618	6	1.6	96	14	US-10-317-833-82	Sequence 82, Appl
546	6	1.6	81	9	US-09-925-300-1641	Sequence 1641, Ap	619	6	1.6	96	15	US-10-424-599-215384	Sequence 215384,
547	6	1.6	81	9	US-09-864-921-172	Sequence 172, App	620	6	1.6	97	9	US-09-764-869-1055	Sequence 1055, Ap
548	6	1.6	81	10	US-09-948-783-134	Sequence 134, App	621	6	1.6	97	14	US-10-091-504-1055	Sequence 1055, Ap
549	6	1.6	81	15	US-10-264-049-3886	Sequence 3886, Ap	622	6	1.6	97	15	US-10-227-577-1055	Sequence 1055, Ap
550	6	1.6	81	15	US-10-424-599-153018	Sequence 153018,	623	6	1.6	97	16	US-10-437-963-115369	Sequence 115369,
551	6	1.6	81	15	US-10-424-599-186385	Sequence 186385,	624	6	1.6	97	16	US-10-437-963-134225	Sequence 134225,
552	6	1.6	81	15	US-10-424-599-206427	Sequence 206427,	625	6	1.6	97	16	US-10-437-963-193790	Sequence 193790,
553	6	1.6	82	10	US-09-892-877-132	Sequence 132, App	626	6	1.6	97	17	US-10-472-928-2286	Sequence 2286, Ap
554	6	1.6	82	15	US-10-424-599-190374	Sequence 190374,	627	6	1.6	98	14	US-10-240-730-2	Sequence 2, Appli
555	6	1.6	83	14	US-10-156-761-11657	Sequence 11657, A	628	6	1.6	98	14	US-10-153-401-5	Sequence 5, Appli
556	6	1.6	83	15	US-10-424-599-185540	Sequence 185540,	629	6	1.6	98	15	US-10-424-599-243891	Sequence 243891,
557	6	1.6	83	15	US-10-424-599-250483	Sequence 250483,	630	6	1.6	98	15	US-10-424-599-244020	Sequence 244020,
558	6	1.6	83	16	US-10-437-963-184334	Sequence 184334,	631	6	1.6	98	16	US-10-437-963-144302	Sequence 144302,
559	6	1.6	84	15	US-10-424-599-271907	Sequence 271907,	632	6	1.6	99	14	US-10-317-833-44	Sequence 44, Appl
560	6	1.6	84	16	US-10-437-963-130740	Sequence 130740,	633	6	1.6	99	15	US-10-424-599-264649	Sequence 264649,
561	6	1.6	84	16	US-10-437-963-161451	Sequence 161451,	634	6	1.6	99	16	US-10-437-963-141270	Sequence 141270,
562	6	1.6	84	16	US-10-767-701-58899	Sequence 58899, A	635	6	1.6	99	16	US-10-437-963-152930	Sequence 152930,
563	6	1.6	85	11	US-09-864-408A-250	Sequence 250, App	636	6	1.6	99	16	US-10-767-701-44721	Sequence 44721, A
564	6	1.6	85	15	US-10-424-599-208916	Sequence 208916,	637	6	1.6	100	11	US-09-864-408A-8622	Sequence 8622, Ap
565	6	1.6	85	15	US-10-424-599-240185	Sequence 240185,	638	6	1.6	100	16	US-10-437-963-119862	Sequence 119862,
566	6	1.6	85	15	US-10-424-599-241996	Sequence 241996,	639	6	1.6	100	16	US-10-437-963-151047	Sequence 151047,
567	6	1.6	85	16	US-10-437-963-143579	Sequence 143579,	640	6	1.6	101	9	US-09-828-708-10	Sequence 10, Appl
568	6	1.6	86	14	US-10-080-254-65	Sequence 65, Appl	641	6	1.6	101	15	US-10-424-599-205133	Sequence 205133,
569	6	1.6	86	15	US-10-242-355-609	Sequence 242, App	642	6	1.6	101	15	US-10-424-599-205134	Sequence 205134,
570	6	1.6	86	15	US-10-424-599-245019	Sequence 245019,	643	6	1.6	101	15	US-10-424-599-275269	Sequence 275269,
571	6	1.6	86	15	US-10-001-885-166	Sequence 166, App	644	6	1.6	102	15	US-10-424-599-217908	Sequence 217908,
572	6	1.6	86	16	US-10-437-963-104144	Sequence 104144,	645	6	1.6	103	15	US-09-974-879-178	Sequence 178, App
573	6	1.6	87	9	US-09-867-550-996	Sequence 996, App	646	6	1.6	103	15	US-10-424-599-197474	Sequence 197474,
574	6	1.6	87	15	US-10-424-599-201905	Sequence 201905,	647	6	1.6	103	15	US-10-424-599-267511	Sequence 267511,
575	6	1.6	87	15	US-10-638-210-7	Sequence 7, Appli	648	6	1.6	103	15	US-10-621-401-178	Sequence 178, App
576	6	1.6	87	15	US-10-638-210-45	Sequence 45, Appl	649	6	1.6	103	16	US-10-437-963-125644	Sequence 125644,
577	6	1.6	87	16	US-10-789-378-12	Sequence 12, Appl	650	6	1.6	104	9	US-09-815-242-5168	Sequence 5168, Ap
578	6	1.6	88	9	US-09-764-887-217	Sequence 217, App	651	6	1.6	104	10	US-09-305-736-178	Sequence 178, App
579	6	1.6	88	14	US-10-073-961-217	Sequence 217, App	652	6	1.6	104	10	US-09-818-683-178	Sequence 178, App
580	6	1.6	88	15	US-10-424-599-198594	Sequence 198594,	653	6	1.6	104	11	US-09-818-683-178	Sequence 178, App
581	6	1.6	88	15	US-10-424-599-232362	Sequence 232362,	654	6	1.6	104	15	US-10-108-260A-3928	Sequence 3928, Ap
582	6	1.6	88	15	US-10-425-114-53154	Sequence 53154, A	655	6	1.6	104	15	US-10-282-122A-43483	Sequence 43483, A
583	6	1.6	88	16	US-10-767-701-60463	Sequence 60463, A	656	6	1.6	104	15	US-10-282-122A-67824	Sequence 67824, A
584	6	1.6	89	15	US-10-424-599-238357	Sequence 238357,	657	6	1.6	104	15	US-10-282-122A-69234	Sequence 69234, A
585	6	1.6	89	16	US-10-437-963-106179	Sequence 106179,	658	6	1.6	104	15	US-10-424-599-203898	Sequence 203898,
586	6	1.6	90	14	US-10-083-357-741	Sequence 741, App	659	6	1.6	104	15	US-10-424-599-216327	Sequence 216327,
587	6	1.6	90	15	US-10-424-599-195600	Sequence 195600,	660	6	1.6	104	16	US-10-437-963-135545	Sequence 135545,
588	6	1.6	90	15	US-10-424-599-233485	Sequence 233485,	661	6	1.6	104	16	US-10-437-963-204622	Sequence 204622,
589	6	1.6	90	15	US-10-424-599-289419	Sequence 289419,	662	6	1.6	105	9	US-09-864-761-42752	Sequence 42752, A
590	6	1.6	90	16	US-10-437-963-128220	Sequence 128220,	663	6	1.6	105	15	US-10-424-599-215170	Sequence 215170,
591	6	1.6	90	16	US-10-437-963-138206	Sequence 138206,	664	6	1.6	105	15	US-10-424-599-278225	Sequence 278225,
592	6	1.6	91	11	US-09-864-408A-1904	Sequence 1904, Ap	665	6	1.6	105	16	US-10-437-963-139789	Sequence 139789,
593	6	1.6	91	14	US-10-029-386-34100	Sequence 34100, A	666	6	1.6	106	15	US-10-424-599-235720	Sequence 235720,
594	6	1.6	91	15	US-10-282-122A-46443	Sequence 46443, A	667	6	1.6	106	15	US-10-424-599-258137	Sequence 258137,
595	6	1.6	91	15	US-10-424-599-165858	Sequence 165858,	668	6	1.6	106	15	US-10-424-599-273183	Sequence 273183,
596	6	1.6	91	15	US-10-335-977-6836	Sequence 6836, Ap	669	6	1.6	106	16	US-10-767-701-59987	Sequence 59987, A
597	6	1.6	91	16	US-10-437-963-155786	Sequence 155786,	670	6	1.6	107	16	US-10-437-963-111994	Sequence 111994,

671	6	1.6	107	16	US-10-437-963-191176	Sequence 191176,	744	14	US-10-012-543-355	Sequence 355, App
672	6	1.6	108	15	US-10-264-237-1506	Sequence 1506, Ap	745	14	US-10-115-123-355	Sequence 355, App
673	6	1.6	109	15	US-10-424-599-175617	Sequence 175617,	746	15	US-10-289-762-1225	Sequence 1225, Ap
674	6	1.6	108	16	US-10-767-701-49690	Sequence 49690, A	747	15	US-10-425-114-61655	Sequence 61655, A
675	6	1.6	108	16	US-10-767-701-59593	Sequence 59593, A	748	16	US-10-437-963-139692	Sequence 139692,
676	6	1.6	109	15	US-10-424-599-154412	Sequence 154412,	749	6	US-09-984-245-169	Sequence 169, App
677	6	1.6	109	15	US-10-424-599-271737	Sequence 271737,	750	6	US-09-984-245-169	Sequence 169, App
678	6	1.6	110	9	US-09-864-761-46752	Sequence 46752, A	751	6	US-10-424-599-251992	Sequence 251992,
679	6	1.6	110	15	US-10-369-493-12685	Sequence 12685, A	752	6	US-10-335-977-5125	Sequence 5125, Ap
680	6	1.6	110	15	US-10-437-963-146902	Sequence 146902,	753	6	US-10-632-983-173	Sequence 173, App
681	6	1.6	111	14	US-10-156-761-8026	Sequence 8026, Ap	754	6	US-10-471-115-4	Sequence 4, Appli
682	6	1.6	111	15	US-10-424-599-172044	Sequence 172044,	755	6	US-10-818-068-2	Sequence 2, Appli
683	6	1.6	111	15	US-10-424-599-205630	Sequence 205630,	756	6	US-10-818-068-3	Sequence 3, Appli
684	6	1.6	111	15	US-10-424-599-257944	Sequence 257944,	757	6	US-10-818-068-5	Sequence 5, Appli
685	6	1.6	111	16	US-10-437-963-165536	Sequence 165536,	758	6	US-10-818-068-6	Sequence 6, Appli
686	6	1.6	112	9	US-09-828-708-8	Sequence 8, Appli	759	6	US-10-818-068-6	Sequence 6, Appli
687	6	1.6	112	11	US-09-978-3608-507	Sequence 507, App	760	6	US-10-424-599-167136	Sequence 167136,
688	6	1.6	112	15	US-10-424-599-191335	Sequence 191335,	761	6	US-10-437-963-195607	Sequence 195607,
689	6	1.6	112	15	US-10-424-599-236211	Sequence 236211,	762	6	US-10-104-047-2610	Sequence 2610, Ap
690	6	1.6	112	15	US-10-425-114-42211	Sequence 42211, A	763	6	US-10-104-047-2610	Sequence 2610, Ap
691	6	1.6	112	15	US-10-425-114-53352	Sequence 53352, A	764	6	US-10-282-122A-45640	Sequence 45640, A
692	6	1.6	112	15	US-10-425-114-57383	Sequence 57383, A	765	6	US-10-282-122A-52394	Sequence 52394, A
693	6	1.6	112	15	US-10-425-114-59445	Sequence 59445, A	766	6	US-10-425-114-41476	Sequence 41476, A
694	6	1.6	113	13	US-10-160-865-18	Sequence 18, Appl	767	6	US-10-408-768A-1250	Sequence 1250, Ap
695	6	1.6	113	14	US-10-097-111-344	Sequence 344, App	768	6	US-10-437-963-102732	Sequence 102732,
696	6	1.6	113	15	US-10-424-599-223450	Sequence 223450,	769	6	US-10-767-701-33544	Sequence 33544, A
697	6	1.6	113	16	US-10-803-622-218	Sequence 218, App	770	6	US-10-767-701-33544	Sequence 33544, A
698	6	1.6	113	16	US-10-803-653-218	Sequence 218, App	771	6	US-10-767-701-33544	Sequence 33544, A
699	6	1.6	114	9	US-09-865-483-8	Sequence 8, Appli	772	6	US-10-767-701-33544	Sequence 33544, A
700	6	1.6	114	14	US-10-012-819-140	Sequence 140, App	773	6	US-10-767-701-33544	Sequence 33544, A
701	6	1.6	114	15	US-10-424-599-146860	Sequence 146860,	774	6	US-10-767-701-33544	Sequence 33544, A
702	6	1.6	114	15	US-10-425-114-54750	Sequence 54750, A	775	6	US-10-767-701-33544	Sequence 33544, A
703	6	1.6	114	15	US-10-425-114-71072	Sequence 71072, A	776	6	US-10-767-701-33544	Sequence 33544, A
704	6	1.6	114	15	US-10-425-114-71072	Sequence 71072, A	777	6	US-10-767-701-33544	Sequence 33544, A
705	6	1.6	114	15	US-10-726-555-8	Sequence 8, Appli	778	6	US-10-767-701-33544	Sequence 33544, A
706	6	1.6	115	9	US-10-424-599-148792	Sequence 148792,	779	6	US-10-767-701-33544	Sequence 33544, A
707	6	1.6	116	9	US-09-881-823-18	Sequence 18, Appl	780	6	US-10-767-701-33544	Sequence 33544, A
708	6	1.6	116	14	US-10-194-975-100	Sequence 100, App	781	6	US-10-767-701-33544	Sequence 33544, A
709	6	1.6	116	14	US-10-169-351-108	Sequence 108, App	782	6	US-10-767-701-33544	Sequence 33544, A
710	6	1.6	116	15	US-10-424-599-176186	Sequence 176186,	783	6	US-10-767-701-33544	Sequence 33544, A
711	6	1.6	116	15	US-10-424-599-225567	Sequence 225567,	784	6	US-10-767-701-33544	Sequence 33544, A
712	6	1.6	116	15	US-10-435-299-4	Sequence 4, Appli	785	6	US-10-767-701-33544	Sequence 33544, A
713	6	1.6	116	16	US-10-437-963-182706	Sequence 182706,	786	6	US-10-767-701-33544	Sequence 33544, A
714	6	1.6	116	16	US-10-682-845-53	Sequence 53, Appl	787	6	US-10-767-701-33544	Sequence 33544, A
715	6	1.6	117	10	US-09-764-891-2956	Sequence 2956, Ap	788	6	US-10-767-701-33544	Sequence 33544, A
716	6	1.6	117	14	US-10-174-693-400	Sequence 400, App	789	6	US-10-767-701-33544	Sequence 33544, A
717	6	1.6	117	15	US-10-372-481-11	Sequence 11, Appl	790	6	US-10-767-701-33544	Sequence 33544, A
718	6	1.6	117	15	US-10-371-797-11	Sequence 11, Appl	791	6	US-10-767-701-33544	Sequence 33544, A
719	6	1.6	117	15	US-10-264-237-2560	Sequence 2560, Ap	792	6	US-10-767-701-33544	Sequence 33544, A
720	6	1.6	117	15	US-10-264-237-2728	Sequence 2728, Ap	793	6	US-10-767-701-33544	Sequence 33544, A
721	6	1.6	117	16	US-10-767-701-56500	Sequence 56500, A	794	6	US-10-767-701-33544	Sequence 33544, A
722	6	1.6	118	10	US-09-820-649-136	Sequence 136, App	795	6	US-10-767-701-33544	Sequence 33544, A
723	6	1.6	118	14	US-10-056-052-8	Sequence 8, Appli	796	6	US-10-767-701-33544	Sequence 33544, A
724	6	1.6	118	14	US-10-160-162-136	Sequence 136, App	797	6	US-10-767-701-33544	Sequence 33544, A
725	6	1.6	119	13	US-10-140-555-2	Sequence 2, Appli	798	6	US-10-767-701-33544	Sequence 33544, A
726	6	1.6	119	14	US-10-144-644-15	Sequence 15, Appl	799	6	US-10-767-701-33544	Sequence 33544, A
727	6	1.6	119	14	US-10-232-187-2	Sequence 2, Appli	800	6	US-10-767-701-33544	Sequence 33544, A
728	6	1.6	119	14	US-10-153-401-16	Sequence 16, Appl	801	6	US-10-767-701-33544	Sequence 33544, A
729	6	1.6	119	15	US-10-389-155-19	Sequence 19, Appl	802	6	US-10-767-701-33544	Sequence 33544, A
730	6	1.6	119	15	US-10-339-656-23	Sequence 23, Appl	803	6	US-10-767-701-33544	Sequence 33544, A
731	6	1.6	119	15	US-10-389-417-19	Sequence 19, Appl	804	6	US-10-767-701-33544	Sequence 33544, A
732	6	1.6	119	16	US-10-452-357-60	Sequence 60, Appl	805	6	US-10-767-701-33544	Sequence 33544, A
733	6	1.6	119	16	US-10-700-740-15	Sequence 15, Appl	806	6	US-10-767-701-33544	Sequence 33544, A
734	6	1.6	120	14	US-10-194-975-112	Sequence 112, App	807	6	US-10-767-701-33544	Sequence 33544, A
735	6	1.6	120	15	US-10-239-656-33	Sequence 33, Appl	808	6	US-10-767-701-33544	Sequence 33544, A
736	6	1.6	120	15	US-10-239-656-43	Sequence 43, Appl	809	6	US-10-767-701-33544	Sequence 33544, A
737	6	1.6	120	16	US-10-437-963-158380	Sequence 158380,	810	6	US-10-767-701-33544	Sequence 33544, A
738	6	1.6	120	16	US-10-767-701-339809	Sequence 339809, A	811	6	US-10-767-701-33544	Sequence 33544, A
739	6	1.6	121	13	US-10-078-929-118	Sequence 118, App	812	6	US-10-767-701-33544	Sequence 33544, A
740	6	1.6	121	14	US-10-056-052-12	Sequence 12, Appl	813	6	US-10-767-701-33544	Sequence 33544, A
741	6	1.6	121	14	US-10-056-052-20	Sequence 20, Appl	814	6	US-10-767-701-33544	Sequence 33544, A
742	6	1.6	121	15	US-10-424-599-201530	Sequence 201530,	815	6	US-10-767-701-33544	Sequence 33544, A
743	6	1.6	121	16	US-10-437-963-141451	Sequence 141451,	816	6	US-10-767-701-33544	Sequence 33544, A

817	6	1.6	135	16	US-10-351-748-31	Sequence 31, Appl	890	6	1.6	160	10	US-09-394-142B-10	Sequence 10, Appl
818	6	1.6	136	15	US-10-094-749-2334	Sequence 2334, Ap	891	6	1.6	160	15	US-10-425-114-69519	Sequence 69519, A
819	6	1.6	136	16	US-10-437-963-150496	Sequence 150496,	892	6	1.6	160	15	US-10-210-172-30	Sequence 30, Appl
820	6	1.6	137	16	US-10-437-963-198795	Sequence 198795,	893	6	1.6	160	16	US-10-782-627-10	Sequence 10, Appl
821	6	1.6	137	16	US-10-767-701-36077	Sequence 36077, A	894	6	1.6	160	16	US-10-767-701-41173	Sequence 41173, A
822	6	1.6	138	15	US-10-389-155-46	Sequence 46, Appl	895	6	1.6	161	15	US-10-108-2608-3620	Sequence 3620, Ap
823	6	1.6	138	15	US-10-389-493-9126	Sequence 9126, Ap	896	6	1.6	161	15	US-10-408-765A-2845	Sequence 2845, Ap
824	6	1.6	138	15	US-10-424-599-163385	Sequence 163385,	897	6	1.6	161	16	US-10-408-765A-2845	Sequence 137534,
825	6	1.6	138	15	US-10-389-417-46	Sequence 46, Appl	898	6	1.6	162	16	US-10-437-963-137524	Sequence 142605,
826	6	1.6	138	15	US-10-452-357-33	Sequence 33, Appl	899	6	1.6	162	16	US-10-437-963-137524	Sequence 169927,
827	6	1.6	138	16	US-10-437-963-203261	Sequence 203261,	900	6	1.6	162	16	US-10-437-963-169927	Sequence 169927,
828	6	1.6	138	16	US-10-437-963-203633	Sequence 36333, A	901	6	1.6	163	15	US-10-424-599-151490	Sequence 151490,
829	6	1.6	139	8	US-08-773-784-37	Sequence 37, Appl	902	6	1.6	163	15	US-10-424-599-151490	Sequence 157154,
830	6	1.6	139	9	US-09-881-823-4	Sequence 4, Appl	903	6	1.6	163	15	US-10-424-599-175993	Sequence 175993,
831	6	1.6	139	15	US-10-425-114-41659	Sequence 41659, A	904	6	1.6	163	15	US-10-424-599-187125	Sequence 187125,
832	6	1.6	140	16	US-10-437-963-179933	Sequence 179933,	905	6	1.6	164	15	US-10-389-566-969	Sequence 969, App
833	6	1.6	140	16	US-10-437-963-185178	Sequence 185178,	906	6	1.6	164	15	US-10-424-599-187123	Sequence 187123,
834	6	1.6	140	16	US-10-767-701-39092	Sequence 39092, A	907	6	1.6	164	16	US-10-767-701-40547	Sequence 40547, A
835	6	1.6	140	16	US-10-767-701-56723	Sequence 56723, A	908	6	1.6	165	10	US-09-764-891-3994	Sequence 3994, Ap
836	6	1.6	141	15	US-10-424-599-284856	Sequence 284856,	909	6	1.6	165	10	US-09-769-787-92	Sequence 92, Appl
837	6	1.6	142	9	US-09-772-103-4	Sequence 4, Appl	910	6	1.6	165	15	US-10-424-599-172746	Sequence 172746,
838	6	1.6	142	14	US-10-029-386-32549	Sequence 32549, A	911	6	1.6	165	15	US-10-424-599-235756	Sequence 235756,
839	6	1.6	142	15	US-10-282-122A-67106	Sequence 67106, A	912	6	1.6	165	15	US-10-335-977-6192	Sequence 6192, Ap
840	6	1.6	142	16	US-10-437-963-134512	Sequence 134512,	913	6	1.6	165	16	US-10-437-963-152577	Sequence 152577,
841	6	1.6	142	16	US-10-437-963-141271	Sequence 141271,	914	6	1.6	165	16	US-10-767-701-32177	Sequence 32177, A
842	6	1.6	143	16	US-10-437-963-143435	Sequence 143435,	915	6	1.6	166	15	US-10-472-928-1684	Sequence 1684, Ap
843	6	1.6	144	15	US-10-094-749-2148	Sequence 2148, Ap	916	6	1.6	166	15	US-10-282-122A-64273	Sequence 64273, A
844	6	1.6	144	15	US-10-424-599-143966	Sequence 143966,	917	6	1.6	166	15	US-10-424-599-283375	Sequence 283375,
845	6	1.6	144	15	US-10-425-114-55635	Sequence 55635, A	918	6	1.6	166	15	US-10-425-114-61855	Sequence 61855, A
846	6	1.6	144	15	US-10-425-114-56488	Sequence 56488, A	919	6	1.6	166	15	US-10-425-114-64112	Sequence 64112, A
847	6	1.6	145	9	US-09-821-839-5	Sequence 5, Appl	920	6	1.6	167	16	US-10-437-963-134987	Sequence 134987,
848	6	1.6	145	15	US-10-425-114-36905	Sequence 36905, A	921	6	1.6	168	15	US-10-289-762-72	Sequence 72, Appl
849	6	1.6	145	16	US-10-437-963-129399	Sequence 129399,	922	6	1.6	169	15	US-10-369-493-17361	Sequence 17361, A
850	6	1.6	146	9	US-09-764-869-644	Sequence 644, App	923	6	1.6	169	16	US-10-767-701-36423	Sequence 36423, A
851	6	1.6	146	14	US-10-091-504-644	Sequence 644, App	924	6	1.6	169	16	US-10-767-701-36426	Sequence 36426, A
852	6	1.6	146	15	US-10-389-493-11808	Sequence 11808, A	925	6	1.6	169	16	US-10-767-701-57523	Sequence 57523, A
853	6	1.6	146	15	US-10-227-577-644	Sequence 644, App	926	6	1.6	170	15	US-10-425-114-36746	Sequence 36746, A
854	6	1.6	146	15	US-10-424-599-155439	Sequence 155439,	927	6	1.6	170	16	US-10-425-114-51752	Sequence 51752, A
855	6	1.6	146	15	US-10-424-599-247022	Sequence 247022,	928	6	1.6	170	16	US-10-437-963-110548	Sequence 110548,
856	6	1.6	146	15	US-10-425-114-62197	Sequence 62197, A	929	6	1.6	170	16	US-10-437-963-186646	Sequence 186646,
857	6	1.6	146	15	US-10-425-114-70902	Sequence 70902, A	930	6	1.6	170	16	US-10-767-701-32869	Sequence 32869, A
858	6	1.6	147	15	US-10-424-599-207156	Sequence 207156, A	931	6	1.6	171	10	US-09-892-877-277	Sequence 277, App
859	6	1.6	147	15	US-10-425-114-66983	Sequence 66983, A	932	6	1.6	171	10	US-09-948-783-279	Sequence 279, App
860	6	1.6	147	16	US-10-437-963-101116	Sequence 101116,	933	6	1.6	171	15	US-10-094-749-2193	Sequence 2193, Ap
861	6	1.6	147	16	US-10-767-701-41809	Sequence 41809, A	934	6	1.6	172	9	US-09-864-761-34586	Sequence 34586, A
862	6	1.6	148	15	US-10-425-114-41217	Sequence 41217, A	935	6	1.6	172	9	US-09-864-761-42700	Sequence 42700, A
863	6	1.6	148	16	US-10-437-963-198902	Sequence 198902,	936	6	1.6	172	9	US-09-738-626-6958	Sequence 6958, Ap
864	6	1.6	148	16	US-10-767-701-38117	Sequence 38117, A	937	6	1.6	172	15	US-10-425-114-60659	Sequence 60659, A
865	6	1.6	149	15	US-10-424-599-266128	Sequence 266128,	938	6	1.6	172	15	US-10-425-114-63902	Sequence 63902, A
866	6	1.6	150	15	US-10-424-599-178119	Sequence 178119,	939	6	1.6	172	16	US-10-437-963-176354	Sequence 176354,
867	6	1.6	150	15	US-10-424-599-212497	Sequence 212497,	940	6	1.6	172	16	US-10-437-963-176354	Sequence 59998, A
868	6	1.6	150	15	US-10-424-599-282596	Sequence 282596,	941	6	1.6	172	16	US-10-767-701-59998	Sequence 236, App
869	6	1.6	150	16	US-10-767-701-58488	Sequence 58488, A	942	6	1.6	173	9	US-09-764-868-1052	Sequence 1052, Ap
870	6	1.6	151	16	US-10-767-701-62023	Sequence 62023, A	943	6	1.6	173	13	US-10-052-586-506	Sequence 506, App
871	6	1.6	152	9	US-09-990-205-4	Sequence 4, Appl	944	6	1.6	173	14	US-10-174-590-506	Sequence 506, App
872	6	1.6	152	14	US-10-153-401-4	Sequence 4, Appl	945	6	1.6	173	14	US-10-174-590-506	Sequence 506, App
873	6	1.6	152	15	US-10-424-599-175161	Sequence 175161,	946	6	1.6	173	14	US-10-175-737-506	Sequence 506, App
874	6	1.6	153	15	US-10-424-599-267234	Sequence 267234,	947	6	1.6	173	14	US-10-174-581-506	Sequence 506, App
875	6	1.6	153	15	US-10-767-701-35028	Sequence 35028, A	948	6	1.6	173	14	US-10-176-483-506	Sequence 506, App
876	6	1.6	154	15	US-10-282-122A-46514	Sequence 46514, A	949	6	1.6	173	14	US-10-176-749-506	Sequence 506, App
877	6	1.6	155	16	US-10-437-963-186816	Sequence 186816,	950	6	1.6	173	14	US-10-176-914-506	Sequence 506, App
878	6	1.6	156	14	US-10-029-386-32077	Sequence 32077, A	951	6	1.6	173	14	US-10-176-915-506	Sequence 506, App
879	6	1.6	156	15	US-10-424-599-181140	Sequence 181140,	952	6	1.6	173	14	US-10-173-706-506	Sequence 506, App
880	6	1.6	156	15	US-10-424-599-245615	Sequence 245615,	953	6	1.6	173	14	US-10-175-738-506	Sequence 506, App
881	6	1.6	156	16	US-10-767-701-32834	Sequence 32834, A	954	6	1.6	173	14	US-10-175-752-506	Sequence 506, App
882	6	1.6	157	15	US-10-425-114-51936	Sequence 51936, A	955	6	1.6	173	14	US-10-176-482-506	Sequence 506, App
883	6	1.6	158	14	US-10-152-886-55	Sequence 55, Appl	956	6	1.6	173	14	US-10-176-757-506	Sequence 506, App
884	6	1.6	158	14	US-10-157-031-134	Sequence 134, App	957	6	1.6	173	14	US-10-176-913-506	Sequence 506, App
885	6	1.6	158	15	US-10-424-599-279167	Sequence 279167,	958	6	1.6	173	14	US-10-180-552-506	Sequence 506, App
886	6	1.6	158	16	US-10-437-963-144197	Sequence 144197,	959	6	1.6	173	14	US-10-180-557-506	Sequence 506, App
887	6	1.6	158	16	US-10-767-701-35595	Sequence 35595, A	960	6	1.6	173	14	US-10-173-700-506	Sequence 506, App
888	6	1.6	159	15	US-10-424-599-158470	Sequence 158470,	961	6	1.6	173	14	US-10-174-572-506	Sequence 506, App
889	6	1.6	159	16	US-10-437-963-147590	Sequence 147590,	962	6	1.6	173	14	US-10-174-579-506	Sequence 506, App

963 6 1.6 173 14 US-10-174-582-506 Sequence 506, App
 964 6 1.6 173 14 US-10-174-588-506 Sequence 506, App
 965 6 1.6 173 14 US-10-175-739-506 Sequence 506, App
 966 6 1.6 173 14 US-10-175-740-506 Sequence 506, App
 967 6 1.6 173 14 US-10-175-743-506 Sequence 506, App
 968 6 1.6 173 14 US-10-176-488-506 Sequence 506, App
 969 6 1.6 173 14 US-10-176-492-506 Sequence 506, App
 970 6 1.6 173 14 US-10-176-747-506 Sequence 506, App
 971 6 1.6 173 14 US-10-176-750-506 Sequence 506, App
 972 6 1.6 173 14 US-10-176-985-506 Sequence 506, App
 973 6 1.6 173 14 US-10-176-987-506 Sequence 506, App
 974 6 1.6 173 14 US-10-176-992-506 Sequence 506, App
 975 6 1.6 173 14 US-10-176-993-506 Sequence 506, App
 976 6 1.6 173 14 US-10-184-658-506 Sequence 506, App
 977 6 1.6 173 14 US-10-176-991-506 Sequence 506, App
 978 6 1.6 173 14 US-10-173-695-506 Sequence 506, App
 979 6 1.6 173 14 US-10-173-697-506 Sequence 506, App
 980 6 1.6 173 14 US-10-173-705-506 Sequence 506, App
 981 6 1.6 173 14 US-10-174-576-506 Sequence 506, App
 982 6 1.6 173 14 US-10-174-585-506 Sequence 506, App
 983 6 1.6 173 14 US-10-174-586-506 Sequence 506, App
 984 6 1.6 173 14 US-10-175-747-506 Sequence 506, App
 985 6 1.6 173 14 US-10-176-481-506 Sequence 506, App
 986 6 1.6 173 14 US-10-176-485-506 Sequence 506, App
 987 6 1.6 173 14 US-10-176-487-506 Sequence 506, App
 988 6 1.6 173 14 US-10-176-493-506 Sequence 506, App
 989 6 1.6 173 14 US-10-176-756-506 Sequence 506, App
 990 6 1.6 173 14 US-10-176-911-506 Sequence 506, App
 991 6 1.6 173 14 US-10-176-919-506 Sequence 506, App
 992 6 1.6 173 14 US-10-176-925-506 Sequence 506, App
 993 6 1.6 173 14 US-10-176-978-506 Sequence 506, App
 994 6 1.6 173 14 US-10-179-510-506 Sequence 506, App
 995 6 1.6 173 14 US-10-180-543-506 Sequence 506, App
 996 6 1.6 173 14 US-10-180-544-506 Sequence 506, App
 997 6 1.6 173 14 US-10-180-546-506 Sequence 506, App
 998 6 1.6 173 14 US-10-180-547-506 Sequence 506, App
 999 6 1.6 173 14 US-10-180-549-506 Sequence 506, App
 1000 6 1.6 173 14 US-10-180-555-506 Sequence 506, App

ALIGNMENTS

RESULT 1
 US-09-736-250-1
 ; Sequence 1, Application US/09736250
 ; Publication No. US20050014139A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
 ; APPLICANT: NAKAMURA, Takeshi
 ; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
 ; FILE REFERENCE: 050212-0278
 ; CURRENT APPLICATION NUMBER: US/09/736,250
 ; CURRENT FILING DATE: 2000-12-15
 ; PRIOR APPLICATION NUMBER: 09/054,492
 ; PRIOR FILING DATE: 1998-04-03
 ; PRIOR APPLICATION NUMBER: PCT/JP96/02905
 ; PRIOR FILING DATE: 1996-10-07
 ; PRIOR APPLICATION NUMBER: 284663/1995
 ; PRIOR FILING DATE: 1995-10-05
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patent in version 3.3
 ; SEQ ID NO 1
 ; LENGTH: 377
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-736-250-1
 Query Match 100.0%; Score 377; DB 12; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MKFPGPLENQLSFLLEKAITREAOQMWKVNVRKMPNSQNVSPSORDEVIQWLAKLYQFN 60

Db 1 MKFPGPLENQLSFLLEKAITREAOQMWKVNVRKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 Qy 61 LYPTETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 Db 61 LYPTETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 Qy 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 180
 Db 121 GCSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAVSTRPQLFLSLPKLSPSOHLAV 180
 Qy 181 LTKQLLHCMAQNQLQPRGSMALAMVSEMEKLIIPDWLSLITTELLOKAQMDSSQLIHCR 240
 Db 181 LTKQLLHCMAQNQLQPRGSMALAMVSEMEKLIIPDWLSLITTELLOKAQMDSSQLIHCR 240
 Qy 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFLHPSSVPGDFSKDASKPEVPV 300
 Db 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFLHPSSVPGDFSKDASKPEVPV 300
 Qy 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDYFDGIKRLYNEDNVSENVSGVCGTDLR 360
 Db 301 RGTAAFYHHLPAASGCKQTSTKRVEMEVDYFDGIKRLYNEDNVSENVSGVCGTDLR 360
 Qy 361 QEGHASPCLPPLQPVSV 377
 Db 361 QEGHASPCLPPLQPVSV 377

RESULT 2

US-09-796-149-4
 ; Sequence 4, Application US/09796149
 ; Patent No. US20020035079A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Univ. of Southern California
 ; TITLE OF INVENTION: Mutated cyclin G1 protein
 ; FILE REFERENCE: 4-31342A/USC
 ; CURRENT APPLICATION NUMBER: US/09/796,149
 ; CURRENT FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 254
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-796-149-4

Query Match 67.4%; Score 254; DB 9; Length 254;
 Best Local Similarity 100.0%; Pred. No. 3.5e-239;
 Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 VSPSORDEVIQWLAKLYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 99
 Db 1 VSPSORDEVIQWLAKLYQFNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAA 60
 Qy 100 KTVVEEDERIPVLKVLARDSFCGSSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAV 159
 Db 61 KTVVEEDERIPVLKVLARDSFCGSSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIAV 120
 Qy 160 STRPQLFLSLPKLSPSOHLAVLTKQLLHCMAQNQLQPRGSMALAMVSEMEKLIIPDWL 219
 Db 121 STRPQLFLSLPKLSPSOHLAVLTKQLLHCMAQNQLQPRGSMALAMVSEMEKLIIPDWL 180
 Qy 220 SLTIELLOKAQMDSSQLIHCHRELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFL 279
 Db 181 SLTIELLOKAQMDSSQLIHCHRELVAHHLSTLQSSPLNSVYVYRPLKHTLVTCDKGVFL 240
 Qy 280 HPSSVPGDFPSKDN 293
 Db 241 HPSSVPGDFPSKDN 254

RESULT 3

US-09-736-250-5

; Sequence 5, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: NIKITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: SAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-09-736-250-5

Query Match 3.7%; Score 14; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 4.5e+06; Length 9;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 343 EDNVSENVGVCVT 356
| | | | | | | | | | | | | | | | | |
Db 1 EDNVSENVGVCVT 14

RESULT 4
US-09-865-548A-151
; Sequence 151, Application US/09865548A
; Publication No. US20030096298A1
; GENERAL INFORMATION:
; APPLICANT: Barnea, Eilon
; APPLICANT: Beer, Ilan
; APPLICANT: Ziv, Tamar
; APPLICANT: Admon, Arie
; TITLE OF INVENTION: METHOD OF IDENTIFYING PEPTIDES CAPABLE OF BINDING TO MHC MOLECULE
; TITLE OF INVENTION: PEPTIDES IDENTIFIED THEREBY AND THEIR USES
; FILE REFERENCE: 01/22080
; CURRENT APPLICATION NUMBER: US/09/865,548A
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/290,958
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 204
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 151
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-09-865-548A-151

Query Match 2.4%; Score 9; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRLFLATV 80
| | | | | | | | | | | | | | | | | |
Db 1 LLDRLFLATV 9

RESULT 5
US-10-006-177-8
; Sequence 8, Application US/10006177
; Publication No. US20030165513A1

; GENERAL INFORMATION:
; APPLICANT: Ramakrishna, Venky
; APPLICANT: Ross, Mark
; APPLICANT: Philip, Ramila
; TITLE OF INVENTION: Cytotoxic T-Lymphocyte-Inducing Immunogens for Prevention, Treatm
; FILE REFERENCE: 26747-35
; CURRENT APPLICATION NUMBER: US/10/006,177
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US/60/251,022
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: US/60/256,824
; PRIOR FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Epitopic Peptide
US-10-006-177-8

Query Match 2.4%; Score 9; DB 14; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.2e+06; Length 9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 LLDRLFLATV 80
| | | | | | | | | | | | | | | | | |
Db 1 LLDRLFLATV 9

RESULT 6
US-09-129-112-2
; Sequence 2, Application US/09129112
; Patent No. US20020019995A1
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; TITLE OF INVENTION: A No. US20020019995A1 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (52)..(73)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyases
; NAME/KEY: PEPTIDE
; LOCATION: (128)..(144)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyases
; NAME/KEY: PEPTIDE
; LOCATION: (173)..(195)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyases
; NAME/KEY: PEPTIDE
; LOCATION: (200)..(220)
; OTHER INFORMATION: motif identified as conserved region among a
; OTHER INFORMATION: variety of plant and animal apyases
US-09-129-112-2

Query Match 2.4%; Score 9; DB 9; Length 462;
Best Local Similarity 100.0%; Pred. No. 8.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 LLFSLPKLS 173
Db 20 LLFSLPKLS 28

RESULT 7

US-10-425-114-42971
; Sequence 42971, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 42971
; LENGTH: 83
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700673310_FLI.pep
US-10-425-114-42971

Query Match 2.1%; Score 8; DB 15; Length 83;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 SLPKLSPS 175
Db 36 SLPKLSPS 43

RESULT 8

US-10-424-599-245711
; Sequence 245711, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 245711
; LENGTH: 99
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_63909C.1.pep
US-10-424-599-245711

Query Match 2.1%; Score 8; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 279 LHPSSVPG 286
Db 51 LHPSSVPG 58

RESULT 9

US-10-424-599-196677
; Sequence 196677, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196677
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)...(216)
; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19626C.1.pep
US-10-424-599-196677

Query Match 2.1%; Score 8; DB 15; Length 216;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 SLPKLSPS 175
Db 185 SLPKLSPS 192

RESULT 10

US-10-424-599-196680
; Sequence 196680, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 196680
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_19629C.1.pep
US-10-424-599-196680

Query Match 2.1%; Score 8; DB 15; Length 289;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 168 SLPKLSPS 175
Db 242 SLPKLSPS 249

RESULT 11

US-10-437-963-145582
; Sequence 145582, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:

; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 145582
; LENGTH: 379
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_46289C.1.pap
US-10-437-963-145582

Query Match 2.1%; Score 8; DB 16; Length 379;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 YRPLKHTL 269
Db 148 YRPLKHTL 155
|||||

RESULT 12
US-09-866-562-62
; Sequence 62, Application US/09866562
; Patent No. US20020009758A1
; GENERAL INFORMATION:
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Klee, Jennifer
; APPLICANT: Switzer, Anne
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER.
; FILE REFERENCE: 210121.502
; CURRENT APPLICATION NUMBER: US/09/866,562
; CURRENT FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 96
; SEQ ID NO 62
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-562-62

Query Match 2.1%; Score 8; DB 9; Length 391;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LSTLQSSL 254
Db 84 LSTLQSSL 91
|||||

RESULT 13
US-10-236-392-92
; Sequence 92, Application US/10236392
; Publication No. US20040067490A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, David W
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Burgess, Catherine, E
; APPLICANT: Casman, Stacie J
; APPLICANT: Catterton, Elina
; APPLICANT: Chapoval, Andrei

; APPLICANT: Crabtree, Julie
; APPLICANT: Edinger, Shlomit, R
; APPLICANT: Ellerman, Karen
; APPLICANT: Gerlach, Valerie
; APPLICANT: Gorman, Linda
; APPLICANT: Grosse, William M
; APPLICANT: Gusev, Vladamir
; APPLICANT: Kekuda, Ramesh
; APPLICANT: LaRochelle, William J
; APPLICANT: Li, Li
; APPLICANT: MacDougall, John R
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Miller, Charles E
; APPLICANT: Millet, Isabelle
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Pena, Carol A
; APPLICANT: Peyman, John A
; APPLICANT: Rastelli, Luca
; APPLICANT: Reiger, Daniel K
; APPLICANT: Rothenberg, Mark E
; APPLICANT: Shenoy, Suresh
; APPLICANT: Shimkets, Richard A
; APPLICANT: Smithson, Glennda
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-442A
; CURRENT APPLICATION NUMBER: US/10/236,392
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US09/540,763
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: US60/390,155
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US09/635,949
; PRIOR FILING DATE: 2000-08-10
; PRIOR APPLICATION NUMBER: US60/318,765
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/357,303
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US60/367,753
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US60/369,479
; PRIOR FILING DATE: 2002-04-02
; PRIOR APPLICATION NUMBER: US09/659,634
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: US60/318,120
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US60/318,130
; PRIOR FILING DATE: 2001-09-07
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 794
; SOFTWARE: Custom
; SEQ ID NO 92
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-392-92

Query Match 2.1%; Score 8; DB 15; Length 416;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 247 LSTLQSSL 254
Db 84 LSTLQSSL 91
|||||

RESULT 14
US-10-425-114-51949
; Sequence 51949, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 51949
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700103547_FLI.pep
US-10-425-114-51949

Query Match 2.1%; Score 8; DB 15; Length 418;
Best Local Similarity 100.0%; Pred.No. 75;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LSPSQHLA 179
|||||||
Db 166 LSPSQHLA 173

RESULT 15
US-10-767-701-44456
; Sequence 44456, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 44456
; LENGTH: 514
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C7731_1.pep
US-10-767-701-44456

Query Match 2.1%; Score 8; DB 16; Length 514;
Best Local Similarity 100.0%; Pred.No. 91;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 LSPSQHLA 179
|||||||
Db 262 LSPSQHLA 269

Search completed: February 11, 2005, 03:25:20
Job time : 107.777 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:06:34 , Search time 28.9258 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKPQPLENQRLSLLEKAI.....LSRQEGHSCPPLQPVSV 377

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: Pirl.*

2: Pirl.*

3: Pirl.*

4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	103	27.3	178	2 J80264	cyclin I - human
2	8	2.1	842	2 A87341	sensory box/GGDEF
3	8	2.1	1715	2 G84429	hypothetical prote
4	7	1.9	61	2 D82732	hypothetical prote
5	7	1.9	85	2 G84490	hypothetical prote
6	7	1.9	95	2 D71534	hypothetical prote
7	7	1.9	95	2 C81692	conserved hypotet
8	7	1.9	108	2 D44221	orf4 protein - Aut
9	7	1.9	108	2 C72852	AcOrf-19 protein -
10	7	1.9	110	2 T41765	AcMPV orf19 - Bom
11	7	1.9	113	2 G83745	hypothetical prote
12	7	1.9	123	2 H87603	transcription regu
13	7	1.9	126	2 B69320	conserved hypotet
14	7	1.9	131	2 AD0633	probable secreted
15	7	1.9	154	2 T35544	probable quinolina
16	7	1.9	155	2 G82534	30S ribosomal prot
17	7	1.9	184	2 S85816	RNA-directed DNA p
18	7	1.9	188	2 B82696	cytochrome B561 XF
19	7	1.9	189	2 AB2169	hypothetical prote
20	7	1.9	214	2 T42530	hypothetical prote
21	7	1.9	230	2 C71548	probable ABC trans
22	7	1.9	237	2 D88095	protein f39E9.1 [i
23	7	1.9	238	2 T40721	hypothetical prote
24	7	1.9	238	2 A83233	conserved hypotet
25	7	1.9	242	2 S49462	cyclin - rice
26	7	1.9	269	2 T04394	NBS-LRR type resis
27	7	1.9	284	1 S74516	(adenine-N6,N6-)-d
28	7	1.9	294	2 T05604	hypothetical prote
29	7	1.9	301	2 T37172	probable lysr-fami

hypothetical prote
probable transcrip
hypothetical prote
transcription fact
hypothetical prote
prostatic spermine
alcohol dehydrogen
isocitrate dehydro
peroxin-like prot
RING-H2 finger pro
hypothetical prote
aminoalcoholphosph
alpha-1-antiprotei
protein kinase-lik
corticosteroid-bin
unknown protein [i
coenzyme F420 hydr
contrapsin precurs
hypothetical prote
hypothetical prote
hedgehog homolog v
taxadienol acetyl
probable UDP-n-ace
hypothetical prote
tyrosine kinase (f
53K glycoprotein -
hypothetical prote
homeotic protein B
oligopeptide ABC t
plasma hyaluronan-
probable fumarate
hypothetical prote
hypothetical prote
hypothetical prote
translation regula
probable translati
hypothetical prote
hypothetical prote
hypothetical prote
ent-kaurene syntha
hypothetical prote
beta-glucosidase (
probable tail leng
probable tail comp
probable AAA-type
probable tail leng
probable tail leng
probable tail comp
sucrose-phosphate
exodeoxyribonuclea
probable tail leng
probable regulator
chromosome segrega
apical endosomal p
multimerin, endoth
structural mainten
cell surface prote
cystic fibrosis tr
oxfX protein - Esc
25-hydroxyvitamin
splenin - human
thymopoietin - hum
probable photosyst
phosphoenolpyruvat
puc3A protein - Rh
puc2A protein - Rh
hypothetical prote
hypothetical prote
pepsin B (EC 3.4.2
transcription regu
hypothetical prote
transcription fact
hypothetical prote

103 1.6 6 88 2 A97936 conserved hypotet
104 1.6 6 93 2 S75571 hypotetrical prote
105 1.6 6 95 2 S17605 Ig heavy chain v r
106 1.6 6 97 2 S55372 Ig heavy chain v r
107 1.6 6 97 2 S95132 conserved hypotet
108 1.6 6 97 2 AC2732 hypotetrical prote
109 1.6 6 98 2 S21812 Ig heavy chain v r
110 1.6 6 98 2 AB3072 conserved hypotet
111 1.6 6 98 2 G98214 hypotetrical prote
112 1.6 6 100 2 A25913 Ig heavy chain pre
113 1.6 6 100 2 S14490 Ig heavy chain v r
114 1.6 6 100 2 B71102 hypotetrical prote
115 1.6 6 101 2 S03466 Ig heavy chain v r
116 1.6 6 102 2 AC0674 insulin-like growt
117 1.6 6 103 2 T28354 hypotetrical prote
118 1.6 6 104 2 B83115 50S ribosomal prot
119 1.6 6 104 2 F72753 hypotetrical prote
120 1.6 6 105 2 B55208 frdb homolog socA2
121 1.6 6 105 2 T32799 hypotetrical prote
122 1.6 6 106 2 S14489 Ig heavy chain v r
123 1.6 6 106 2 S26322 Ig heavy chain v r
124 1.6 6 106 2 C96086 hypotetrical prote
125 1.6 6 107 2 P00322 exo-alpha-sialidas
126 1.6 6 107 2 S14492 Ig heavy chain v r
127 1.6 6 107 2 S14493 Ig heavy chain v r
128 1.6 6 107 2 S14491 Ig heavy chain v r
129 1.6 6 108 2 S07331 Ig heavy chain v r
130 1.6 6 109 2 PH1026 Ig heavy chain v r
131 1.6 6 109 2 PH1035 Ig heavy chain v r
132 1.6 6 109 2 G82935 ATP synthase C cha
133 1.6 6 110 2 S26323 Ig heavy chain v r
134 1.6 6 110 2 PH1024 Ig heavy chain v r
135 1.6 6 111 2 S26324 Ig heavy chain v r
136 1.6 6 111 2 C69168 conserved hypotet
137 1.6 6 111 2 G70521 hypotetrical prote
138 1.6 6 112 2 S11108 Ig heavy chain v r
139 1.6 6 112 2 S11100 Ig heavy chain v r
140 1.6 6 112 2 S11098 Ig heavy chain v r
141 1.6 6 113 2 E81138 succinate dehydrog
142 1.6 6 113 2 S11101 Ig heavy chain v r
143 1.6 6 113 2 D72454 hypotetrical prote
144 1.6 6 114 2 S11099 Ig heavy chain v r
145 1.6 6 114 2 S11104 Ig heavy chain v r
146 1.6 6 114 2 S11106 Ig heavy chain v r
147 1.6 6 114 2 S11105 Ig heavy chain v r
148 1.6 6 114 2 S57692 probable membrane
149 1.6 6 114 2 D84852 hypotetrical prote
150 1.6 6 115 1 HWM834 Ig heavy chain pre
151 1.6 6 115 2 S11103 Ig heavy chain v r
152 1.6 6 115 2 S26470 Ig heavy chain v r
153 1.6 6 115 2 S11107 Ig heavy chain v r
154 1.6 6 115 2 S69592 hypotetrical prote
155 1.6 6 115 2 AE2551 conserved hypotet
156 1.6 6 115 2 H75491 anti-DNA autoantib
157 1.6 6 116 1 G1MS10 Ig heavy chain pre
158 1.6 6 116 2 P10198 Ig mu chain precu
159 1.6 6 116 2 A33932 Ig heavy chain v r
160 1.6 6 116 2 S42494 Ig heavy chain v r
161 1.6 6 116 2 S11102 Ig heavy chain v r
162 1.6 6 117 2 S38553 Ig heavy chain v r
163 1.6 6 117 2 S10111 Ig heavy chain v r
164 1.6 6 117 2 JC2282 ribosomal protein
165 1.6 6 118 2 P00266 Ig heavy chain v r
166 1.6 6 118 2 AE1214 hypotetrical prote
167 1.6 6 119 2 E33876 carcinoembryonic a
168 1.6 6 119 2 S84947 phosphoribosyl-AMP
169 1.6 6 120 2 P10087 Ig heavy chain v r
170 1.6 6 120 2 A87462 hypotetrical prote
171 1.6 6 121 2 S77497 ribosomal protein
172 1.6 6 121 2 T25485 hypotetrical prote
173 1.6 6 122 2 A49049 Ig heavy chain v r
174 1.6 6 122 2 A72025 conserved hypotet
175 1.6 6 122 2 G86597 C7716 hypotetrical

176 1.6 6 123 2 S27937
177 1.6 6 124 2 AD3151
178 1.6 6 125 2 F87685 Ig heavy chain v r
179 1.6 6 126 2 S29303 Ig heavy chain v r
180 1.6 6 127 2 B31807 Ig heavy chain v r
181 1.6 6 127 2 T43781 Ig heavy chain v r
182 1.6 6 128 2 PN0647 epiN protein - Vib
183 1.6 6 129 2 A11705 hypotetrical prote
184 1.6 6 130 2 C90052 hypotetrical prote
185 1.6 6 131 2 E36819 Cl3 protein - rabb
186 1.6 6 132 2 JQ0737 RnpA protein - Mic
187 1.6 6 134 2 B71354 Down syndrome crit
188 1.6 6 134 2 JC7301 Ig gamma-2A chain
189 1.6 6 135 2 S31913 hypotetrical prote
190 1.6 6 139 1 D71107 arsenate reductase
191 1.6 6 139 2 F84024 Ig heavy chain pre
192 1.6 6 139 2 A32456 hypotetrical prote
193 1.6 6 139 2 A70881 hypotetrical prote
194 1.6 6 139 2 T28243 hypotetrical prote
195 1.6 6 141 2 S52446 Ig heavy chain v r
196 1.6 6 141 2 H82220 hypotetrical prote
197 1.6 6 142 2 B48648 acetoxyhydroxy acid
198 1.6 6 142 2 T36312 hypotetrical prote
199 1.6 6 143 2 H64000 hypotetrical prote
200 1.6 6 143 2 A54793 ponticulin precurs
201 1.6 6 144 2 S11244 Ig gamma-2a chain
202 1.6 6 144 2 B75054 probable endomucle
203 1.6 6 145 2 S30247 Kin-1 protein - hu
204 1.6 6 146 2 T26379 hypotetrical prote
205 1.6 6 147 2 S53574 probable membrane
206 1.6 6 147 2 C64958 flagellar protein
207 1.6 6 147 2 A89964 flagellar filij pro
208 1.6 6 147 2 A85812 flagellar filij pro
209 1.6 6 149 2 S39910 S-receptor kinase
210 1.6 6 149 2 S75155 hypotetrical prote
211 1.6 6 149 2 T49200 hypotetrical prote
212 1.6 6 149 2 C81959 probable palin NMA
213 1.6 6 150 2 S31411 S-receptor kinase-
214 1.6 6 150 2 E97158 hypotetrical prote
215 1.6 6 151 2 F69212 autotrophic growth
216 1.6 6 152 2 G69487 LSU ribosomal prot
217 1.6 6 152 2 H69129 ribosomal protein
218 1.6 6 153 2 P00255 polyprotein (clone
219 1.6 6 153 2 D70345 conserved hypotet
220 1.6 6 154 1 R5MX30 ribosomal protein
221 1.6 6 154 2 D64359 ribosomal protein
222 1.6 6 155 2 C75145 lsu ribosomal prot
223 1.6 6 155 2 G71184 probable ribosomal
224 1.6 6 158 2 JC7302 Down syndrome crit
225 1.6 6 158 2 H71229 hypotetrical prote
226 1.6 6 162 2 T36686 probable integral
227 1.6 6 163 2 T48132 hypotetrical prote
228 1.6 6 165 2 B64121 nonheme ferritin h
229 1.6 6 165 2 F95099 conserved hypotet
230 1.6 6 165 2 H97967 conserved hypotet
231 1.6 6 165 2 S62563 adaptin complex sm
232 1.6 6 166 1 S07369 interleukin-3 prec
233 1.6 6 166 2 S73928 single-stranded DN
234 1.6 6 167 2 I64221 conserved hypotet
235 1.6 6 167 2 JC2336 hypotetrical prote
236 1.6 6 168 2 JC6566 interleukin-3 beta
237 1.6 6 168 2 A12865 transcription regu
238 1.6 6 168 2 G97642 hypotetrical prote
239 1.6 6 169 2 D83998 acetyl-CoA carboxy
240 1.6 6 169 2 C95919 probable periplasm
241 1.6 6 170 2 H71454 hypotetrical prote
242 1.6 6 172 2 B56684 acetoxyhydroxy acid
243 1.6 6 173 2 T32335 hypotetrical prote
244 1.6 6 174 2 E69213 aspartate carbamoy
245 1.6 6 174 2 B75013 phosphoribosylamin
246 1.6 6 174 2 C69539 conserved hypotet
247 1.6 6 175 2 T08948 hypotetrical prote
248 1.6 6 177 2 T36367 transcription init

249	6	1.6	177	2	E71138	probable phosphori	322	228	2	E89923	hypothetical prote
250	6	1.6	179	2	A4684	hypothetical prote	323	229	2	E95862	probable transcrip
251	6	1.6	180	2	C75171	ssu ribosomal prot	324	230	2	S75576	ribulose-phosphate
252	6	1.6	181	2	E70209	conserved hypoteth	325	230	2	E83554	probable pseudouri
253	6	1.6	181	2	E86654	transcription regu	326	230	2	C72256	rnfB-related prote
254	6	1.6	183	2	D83712	shikimate kinase a	327	231	1	F1SP3	photosystem I chai
255	6	1.6	183	2	G87250	molybdenum cofacto	328	231	2	T20304	hypothetical prote
256	6	1.6	184	2	AC3427	transposase BME114	329	233	2	PV0001	recf protein - pse
257	6	1.6	185	2	G91138	hypothetical prote	330	233	2	F13367	16S pseudouridylat
258	6	1.6	185	2	B85984	hypothetical prote	331	234	2	F86855	conserved hypoteth
259	6	1.6	185	2	B65111	17.3 kD protein in	332	234	2	E64434	hypothetical prote
260	6	1.6	185	2	T49611	hypothetical prote	333	235	2	A56757	14-3-3 regulatory
261	6	1.6	185	2	T24375	hypothetical prote	334	235	2	E83752	hypothetical prote
262	6	1.6	186	2	G59567	hypothetical prote	335	235	2	T26489	hypothetical prote
263	6	1.6	186	2	B90548	50S ribosomal prot	336	235	2	E95876	conserved hypoteth
264	6	1.6	186	2	F86379	protein F219.28 [337	236	2	AB0681	probable ABC trans
265	6	1.6	186	2	T31951	hypothetical prote	338	237	1	A39017	modulation control
266	6	1.6	186	2	F09296	apolipoprotein III	339	238	2	A81422	probable RNA polym
267	6	1.6	187	1	F0VW53	gag polyprotein -	340	238	2	D75513	L-serine dehydrata
268	6	1.6	187	2	D2501	hypothetical prote	341	238	2	T51270	hypothetical prote
269	6	1.6	187	2	A72737	hypothetical prote	342	240	2	E72740	hypothetical prote
270	6	1.6	189	2	T46076	hypothetical prote	343	241	2	D72751	hypothetical prote
271	6	1.6	189	2	A49743	hypothetical prote	344	242	2	A75023	hypothetical prote
272	6	1.6	189	2	AD2916	transcription regu	345	242	2	H97151	hypothetical prote
273	6	1.6	189	2	G97690	hypothetical prote	346	242	2	AH3537	nta operon transcr
274	6	1.6	190	2	T08258	conserved hypoteth	347	243	2	F83429	conserved hypoteth
275	6	1.6	190	2	D88957	protein ZK697.8 [1	348	244	2	S38568	transcription init
276	6	1.6	193	2	E70226	conserved hypoteth	349	244	2	H96934	uncharacterized me
277	6	1.6	194	2	AS2310	hypothetical prote	350	246	2	B96707	hypothetical prote
278	6	1.6	195	2	H96532	hypothetical prote	351	246	2	AF2684	conserved hypoteth
279	6	1.6	195	2	G72697	hypothetical prote	352	246	2	S60883	ATP-binding protei
280	6	1.6	196	2	H95023	hypothetical prote	353	247	2	E95207	conserved hypoteth
281	6	1.6	196	2	B96980	uncharacterized co	354	247	2	JG0016	epidermal cell dif
282	6	1.6	196	2	A37895	hypothetical prote	355	248	2	B97794	hypothetical prote
283	6	1.6	197	2	A83845	hypothetical prote	356	249	1	S68688	myb-related protei
284	6	1.6	197	2	T24133	hypothetical prote	357	249	2	C70436	conserved hypoteth
285	6	1.6	199	2	B86659	hypothetical prote	358	249	2	S38308	SNAP-25 protein -
286	6	1.6	200	2	A86025	probable regulator	359	249	2	S38309	SNAP-25 protein -
287	6	1.6	200	2	H91178	probable transcrip	360	249	2	S37693	cyclin G - mouse
288	6	1.6	200	2	S47740	hypothetical prote	361	249	2	S51621	cyclin G - rat
289	6	1.6	200	2	E99871	hypothetical prote	362	250	2	T04496	hypothetical prote
290	6	1.6	201	2	T29387	hypothetical prote	363	250	2	T31835	conserved hypoteth
291	6	1.6	201	2	I38850	LEKX-4 - human	364	251	2	E98072	conserved hypoteth
292	6	1.6	202	2	T15874	hypothetical prote	365	252	2	T13588	NADH2 dehydrogenas
293	6	1.6	202	2	E75053	hypothetical prote	366	252	2	E82040	general secretion
294	6	1.6	203	2	T45907	hypothetical prote	367	252	2	D82963	conserved hypoteth
295	6	1.6	204	2	T44357	hypothetical prote	368	255	2	G97173	chemotaxis protein
296	6	1.6	206	2	T40519	BAG-family molecu	369	256	2	H83291	conserved hypoteth
297	6	1.6	207	1	LNCHL	hepatic lectin - c	370	256	2	G02523	cyclin G - human
298	6	1.6	209	2	C86736	two-component syst	371	258	2	T09031	hypothetical prote
299	6	1.6	209	2	G70091	ABC transporter (A	372	259	2	D82331	peptidyl-prolyl ci
300	6	1.6	210	2	G75180	hypothetical prote	373	259	2	T36003	hypothetical prote
301	6	1.6	211	2	F81998	mutants block spor	374	260	2	S76509	hypothetical prote
302	6	1.6	212	2	G90056	hypothetical prote	375	260	2	E87431	hypothetical prote
303	6	1.6	212	2	S31707	floral homeotic pr	376	261	2	S20610	calpastatin - mous
304	6	1.6	213	2	A13452	glycerol metabolis	377	261	2	A82106	flagellar L-ring p
305	6	1.6	214	2	F72664	superoxide dismuta	378	261	2	T09075	hypothetical prote
306	6	1.6	216	2	A71445	hypothetical prote	379	262	2	I49361	natural killer cel
307	6	1.6	216	2	T37472	fibroblast growth	380	262	2	A45813	T-cell surface gly
308	6	1.6	217	2	B64092	butyrate-acetoacet	381	262	2	D97466	probable repressor
309	6	1.6	217	2	F83196	probable two-compo	382	264	2	T02174	probable alcohol d
310	6	1.6	217	2	T33926	hypothetical prote	383	264	2	E95410	probable ABC trans
311	6	1.6	219	2	AG0333	heme exporter prot	384	264	2	T32387	hypothetical prote
312	6	1.6	219	2	S22276	ribosomal protein	385	265	2	T27673	hypothetical prote
313	6	1.6	220	1	S22516	S-allele-associate	386	266	2	I49050	Ly-49E-GE antigen
314	6	1.6	222	2	A46658	calcium channel pr	387	267	2	H83426	3-phosphoadenosin
315	6	1.6	222	2	S10728	calcium channel pr	388	267	2	A75131	hypothetical prote
316	6	1.6	223	2	F83034	urease accessory p	389	267	2	I55686	LGL-1 - mouse
317	6	1.6	224	2	S61386	icm1 protein - leg	390	267	2	I49053	Ly-49C.2 antigen -
318	6	1.6	224	2	D87236	conserved membrane	391	267	2	A71087	hypothetical prote
319	6	1.6	227	2	T11329	H4-transporing tw	392	268	2	S08229	chlorophyll a/b-bi
320	6	1.6	227	2	F90616	ATP synthase F0 ch	393	268	2	S00553	MSS18 protein - ye
321	6	1.6	227	2	F90618	ATP synthase F0 ch	394	269	1	WZB524	gene 24 protein -

395	6	1.6	269	2	A70719	probable enoyl-coA	468	302	2	B3163	cobV protein - Pse
396	6	1.6	269	2	T37798	probable coiled-co	469	302	2	T27602	hypothetical prote
397	6	1.6	269	2	S58439	transcription fact	470	303	2	F98284	3-hydroxybutyryl-C
398	6	1.6	270	2	T46961	molybdenum cofacto	471	303	2	AC2399	3-hydroxybutyryl-C
399	6	1.6	270	2	T50952	transposase relate	472	303	2	T00969	probable mitochond
400	6	1.6	272	2	E64182	cysZ protein - Hae	473	303	2	T16004	hypothetical prote
401	6	1.6	272	2	T32438	hypothetical prote	474	304	2	S02284	potassium channel
402	6	1.6	277	2	G75520	hypothetical prote	475	304	2	G82288	conserved hypotet
403	6	1.6	277	2	AF2404	hypothetical prote	476	304	2	D86998	probable secreted
404	6	1.6	279	2	A11189	B. subtilis ycgQ p	477	306	2	AE1394	conserved hypotet
405	6	1.6	279	2	AB1548	B. subtilis ycgQ p	478	306	2	AH1769	conserved hypotet
406	6	1.6	279	2	T25587	hypothetical prote	479	307	1	G64717	pyridoxal phosphat
407	6	1.6	279	2	E37097	methyl-accepting c	480	307	1	ACBPT7	capsid assembly pr
408	6	1.6	279	2	A89920	conserved hypotet	481	307	2	F86865	conserved hypotet
409	6	1.6	280	2	H69228	fumarate hydratase	482	307	2	T75584	hypothetical prote
410	6	1.6	280	2	I49052	Ly-49G.1 antigen -	483	307	2	S47244	C-raf protein - ze
411	6	1.6	280	2	S46059	probable membrane	484	308	2	AE2829	hypothetical prote
412	6	1.6	281	2	A11858	chorismate mutase/	485	309	2	C81317	probable glycosylt
413	6	1.6	281	2	H95085	conserved hypotet	486	309	2	T50797	hypothetical prote
414	6	1.6	281	2	D97953	conserved hypotet	487	310	1	F0MVFB	gag polyprotein -
415	6	1.6	282	2	S29040	Na+-transporting A	488	310	2	A98939	probable kinase [i
416	6	1.6	282	2	T35000	probable protein a	489	310	2	E85787	probable kinase 22
417	6	1.6	282	2	F96946	methyl-accepting c	490	310	2	H87058	l-asparaginase/l-9
418	6	1.6	283	2	C70390	formate dehydrogen	491	310	2	S07522	capsid assembly pr
419	6	1.6	284	2	S45458	PET8 protein - Yea	492	311	2	AH0867	transcription acti
420	6	1.6	284	2	A11423	B. subtilis DNA-bi	493	311	2	H69513	5-methyltetrahydro
421	6	1.6	284	2	G90671	probable ARAC-type	494	311	2	G81402	oxidoreductase Cj0
422	6	1.6	284	2	C85522	probable ARAC-type	495	312	2	T31834	hypothetical prote
423	6	1.6	284	2	A64757	Ykgp protein - Esc	496	313	2	D69336	conserved hypotet
424	6	1.6	286	2	B90156	hypothetical prote	497	313	2	C69803	hypothetical prote
425	6	1.6	287	2	T42968	hypothetical prote	498	313	2	G95883	probable ABC trans
426	6	1.6	288	2	G64102	phosphatidate cyti	499	314	2	AG0485	2-dehydro-3-deoxyg
427	6	1.6	288	2	JC4011	cyclin D2 - rat	500	315	2	G88485	protein F23F12.1 [
428	6	1.6	288	2	I58372	cyclin D2 - rat	501	316	2	H82128	3-oxoacyl-(acyl-ca
429	6	1.6	288	2	S74895	hypothetical prote	502	316	2	B72499	probable carbamate
430	6	1.6	288	2	S40173	ExoU protein - Rhi	503	316	2	AG0121	probable sideropho
431	6	1.6	289	2	A42822	cyclin D2 - human	504	316	2	S75096	hypothetical prote
432	6	1.6	289	2	A41984	cyclin D2 - mouse	505	316	2	T34023	hypothetical prote
433	6	1.6	289	2	S39721	spore coat polysac	506	316	2	D97865	hypothetical prote
434	6	1.6	289	2	E81259	hypothetical prote	507	316	2	AG2977	hypothetical prote
435	6	1.6	291	2	JC4579	cyclin D2 - chicke	508	316	2	B96749	hypothetical prote
436	6	1.6	291	2	S57925	cyclin D2 - Africa	509	316	2	C96020	probable sugar upt
437	6	1.6	291	2	H89894	conserved hypotet	510	317	2	C86479	probable annexin p
438	6	1.6	291	2	A86681	hypothetical prote	511	317	2	G82635	methanol dehydrog
439	6	1.6	291	2	D82491	hypothetical prote	512	317	2	S76961	hypothetical prote
440	6	1.6	292	2	D98096	conserved hypotet	513	317	2	T32101	hypothetical prote
441	6	1.6	292	2	B35232	conserved hypotet	514	319	2	E98305	hypothetical prote
442	6	1.6	292	2	A64624	hypothetical prote	515	319	2	H69882	deacetylase homolo
443	6	1.6	293	2	D86670	pseudouridine synt	516	320	2	S73995	probable lipoprote
444	6	1.6	294	2	T49271	CELL DIVISION CONT	517	320	2	H11259	probable membrane
445	6	1.6	294	2	S23095	protein kinase (EC	518	321	2	T11274	NADH2 dehydrogenas
446	6	1.6	294	2	G83962	hypothetical prote	519	322	1	D64937	probable sugar kin
447	6	1.6	294	2	AB0772	hypothetical prote	520	322	2	A97657	ferrichrome ABC tr
448	6	1.6	294	2	C86802	hypothetical prote	521	322	2	AI2880	ABC transporter, m
449	6	1.6	295	2	T20629	hypothetical prote	522	323	2	S42426	aspartate-semialde
450	6	1.6	295	2	G02401	cyclin G1 - human	523	323	2	S27596	replacation-associ
451	6	1.6	296	2	F71336	probable glutamate	524	324	2	S75735	probable malate de
452	6	1.6	296	2	B75555	probable lipase/es	525	324	2	F70609	hypothetical prote
453	6	1.6	296	2	D71891	hypothetical prote	526	326	2	G70760	asparaginase (EC 3
454	6	1.6	296	2	B84527	hypothetical prote	527	326	2	A83273	fatty acid biosynt
455	6	1.6	297	2	H75449	riboflavin kinase/	528	326	2	S28706	hypothetical prote
456	6	1.6	297	2	AC1706	hypothetical prote	529	326	2	H95867	probable transcrip
457	6	1.6	297	2	AD1335	hypothetical prote	530	327	2	AI0515	thiamin-binding pe
458	6	1.6	298	1	A59879	conserved hypotet	531	327	2	S67168	probable membrane
459	6	1.6	298	2	G89898	hypothetical prote	532	328	2	A99416	alcohol dehydrogen
460	6	1.6	298	2	T25695	hypothetical prote	533	328	2	S29525	cyclin 2 - alfalfa
461	6	1.6	299	2	D81067	hypothetical prote	534	328	2	A70629	probable glnH prot
462	6	1.6	300	1	WMLJBI	bel-1 protein - hu	535	329	2	T31716	hypothetical prote
463	6	1.6	300	1	S75379	MJ1232 protein hom	536	330	2	B88990	protein C36C5.11 [
464	6	1.6	300	2	D87609	conserved hypotet	537	331	2	T08257	cytochrome d ubiqu
465	6	1.6	301	2	G84339	formylmethanofuran	538	331	2	F71943	high-affinity nick
466	6	1.6	301	2	F72029	phosphatidylserine	539	331	2	A87652	hypothetical prote
467	6	1.6	301	2	E86595	phosphatidylserine	540	332	2	F97071	phosphoribosylamin

541	6	1.6	332	2	B82607	conserved hypotet	614	1.6	370	2	S68777	vasopressin recept
542	6	1.6	333	2	B72306	hypothetical prote	615	1.6	370	2	A93073	hypothetical prote
543	6	1.6	334	2	S13734	licheninase (EC 3	616	1.6	370	2	B98213	probable maltose/m
544	6	1.6	335	2	B96810	unknown protein T1	617	1.6	373	2	T34743	hypothetical prote
545	6	1.6	335	1	A49897	anthranilate phosp	618	1.6	373	2	AF2939	oxidoreductase Atu
546	6	1.6	335	2	T31561	hypothetical prote	619	1.6	374	2	T32207	hypothetical prote
547	6	1.6	335	2	T31559	hypothetical prote	620	1.6	375	2	C82842	hypothetical prote
548	6	1.6	335	2	T31560	hypothetical prote	621	1.6	375	2	F88947	protein C39P7.2 [1
549	6	1.6	335	2	T05722	licheninase (EC 3	622	1.6	375	2	T33778	hypothetical prote
550	6	1.6	336	2	AE2922	zinc-binding dehyd	623	1.6	376	2	A55874	DNA-directed DNA p
551	6	1.6	336	2	F97696	hypothetical zinc-	624	1.6	376	2	D71830	hypothetical prote
552	6	1.6	336	2	E75040	hydrogenase expres	625	1.6	376	2	T47519	hypothetical prote
553	6	1.6	336	2	D71121	probable hydrogena	626	1.6	376	2	T49255	protein kinase-lik
554	6	1.6	336	2	S42382	hypothetical prote	627	1.6	377	2	AD3363	conserved hypotet
555	6	1.6	337	2	T32099	hypothetical prote	628	1.6	377	2	A64685	hypothetical prote
556	6	1.6	337	2	C97607	hypothetical prote	629	1.6	377	2	T49604	hypothetical prote
557	6	1.6	337	2	T27615	hypothetical prote	630	1.6	378	2	T18486	hypothetical prote
558	6	1.6	338	1	R5HS3L	ribosomal protein	631	1.6	379	1	S43263	ubiquinol-cytochro
559	6	1.6	338	2	E95251	ornithine carbanoy	632	1.6	379	1	S43264	ubiquinol-cytochro
560	6	1.6	338	2	B98116	ornithine carbanoy	633	1.6	379	2	T20394	hypothetical prote
561	6	1.6	338	2	A83389	probable permease	634	1.6	379	2	T03608	chilling-induced p
562	6	1.6	338	2	T47427	hypothetical prote	635	1.6	379	2	H69478	NADH2 dehydrogenas
563	6	1.6	338	2	H69022	hypothetical prote	636	1.6	380	2	T13758	NADH2 dehydrogenas
564	6	1.6	339	1	F69852	L-iditol 2-dehydro	637	1.6	380	2	S64417	cyclin B5 - yeast
565	6	1.6	339	2	T24725	hypothetical prote	638	1.6	380	2	A94343	hypothetical prote
566	6	1.6	340	2	A72398	transcription regu	639	1.6	381	2	T13701	NADH2 dehydrogenas
567	6	1.6	342	2	A10286	pap operon transcr	640	1.6	381	2	AC1432	DNA polymerase III
568	6	1.6	342	2	E70812	hypothetical prote	641	1.6	381	2	AC1433	DNA polymerase III
569	6	1.6	344	1	D64620	GTP cyclohydrolase	642	1.6	381	2	G97114	uncharacterized me
570	6	1.6	344	2	C71894	GTP cyclohydrolase	643	1.6	383	2	E75589	hypothetical prote
571	6	1.6	345	2	E70794	probable asd prote	644	1.6	383	2	S66729	probable membrane
572	6	1.6	345	2	S51548	killer toxin K28 -	645	1.6	384	1	W2WL41	E2 protein - human
573	6	1.6	345	2	T37139	hypothetical prote	646	1.6	384	2	E83040	hypothetical prote
574	6	1.6	345	2	T25590	hypothetical prote	647	1.6	385	2	E83414	conserved hypotet
575	6	1.6	346	2	AF2596	hypothetical prote	648	1.6	385	2	T20918	hypothetical prote
576	6	1.6	346	2	H97378	malate dehydrogena	649	1.6	387	2	A53586	albumin-binding pr
577	6	1.6	346	2	C88961	probable l-malate	650	1.6	387	2	G82983	probable MFS trans
578	6	1.6	346	2	B75439	protein P59AV.5 [1	651	1.6	389	2	D64333	pyruvate synthase
579	6	1.6	347	2	T50990	hypothetical prote	652	1.6	389	2	S53975	probable membrane
580	6	1.6	349	2	F69205	3-hydroxy-3-methyl	653	1.6	389	2	A25881	lysostaphin precu
581	6	1.6	349	2	T30093	hypothetical prote	654	1.6	389	2	E95422	probable transmemb
582	6	1.6	349	2	S74439	iron(III) dicitrat	655	1.6	390	1	C64996	probable hydro-ly
583	6	1.6	349	2	CH0235	hypothetical 39K p	656	1.6	390	2	D85865	probable enzyme Z3
584	6	1.6	349	2	C59107	hypothetical prote	657	1.6	390	2	E91021	probable enzyme [1
585	6	1.6	350	2	T40466	probable acetyltra	658	1.6	390	2	D69757	multidrug-efflux t
586	6	1.6	350	2	B82230	conserved hypotet	659	1.6	390	2	D83057	probable aminotran
587	6	1.6	351	2	F87199	aspartate semialde	660	1.6	390	2	T09563	hypothetical prote
588	6	1.6	351	2	AB2963	endoglucanase (imp	661	1.6	391	2	A44063	paired box transcr
589	6	1.6	351	2	C98320	hypothetical prote	662	1.6	391	2	S74688	hypothetical prote
590	6	1.6	353	2	E98142	hypothetical prote	663	1.6	392	2	T13722	NADH2 dehydrogenas
591	6	1.6	353	2	AF3145	hypothetical prote	664	1.6	392	2	T30026	hypothetical prote
592	6	1.6	353	2	E95885	probable iron ABC	665	1.6	392	2	G75056	dehydrogenase PAB0
593	6	1.6	355	2	H71812	hypothetical prote	666	1.6	392	2	F81676	heat shock gene re
594	6	1.6	355	2	B64707	hypothetical prote	667	1.6	393	1	XXALAE	acetyl-CoA C-acety
595	6	1.6	355	2	T15471	hypothetical prote	668	1.6	393	2	T12608	NADH2 dehydrogenas
596	6	1.6	355	2	A37348	HD-GYP domain cont	669	1.6	393	2	T13501	NADH2 dehydrogenas
597	6	1.6	356	2	C70025	multidrug-efflux t	670	1.6	393	2	T13565	NADH2 dehydrogenas
598	6	1.6	356	2	G95875	probable spermidin	671	1.6	393	2	T13775	NADH2 dehydrogenas
599	6	1.6	357	2	H81450	chorismate mutase	672	1.6	393	2	T12630	NADH2 dehydrogenas
600	6	1.6	359	2	H65201	pcs system, fructo	673	1.6	393	2	T12609	NADH2 dehydrogenas
601	6	1.6	360	2	A85016	hypothetical prote	674	1.6	393	2	S62335	171-7 protein - ir
602	6	1.6	361	2	B84716	hypothetical prote	675	1.6	394	2	E83213	NADH2 dehydrogenas
603	6	1.6	361	2	T17282	hypothetical prote	676	1.6	394	2	E83213	probable acyl-CoA
604	6	1.6	363	2	AC0244	conserved hypotet	677	1.6	394	2	A70469	aspartate transami
605	6	1.6	364	2	D86253	hypothetical prote	678	1.6	394	2	T19028	hypothetical prote
606	6	1.6	365	2	S21056	recf protein - pse	679	1.6	394	2	T32042	hypothetical prote
607	6	1.6	366	2	F72703	probable heat shoc	680	1.6	395	2	T13756	NADH2 dehydrogenas
608	6	1.6	367	2	T20914	hypothetical prote	681	1.6	395	2	T13779	NADH2 dehydrogenas
609	6	1.6	368	2	E69796	two-component resp	682	1.6	395	2	S52423	protein kinase (EC
610	6	1.6	369	2	G83644	RecF protein PA000	683	1.6	395	2	T29379	hypothetical prote
611	6	1.6	369	2	T36633	probable heavy met	684	1.6	395	2	C88955	protein K04F1.10 [
612	6	1.6	369	2	AD0555	probable ATP-bind	685	1.6	395	2	AD0678	probable membrane
613	6	1.6	369	2	T46950	probable ATPase co	686	1.6	395	2	E90896	probable transport

687	6	1.6	395	2	B85721	probable transport	760	6	1.6	423	2	T14531	S-locus-specific g
688	6	1.6	395	2	A64908	membrane protein y	761	6	1.6	423	2	JC7677	allatostatin recep
689	6	1.6	395	2	B81358	transmembrane tran	762	6	1.6	424	1	XUHUAB	acetyl-CoA C-acylt
690	6	1.6	396	2	A13554	xylose transport s	763	6	1.6	424	2	S71798	WAD-3 protein homo
691	6	1.6	397	2	T139184	bomaphin - human	764	6	1.6	425	2	B81236	nitrogen assimilat
692	6	1.6	397	2	T190299	hypothetical prote	765	6	1.6	425	2	D82009	probable two-compo
693	6	1.6	397	2	T37955	hypothetical prote	766	6	1.6	426	2	F82139	ATP-dependent Clp
694	6	1.6	398	1	W2WL42	E2 protein - human	767	6	1.6	426	2	B87385	chromate-transport
695	6	1.6	398	2	B86353	protein F2E2.6 [im	768	6	1.6	426	2	B84164	neutral proteinase
696	6	1.6	398	2	J00356	phospholipase C (E	769	6	1.6	426	2	D71552	probable oligopept
697	6	1.6	398	2	B49231	phospholipase C, a	770	6	1.6	428	2	G69988	NDF-sugar denydrog
698	6	1.6	398	2	A30565	phospholipase C (E	771	6	1.6	429	2	B84985	hypothetical prote
699	6	1.6	399	2	T22168	hypothetical prote	772	6	1.6	429	2	F71713	glycerol-3-phospha
700	6	1.6	399	2	I38901	UNK-activating pro	773	6	1.6	429	2	D87375	lpsE protein [impo
701	6	1.6	399	2	B64488	hypothetical prote	774	6	1.6	429	2	T14534	S-locus-specific g
702	6	1.6	400	2	I50219	connexin 45.6 - ch	775	6	1.6	431	2	H82237	histidinol dehydro
703	6	1.6	400	2	C30791	probable integrase	776	6	1.6	431	2	B64454	ribulose-bisphosph
704	6	1.6	400	2	B85600	probable P4-family	777	6	1.6	431	2	B81927	probable oxidoredu
705	6	1.6	400	2	C97623	aspartate aminotra	778	6	1.6	431	2	G81179	oxidoreductase, pr
706	6	1.6	400	2	AC2846	aspartate aminotra	779	6	1.6	431	2	AH1027	probable pilus ass
707	6	1.6	401	1	B35177	chromate resistanc	780	6	1.6	432	2	A69056	hypothetical prote
708	6	1.6	401	2	G82737	argininosuccinate	781	6	1.6	433	1	ITHUC	alpha-1-antichymot
709	6	1.6	401	2	D85030	hypothetical prote	782	6	1.6	433	2	AE2658	glycolate oxidase
710	6	1.6	402	2	A87278	flagellin modifika	783	6	1.6	433	2	B97440	glycolate oxidase
711	6	1.6	402	2	T15490	hypothetical prote	784	6	1.6	434	2	T09706	cyclin cymE2, B-t
712	6	1.6	403	2	E95991	probable transcrip	785	6	1.6	435	1	S65982	transport protein
713	6	1.6	405	2	A39088	alpha-1-antiprotei	786	6	1.6	435	2	H75443	aspartyl-tRNA synt
714	6	1.6	405	2	T31912	hypothetical prote	787	6	1.6	435	2	S67205	probable membrane
715	6	1.6	405	2	A36917	probable permease	788	6	1.6	437	1	TVMSRF	protein kinase A-r
716	6	1.6	405	2	AD2164	hypothetical prote	789	6	1.6	437	2	S46613	2e5 proteasome reg
717	6	1.6	406	1	JC5041	fosmidomycin resis	790	6	1.6	440	2	A49425	sonic hedgehog pro
718	6	1.6	406	2	A37986	aminotripeptidase	791	6	1.6	437	2	A36372	membrane transport
719	6	1.6	406	2	S24788	cyclin A - bovine	792	6	1.6	438	2	D84331	hypothetical prote
720	6	1.6	406	2	AH0563	fosmidomycin resis	793	6	1.6	439	2	D64065	exodeoxyribonucle
721	6	1.6	406	2	H85545	fosmidomycin resis	794	6	1.6	440	2	JC2532	secretin receptor
722	6	1.6	406	2	D90635	fosmidomycin resis	795	6	1.6	440	2	AF0615	killing factor Kic
723	6	1.6	406	2	H73215	conserved hypotet	796	6	1.6	440	2	S43911	mukF protein - Esc
724	6	1.6	407	2	C95116	peptidase t [impor	797	6	1.6	440	2	E90754	mukF protein [impo
725	6	1.6	409	1	J80759	membrane dipeptida	798	6	1.6	440	2	C85618	mukF protein (kill
726	6	1.6	409	2	C82072	D-3-phosphoglycera	799	6	1.6	440	2	B75044	hypothetical prote
727	6	1.6	409	2	C82644	transcription regu	800	6	1.6	440	2	S77194	hypothetical prote
728	6	1.6	409	2	S47440	secy protein - red	801	6	1.6	441	2	C95307	probable transport
729	6	1.6	409	2	E91246	probable L-sorbose	802	6	1.6	443	2	AE0458	X-Pro dipeptidase
730	6	1.6	410	1	S18442	membrane dipeptida	803	6	1.6	444	2	T01721	hypothetical prote
731	6	1.6	410	1	S27204	membrane dipeptida	804	6	1.6	445	2	T49924	embryogenic callus
732	6	1.6	410	1	S33757	membrane dipeptida	805	6	1.6	445	2	S44541	hypothetical prote
733	6	1.6	410	2	S75695	hypothetical prote	806	6	1.6	445	2	A56024	GDP dissociation i
734	6	1.6	410	2	S50151	L-sorbose 1-phosph	807	6	1.6	445	2	C56956	GDP dissociation i
735	6	1.6	411	2	A82492	tryptophan-specifi	808	6	1.6	445	2	B54091	rab GDP dissociati
736	6	1.6	411	2	C64052	NADH2 dehydrogenas	809	6	1.6	445	2	E72674	hypothetical prote
737	6	1.6	413	1	S03631	homeotic protein S	810	6	1.6	445	2	S36039	MAP kinase activat
738	6	1.6	413	2	H75628	hypothetical prote	811	6	1.6	447	2	B83015	heat shock protein
739	6	1.6	413	2	B86094	probable L-sorbose	812	6	1.6	447	2	T17299	hypothetical prote
740	6	1.6	414	2	D84111	uracil transport p	813	6	1.6	449	2	T49125	hypothetical prote
741	6	1.6	414	2	A84604	hypothetical prote	814	6	1.6	450	2	T37628	glycerol dehydroge
742	6	1.6	414	2	H84596	hypothetical prote	815	6	1.6	452	2	T43278	cadmium resistanc
743	6	1.6	415	2	D85061	probable adenosine	816	6	1.6	453	2	AG2117	hypothetical prote
744	6	1.6	416	2	S33473	interleukin-1 rece	817	6	1.6	454	2	T47127	glutamate-ammonia
745	6	1.6	418	2	A30556	grp-binding protei	818	6	1.6	454	2	H86231	hypothetical prote
746	6	1.6	418	2	A46286	somatostatin recep	819	6	1.6	455	2	AH0208	probable transport
747	6	1.6	418	2	AE2462	hypothetical prote	820	6	1.6	455	2	H71028	hypothetical prote
748	6	1.6	419	2	G71311	probable phosphogl	821	6	1.6	456	2	T24442	hypothetical prote
749	6	1.6	419	2	F36788	hypothetical prote	822	6	1.6	456	2	T49192	hypothetical prote
750	6	1.6	419	2	C81179	spermidine/putresc	823	6	1.6	457	2	B84725	puflf C-8 protein -
751	6	1.6	420	2	B97843	glycine hydroxymet	824	6	1.6	457	2	S39079	MAP kinase activat
752	6	1.6	420	2	C72774	probable cleavage	825	6	1.6	457	2	A54694	amino acid transpo
753	6	1.6	421	2	AF3316	aspartate transami	826	6	1.6	458	2	AC1173	amino acid transpo
754	6	1.6	421	2	AF1314	hypothetical prote	827	6	1.6	458	2	AD1530	cytosolic axial fi
755	6	1.6	421	2	AF1686	hypothetical prote	828	6	1.6	458	2	D70410	hypothetical prote
756	6	1.6	421	2	D69643	imidazole-5-prop	829	6	1.6	459	2	H96715	hypothetical prote
757	6	1.6	421	2	C64320	probable membrane	830	6	1.6	459	2	AF1397	two-component sens
758	6	1.6	422	2	S37280	cyclin A - mouse	831	6	1.6	459	2	AI1772	probable cytochrom
759	6	1.6	422	2	S38501	cyclin A2 - mouse	832	6	1.6	461	2	T05332	

833	6	1.6	461	2	JN0097	secreted 45K prote	906	512	2	S23355	alpha-amylase (EC
834	6	1.6	462	2	A33170	tube protein - fru	907	512	2	S06115	alpha-amylase (EC
835	6	1.6	462	2	AH1017	probable integral	908	512	2	H87297	thiamin-pyrophosph
836	6	1.6	463	2	G29300	aspartyl/asparagin	909	513	2	D97665	nodr protein homol
837	6	1.6	463	2	T29442	hypothetical prote	910	513	2	S58200	probable membrane
838	6	1.6	464	2	T48339	hypothetical prote	911	519	2	T43756	ATPase subunit 1 (
839	6	1.6	464	2	F89828	conserved hypotet	912	519	2	S17783	tachykinin recepto
840	6	1.6	465	1	JC1318	triacylglycerol li	913	522	2	H72267	conserved hypotet
841	6	1.6	465	2	A83046	probable amino aci	914	522	2	T22484	hypothetical prote
842	6	1.6	467	2	S08618	modulation protein	915	523	2	T51475	RGA-like protein -
843	6	1.6	467	2	S71797	MAD-2 protein homo	916	523	2	G96777	hypothetical prote
844	6	1.6	468	2	S51593	hypothetical prote	917	524	1	GVNVCV	spike glycoprotein
845	6	1.6	469	1	NMIV27	exo-alpha-sialidas	918	524	2	T14870	hypothetical prote
846	6	1.6	469	1	NMIVH3	exo-alpha-sialidas	919	524	2	T29484	hypothetical prote
847	6	1.6	469	1	NMIVN2	exo-alpha-sialidas	920	526	2	S22811	hypothetical prote
848	6	1.6	469	1	NMIV2	exo-alpha-sialidas	921	532	2	T15354	hypothetical prote
849	6	1.6	469	2	JQ1644	exo-alpha-sialidas	922	532	2	A57173	oculocutaneous alb
850	6	1.6	469	2	D72722	probable MRSA prot	923	533	2	A70464	D-3-phosphoglycra
851	6	1.6	469	2	A99656	hypothetical prote	924	533	2	S53320	(N-acetylneuraminy
852	6	1.6	471	2	H71957	probable outer mem	925	535	2	B72268	conserved hypotet
853	6	1.6	471	2	S41407	hypothetical prote	926	536	2	H72268	conserved hypotet
854	6	1.6	471	2	B72314	hypothetical prote	927	536	2	A84474	hypothetical prote
855	6	1.6	472	2	T39028	citrate synthase p	928	537	1	FOMVGV	gag polyprotein -
856	6	1.6	474	2	G97033	beta-glucosidase f	929	537	2	C90389	conserved hypotet
857	6	1.6	474	2	AC0402	conserved hypotet	930	539	2	T03469	probable hydrogena
858	6	1.6	475	2	JN0578	p-Aminobenzoic aci	931	541	2	B70532	transporter, proba
859	6	1.6	476	2	S59339	proline oxidase -	932	541	2	C90506	hypothetical prote
860	6	1.6	477	2	C85361	hypothetical prote	933	543	2	C86212	hypothetical prote
861	6	1.6	478	2	H71345	probable polynucle	934	545	2	S28117	gas-vesicle operon
862	6	1.6	479	2	A55382	nicotinic acetylch	935	547	2	AB2639	pH adaptation potass
863	6	1.6	479	2	S67202	probable membrane	936	547	2	T45835	hypothetical prote
864	6	1.6	479	2	T34348	hypothetical prote	937	548	2	T30369	DNA ligase-like pr
865	6	1.6	480	2	S01079	lysostaphin precu	938	548	2	AD0287	peptide transport
866	6	1.6	481	2	T15440	hypothetical prote	939	548	2	C97421	phad protein (X933
867	6	1.6	482	2	S08384	modulation protein	940	548	2	S52735	Cw17R protein - mo
868	6	1.6	482	2	S10133	cysteine-trna liga	941	550	2	G95359	Probable ABC trans
869	6	1.6	483	1	S76165	modulation protein	942	551	2	AC2376	hypothetical prote
870	6	1.6	484	2	AG2889	hypothetical prote	943	551	2	H98306	hypothetical prote
871	6	1.6	485	2	G83359	hypothetical prote	944	553	2	G83786	glycerol-3-phospha
872	6	1.6	485	2	T19853	hypothetical prote	945	553	2	C84920	hypothetical prote
873	6	1.6	487	2	T38641	probable metal tra	946	553	2	G81181	electron transfer
874	6	1.6	488	2	D70876	probable polyketid	947	555	2	B87576	choline dehydrogen
875	6	1.6	488	2	T30914	Xylan 1,4-beta-xyl	948	557	2	S56292	hypothetical prote
876	6	1.6	489	1	NM8E1	UL41 protein - hum	949	560	2	S27387	interferon alpha r
877	6	1.6	491	1	A62938	MJ0100 protein hom	950	563	2	AH1245	DNA repair and gen
878	6	1.6	491	1	S24334	p53-binding protei	951	563	2	AD1608	DNA repair and gen
879	6	1.6	492	2	A35354	UL 41 protein - hu	952	564	2	S41974	DNA ligase (ATP) (
880	6	1.6	493	2	T48630	high affinity nitr	953	565	2	S73707	Na(+) translocatin
881	6	1.6	494	2	F89810	NADH dehydrogenase	954	567	2	A33974	membrane transport
882	6	1.6	494	2	D64944	probable permease	955	568	2	E75502	threonine ammonia-
883	6	1.6	494	2	F85794	probable transport	956	569	2	T11357	NADH2 dehydrogenas
884	6	1.6	494	2	B90946	probable transport	957	569	2	B84904	probable laccase (
885	6	1.6	494	2	T08751	hypothetical prote	958	569	2	S47277	gp88 protein - mur
886	6	1.6	495	1	S77406	protein kinase pkn	959	570	2	T38489	helicase - fission
887	6	1.6	495	2	A75608	aldehyde dehydroge	960	570	2	G72595	hypothetical prote
888	6	1.6	495	2	C84089	hypothetical prote	961	571	2	C71528	probable pts pep p
889	6	1.6	495	2	C83598	hypothetical prote	962	572	2	T29880	hypothetical prote
890	6	1.6	496	2	E83849	spore germination	963	573	2	C84645	hypothetical prote
891	6	1.6	496	2	T48547	diaminopimelate de	964	575	2	B64174	hypothetical prote
892	6	1.6	496	2	T09936	hypothetical prote	965	576	2	AE0409	sulfite reductase
893	6	1.6	498	2	AF3279	malonate-semialden	966	578	2	S51379	probable phosphoes
894	6	1.6	499	2	C70405	hypothetical prote	967	579	2	A56740	spem-egg recognit
895	6	1.6	499	2	B85507	hypothetical prote	968	580	2	S72211	N-acetyl-beta-D-gl
896	6	1.6	500	1	JC5819	cytochrome P450 2D	969	581	2	G71520	proline-trna ligas
897	6	1.6	504	2	T37164	probable monooxyge	970	581	2	T31745	hypothetical prote
898	6	1.6	505	2	C86443	unknown protein li	971	583	2	T07848	pectinesterase (EC
899	6	1.6	506	2	AD3338	cobryric acid synth	972	584	2	E71843	poly-beta-hydroxyb
900	6	1.6	506	2	F88954	protein K04Fl.14 [973	584	2	E72308	hypothetical prote
901	6	1.6	509	2	S46314	hydroxymethylgluta	974	585	2	G96731	probable phosphogl
902	6	1.6	510	2	T20276	hypothetical prote	975	585	2	G81920	probable electron
903	6	1.6	511	1	IKECBB	colicin B - Escher	976	585	2	AE3240	chromosome partiti
904	6	1.6	511	2	G90321	hypothetical prote	977	588	2	AC0169	conserved hypotet
905	6	1.6	511	2	T26124	hypothetical prote	978	588	2	I37202	B-CAM protein - hu

979 1.6 589 2 D84530 probable Tail-like
 980 1.6 590 2 A25680 nuclear histone-bi
 981 1.6 591 2 F69901 DNA helicase recQ
 982 1.6 592 2 T13742 hypothetical prote
 983 1.6 593 2 G71301 hypothetical prote
 984 1.6 594 1 A44073 CtkI protein - yea
 985 1.6 594 2 C96638 hypothetical prote
 986 1.6 595 2 F71650 DNA mismatch repai
 987 1.6 596 2 S59944 hydroxymethylgluta
 988 1.6 596 2 E82728 succinate dehydrog
 989 1.6 597 2 S65672 GABA transport pro
 990 1.6 597 2 D89765 hypothetical prote
 991 1.6 598 2 D84242 hypothetical prote
 992 1.6 598 2 B90589 sugar ABC transpor
 993 1.6 601 2 F84979 sulfite reductase
 994 1.6 601 2 R87548 hypothetical prote
 995 1.6 602 2 H97365 DNA helicase XFL38
 996 1.6 602 2 AH2583 ATP-dependent DNA
 997 1.6 603 2 S15074 calpastatin - rat
 998 1.6 603 2 T27901 hypothetical prote
 999 1.6 604 1 S00726 protein kinase A-r
 1000 1.6 605 2 AG0123 probable antigenic

ALIGNMENTS

RESULT 1
 JE0264
 Cyclin I - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 09-Jul-2004
 C:Accession: JE0264
 R:Zhu, X.; Naz, R.K.
 Biochem. Biophys. Res. Commun. 249, 56-60, 1998
 A:Title: Expression of a novel isoform of cyclin I in human testis.
 A:Reference number: JE0264; MUID:98381026; PMID:9705831
 A:Accession: JE0264
 A:Molecule type: mRNA
 A:Residues: 1-178 <ZHU>
 A:Cross-references: UNIPROT:Q14094
 C:Comment: This protein may have a physiological role in spermatogenesis and/or human sp

Query Match 27.3%; Score 103; DB 2; Length 178;
 Best Local Similarity 100.0%; Pred. No. 7.3e-97;
 Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 FLATVKAHPKYLSCIAISCFFLAAKTVEEDRIIPVLKVLARDSPCGSSSSIIIRMERIIL 135
 |||||
 Db 76 FLATVKAHPKYLSCIAISCFFLAAKTVEEDRIIPVLKVLARDSPCGSSSSIIIRMERIIL 135
 |||||

Qy 136 DKLAWDLHTATPLDPLHLHFHAIIVSTRPQLLFSLPKLSPSQHL 178
 |||||
 Db 136 DKLAWDLHTATPLDPLHLHFHAIIVSTRPQLLFSLPKLSPSQHL 178
 |||||

RESULT 2
 A87341
 sensory box/GGDEF family protein [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C:Accession: A87341
 R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of Caulobacter crescentus.
 A:Reference number: A87249; MUID:21173698; PMID:11259647
 A:Accession: A87341
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-842 <STO>
 A:Cross-references: UNIPROT:Q9AA66; GB:AE005673; NID:gl13421971; PIDN:AAK22725.1; GSPDB:G

C:Genetics:
 A:Gene: CC0740

Query Match 2.1%; Score 8; DB 2; Length 842;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 69 ASSLLDRF 76
 |||||
 Db 40 ASSLLDRF 47

RESULT 3
 G84429
 hypothetical protein At2g01840 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: G84429
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; L
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
 euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: G84429
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1715 <STO>
 A:Cross-references: UNIPROT:Q9SIS9; GB:AE002093; NID:g4522005; PIDN:AAD21778.1; GSPDB:GNI
 C:Genetics:
 A:Gene: At2g01840
 A:Map position: 2

Query Match 2.1%; Score 8; DB 2; Length 1715;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 303 TAAFYHHL 310
 |||||
 Db 814 TAAFYHHL 821

RESULT 4
 D82732
 hypothetical protein XF1033 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: D82732
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82732
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-61 <SIM>
 A:Cross-references: UNIPROT:Q9PEJ5; GB:AE003940; NID:g9105966; PIDN:AAF8384
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Laig
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.
 as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to Genbank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 , F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation

C;Genetics:
A;Gene: XF1033

Query Match 1.9%; Score 7; DB 2; Length 61;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Gaps 0;

Qy 154 FHATAVS 160
|||||
Db 15 FHATAVS 21

RESULT 5

G84490
Hypothetical protein At2g10340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: G84490
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.D.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: G84490
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-85 <STO>
A;Cross-references: UNIPROT:Q9SHW3; GB:AE002093; NID:G4733979; PIDN:AAD28661.1; GSPDB:GN
C;Genetics:
A;Gene: At2g10340
A;Map position: 2

Query Match 1.9%; Score 7; DB 2; Length 85;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 LAATKVE 103
|||||
Db 34 LAATKVE 40

RESULT 6

D71534
Hypothetical protein CT271 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: D71534
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tra
A;Reference number: A71570; MUID:99000809; PMID:9784136
A;Accession: D71534
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <ARN>
A;Cross-references: UNIPROT:O84273; GB:AE001300; NID:G3328682; PIDN:AAC6786
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: CT271

Query Match 1.9%; Score 7; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
|||||
Db 54 LSFLLK 60

RESULT 7

CS1692
conserved hypothetical protein TC0543 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: C81692
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: C81692
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-95 <TET>
A;Cross-references: UNIPROT:Q9PKC3; GB:AE002322; GB:AE002160; NID:G7190572; PIDN:AAF3938
A;Experimental source: strain Nigg (MoPn)
C;Genetics:
A;Gene: TC0543

Query Match 1.9%; Score 7; DB 2; Length 95;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
|||||
Db 54 LSFLLK 60

RESULT 8

D44221
orf4 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACNPNV
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D44221
R;Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
Virology 191, 1003-1008, 1992
A;Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californi
VP8 of rotavirus.
A;Reference number: A44221; MUID:93079853; PMID:1333113
A;Accession: D44221
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <BRA>
A;Cross-references: UNIPROT:P41424; GB:S52569
C;Superfamily: ACNPNV hypothetical protein 19

Query Match 1.9%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 LSFLLK 18
|||||
Db 100 LSFLLK 106

RESULT 9

C72852
AcOrf-19 protein - Autographa californica nuclear polyhedrosis virus
C;Species: Autographa californica nuclear polyhedrosis virus, ACNPNV
A;Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C;Accession: C72852
R;Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
Virology 202, 586-605, 1994
A;Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
A;Reference number: A72850; MUID:94303173; PMID:8030224
A;Accession: C72852
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <AYR>
A;Cross-references: UNIPROT:P41424; GB:L22858; NID:G510708; PIDN:AAA66649.1; PID:G559088
C;Genetics:
A;Gene: AcOrf-19
C;Superfamily: ACNPNV hypothetical protein 19

Mon Feb 14 12:27:13 2005

```

Query Match      1.9%; Score 7; DB 2; Length 108;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSFLEK 18
    |||||
Db 100 LSFLEK 106

RESULT 10
T41765
AcMNPV orf19 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41765
R:Goni, S.; Majima, K.; Maeda, S.
J.Gen. Virol. 80, 1323-1337, 1999
A>Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z22020; MUID:99281911; PMID:10355780
A;Accession: T41765
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A;Residues: 1-110 <KAM>
A;Cross-references: UNIPROT:O92387; EMBL:L33180; NID:g3745835; PIDN:AAC63694.1; PID:g374
A;Experimental source: isolate T3
C:Genetics:
A;Note: Orf 11
C:Superfamily: AcMNPV hypothetical protein 19

Query Match      1.9%; Score 7; DB 2; Length 110;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 LSFLEK 18
    |||||
Db 102 LSFLEK 108

RESULT 11
G83746
hypothetical protein BH0775 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: G83746
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83746
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-113 <STO>
A;Cross-references: UNIPROT:O9KES4; GB:AP001509; GB:BA000004; NID:g10173176; PIDN:BA04
A;Experimental source: strain C-125
C:Genetics:
A;Gene: BH0775

Query Match      1.9%; Score 7; DB 2; Length 113;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 164 QLLFSLP 170
    |||||
Db 77 QLLFSLP 83

RESULT 12
H87603
transcription regulator, ArsrR family [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C:Accession: H87603

```

```

R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A>Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87603
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-123 <STO>
A;Cross-references: UNIPROT:Q9A4H0; GB:AE005673; NID:gl3424478; PIDN:AAK24828.1; GSPDB:G
C;Genetics:
A;Gene: CC2864

Query Match      1.9%; Score 7; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 SQHLAVL 181
    |||||
Db 63 SQHLAVL 69

RESULT 13
B69320
conserved hypothetical protein AF0562 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: B69320
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: B69320
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A;Residues: 1-126 <KLE>
A;Cross-references: UNIPROT:O29691; GB:AE001066; GB:AE000782; NID:g2689389; PIDN:AAB90675

Query Match      1.9%; Score 7; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 367 PCPLPQP 373
    |||||
Db 93 PCPLPQP 99

RESULT 14
AD0633
probable secreted protein STY1158 [imported] - Salmonella enterica subsp. enterica serov
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C:Accession: AD0633
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Comerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AD0633
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-131 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08247.1; PID:g16502294; GSPDB:GN00176
C;Genetics:
A;Gene: STY1158

```

Query Match 1.9%; Score 7; DB 2; Length 131;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 224 ELLOKQAQ 230
|||||
Db 63 ELLOKQAQ 69

RESULT 15
T35544
Probable quinolinate synthetase - Streptomyces coelicolor (fragment)
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 26-May-2000
C;Accession: T35544
R;Seeger, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21581
A;Accession: T35544
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-154 <SEE>
A;Cross-references: EMBL:AL049497; PIDN:CAB39889.1; GSPDB:GN00070; SCOEDB:SC6G10.35
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: SCOEDB:SC6G10.35
C;Superfamily: Helicobacter pylori quinolinate synthetase A

Query Match 1.9%; Score 7; DB 2; Length 154;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 44 QRDEVIQ 50
|||||
Db 70 QRDEVIQ 76

Search completed: February 11, 2005, 03:16:11
Job time : 56.9258 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:19 ; Search time 100.276 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKPFGPLENORLSFLEKAI.....LSRQGHASCPPLQPVSVW 377

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	377	100.0	377	1	CYCI_HUMAN
2	240	63.7	377	2	Q6FHH0
3	90	23.9	377	2	Q99LF2
4	53	14.1	377	2	Q8C7E2
5	51	13.5	377	1	CYCI_MOUSE
6	29	7.7	382	2	Q6DJQ8
7	29	7.7	382	2	Q6P7H3
8	13	3.4	355	2	Q6NUZ7
9	13	3.4	355	2	Q803P0
10	9	2.4	462	2	Q9XFC9
11	8	2.1	227	2	Q83YJ9
12	8	2.1	231	2	Q86FL6
13	8	2.1	332	2	Q6NWA8
14	8	2.1	359	2	Q66I20
15	8	2.1	364	2	Q947Z5
16	8	2.1	374	2	Q899B7
17	8	2.1	379	2	Q8H088
18	8	2.1	379	2	Q87MS1
19	8	2.1	397	2	Q82S78
20	8	2.1	422	2	Q8BGF8
21	8	2.1	600	2	Q6BXL7
22	8	2.1	667	2	Q35267
23	8	2.1	764	2	Q3LRH7
24	8	2.1	842	2	Q9AA66
25	8	2.1	959	2	Q6BQ15
26	8	2.1	1325	1	RIP2_CHICK
27	8	2.1	1715	2	Q9SIS9
28	7	1.9	59	2	Q81R19
29	7	1.9	61	2	Q3PEJ5
30	7	1.9	62	2	Q69X51
31	7	1.9	62	2	Q82BE3

32	7	1.9	70	2	Q6HZR5	Q6hzr5 bacillus an
33	7	1.9	70	2	Q63CB1	Q63cb1 bacillus ce
34	7	1.9	70	2	Q6HJS3	Q6hjs3 bacillus th
35	7	1.9	72	2	Q81EE1	Q81ee1 bacillus ce
36	7	1.9	85	2	Q9SHW3	Q9shw3 arabisdopsis
37	7	1.9	87	2	Q6MCG8	Q6mcg8 parachlamyd
38	7	1.9	91	2	Q8MSZ0	Q8msz0 drosophila
39	7	1.9	91	2	Q6T3A6	Q6t3a6 gallus gall
40	7	1.9	95	2	Q84273	Q84273 chlamydia t
41	7	1.9	95	2	Q9PKC3	Q9pkc3 chlamydia m
42	7	1.9	101	2	Q72J99	Q72j99 thermus the
43	7	1.9	102	2	Q8EXR4	Q8ekr4 shewanella
44	7	1.9	104	2	Q98M40	Q98m40 rhizobium l
45	7	1.9	104	2	Q89WR9	Q89wr9 bradyrhizob
46	7	1.9	105	2	Q739L5	Q739l5 bacillus ce
47	7	1.9	105	2	Q9D9I8	Q9d9i8 mus musculu
48	7	1.9	106	2	Q7Q3J4	Q7q3j4 anopheles g
49	7	1.9	108	1	Y019 NPVAC	P41424 autographa
50	7	1.9	108	2	Q8B9K9	Q8b9m9 rachiplusia
51	7	1.9	110	2	Q92387	Q92387 bombyx mori
52	7	1.9	111	2	Q83XW4	Q83xw4 flavobacter
53	7	1.9	113	2	Q9KES4	Q9kes4 bacillus ha
54	7	1.9	114	2	Q6XFG9	Q6xfg9 nectarinia
55	7	1.9	115	2	Q6XFH2	Q6xfh2 nectarinia
56	7	1.9	116	2	Q6XFP4	Q6xff4 nectarinia
57	7	1.9	116	2	Q6XFP5	Q6xff5 nectarinia
58	7	1.9	116	2	Q6XFP6	Q6xff6 nectarinia
59	7	1.9	116	2	Q6XFP8	Q6xff8 nectarinia
60	7	1.9	116	2	Q6XFG1	Q6xfg1 nectarinia
61	7	1.9	116	2	Q6XFG4	Q6xfg4 nectarinia
62	7	1.9	116	2	Q6XFG7	Q6xfg7 nectarinia
63	7	1.9	116	2	Q6XFG8	Q6xfg8 nectarinia
64	7	1.9	116	2	Q6XPH0	Q6xfh0 nectarinia
65	7	1.9	116	2	Q6XPH3	Q6xfh3 nectarinia
66	7	1.9	116	2	Q6XPH5	Q6xfh5 nectarinia
67	7	1.9	122	2	Q6ZV25	Q6zv25 homo sapien
68	7	1.9	123	2	Q7UG57	Q7ug57 rhodopirell
69	7	1.9	123	2	Q9A4H0	Q9a4h0 caulobacter
70	7	1.9	126	1	Y562 ARCFU	Q29691 archaeoglob
71	7	1.9	127	2	Q706Q4	Q706q4 pseudomonas
72	7	1.9	127	2	Q727X0	Q727x0 desulfovibr
73	7	1.9	128	2	Q9BQK6	Q9bqk6 homo sapien
74	7	1.9	129	2	Q67MF9	Q67mf9 symbiobacte
75	7	1.9	131	2	Q6K4C4	Q6k4c4 oryza sativ
76	7	1.9	131	2	Q8Z7N6	Q8z7n6 salmomella
77	7	1.9	131	2	Q8ZQ37	Q8zq37 salmonella
78	7	1.9	133	2	Q8FR22	Q8fr22 corynebacte
79	7	1.9	135	2	Q9W219	Q9w219 drosophila
80	7	1.9	136	2	Q7VJM3	Q7vjm3 helicobacte
81	7	1.9	155	1	RS7_XYLFA	Q9pa89 xyella fas
82	7	1.9	155	1	RS7_XYLFT	Q87a34 xyella fas
83	7	1.9	158	2	Q6K2D2	Q6k2d2 oryza sativ
84	7	1.9	159	2	Q67JP3	Q67jp3 symbiobacte
85	7	1.9	187	2	Q8P165	Q8pi65 xanthomonas
86	7	1.9	188	2	Q9PDQ1	Q9pdqi xyella fas
87	7	1.9	189	2	Q8YR22	Q8yt22 anaena sp
88	7	1.9	194	2	Q67T42	Q67t42 symbiobacte
89	7	1.9	195	2	Q9N2Z8	Q9n2z8 caenorhabdi
90	7	1.9	196	2	Q6DUU8	Q6duu8 medicago sa
91	7	1.9	197	2	Q86S66	Q86s66 caenorhabdi
92	7	1.9	197	2	Q945D3	Q945d3 castanea sa
93	7	1.9	198	2	Q7PLD2	Q7pld2 drosophila
94	7	1.9	198	2	Q9MM84	Q9mm84 darevskia l
95	7	1.9	198	2	Q9MM85	Q9mm85 darevskia b
96	7	1.9	198	2	Q9MM89	Q9mm89 darevskia s
97	7	1.9	198	2	Q8PIG7	Q8pig7 xanthomonas
98	7	1.9	199	2	Q9Z3X5	Q9z3x5 ralstonia s
99	7	1.9	199	2	Q7NIF3	Q7nif3 gloeobacter
100	7	1.9	207	2	Q72U42	Q72u42 leptospira
101	7	1.9	207	2	Q8F103	Q8f103 leptospira
102	7	1.9	208	2	Q92QA2	Q92qa2 rhizobium m
103	7	1.9	209	2	Q7QY62	Q7qy62 giardia lam
104	7	1.9	216	2	Q9FY89	Q9fy89 arabisdopsis

105 Q6ER63 oryza sativ 1.9 217 2 Q6ER63
106 Q9zh6 homo sapien 7 1.9 218 1 11F7_HUMAN
107 Q7ru00 7 1.9 219 2 Q7RU00
108 Q9nv10 7 1.9 220 2 Q9NV10
109 Q8ih84 7 1.9 225 2 Q8IH84
110 Q84183 7 1.9 230 2 Q84183
111 Q9PKL3 7 1.9 230 2 Q9PKL3
112 Q6KiH0 7 1.9 231 2 Q6KIH0
113 Q73DK8 7 1.9 234 2 Q73DK8
114 Q835P8 7 1.9 235 2 Q835P8
115 Q17116 7 1.9 237 2 Q17116
116 Q9P723 7 1.9 238 1 YHRE_SCHPO
117 Q9R6N1 7 1.9 238 2 Q9R6N1
118 Q65M11 7 1.9 238 2 Q65M11
119 Q8u685 7 1.9 238 2 Q8U685
120 Q82N00 7 1.9 239 2 Q82N00
121 Q40670 7 1.9 242 2 Q40670
122 Q8XP16 7 1.9 242 2 Q8XP16
123 Q7V465 7 1.9 247 2 Q7V465
124 PCNA_PYRFU 7 1.9 249 1 PCNA_PYRFU
125 Q8K5K7 7 1.9 254 2 Q8K5K7
126 Q829U0 7 1.9 256 2 Q829U0
127 Q75FF8 7 1.9 257 2 Q75FF8
128 Q8EXB2 7 1.9 257 2 Q8EXB2
129 Q7WX06 7 1.9 261 2 Q7WX06
130 Q72UY5 7 1.9 263 2 Q72UY5
131 Q8EZY8 7 1.9 263 2 Q8EZY8
132 Q84LD1 7 1.9 265 2 Q84LD1
133 Q48980 7 1.9 269 2 Q48980
134 Q8G3K6 7 1.9 269 2 Q8G3K6
135 Q81L10 7 1.9 273 2 Q81L10
136 Q8AYG9 7 1.9 273 2 Q8AYG9
137 Q75LH4 7 1.9 278 2 Q75LH4
138 KSGA_SYNY3 7 1.9 284 1 KSGA_SYNY3
139 Q99XQ2 7 1.9 285 2 Q99XQ2
140 Q69780 7 1.9 287 2 Q69780
141 Q8KLH5 7 1.9 287 2 Q8KLH5
142 Q9KXV2 7 1.9 291 2 Q9KXV2
143 Q7BAA7 7 1.9 292 2 Q7BAA7
144 Q8U0U5 7 1.9 294 2 Q8U0U5
145 Q85J80 7 1.9 294 2 Q85J80
146 Q87PG9 7 1.9 297 2 Q87PG9
147 Q6NY19 7 1.9 299 2 Q6NY19
148 Q6TEN3 7 1.9 299 2 Q6TEN3
149 Q7ZTX1 7 1.9 299 2 Q7ZTX1
150 Q538G9 7 1.9 301 2 Q538G9
151 Q8F8Q3 7 1.9 301 2 Q8F8Q3
152 Q9H7A0 7 1.9 303 2 Q9H7A0
153 Q20844 7 1.9 307 2 Q20844
154 Q8SYJ3 7 1.9 310 2 Q8SYJ3
155 Q8EN25 7 1.9 313 2 Q8EN25
156 Q65MX4 7 1.9 315 2 Q65MX4
157 Q9ILR1 7 1.9 315 2 Q9ILR1
158 Q62YB6 7 1.9 319 2 Q62YB6
159 Q7VAR7 7 1.9 322 2 Q7VAR7
160 Q9XTY9 7 1.9 324 2 Q9XTY9
161 Q57599 7 1.9 327 2 Q57599
162 Q9UG89 7 1.9 330 2 Q9UG89
163 Q8S6X8 7 1.9 330 2 Q8S6X8
164 Q7XG76 7 1.9 330 2 Q7XG76
165 Q7XPU3 7 1.9 330 2 Q7XPU3
166 Q7VGA5 7 1.9 330 2 Q7VGA5
167 Q6NZ31 7 1.9 330 2 Q6NZ31
168 Q8ZSP5 7 1.9 333 2 Q8ZSP5
169 Q8BTR1 7 1.9 335 2 Q8BTR1
170 Q6BTR2 7 1.9 336 2 Q6BTR2
171 ADH1_ZYMMO 7 1.9 337 1 ADH1_ZYMMO
172 Q6Y8J4 7 1.9 337 2 Q6Y8J4
173 Q6T7F5 7 1.9 338 2 Q6T7F5
174 Q9D4G2 7 1.9 338 2 Q9D4G2
175 Q82FE3 7 1.9 344 2 Q82FE3
176 Q63XJ6 7 1.9 344 2 Q63XJ6
177 Q75H97 7 1.9 345 2 Q75H97

178 Q6ER63 7 1.9 350 2 Q6ER63
179 Q8ng15 7 1.9 350 2 Q8NG15
180 Q96LB5 7 1.9 350 2 Q96LB5
181 Q9H2P8 7 1.9 350 2 Q9H2P8
182 Q8ih84 7 1.9 350 2 Q8IH84
183 Q84183 7 1.9 353 2 Q84183
184 Q9PKL3 7 1.9 355 2 Q9PKL3
185 Q6KiH0 7 1.9 357 2 Q6KIH0
186 Q73DK8 7 1.9 357 2 Q73DK8
187 Q835P8 7 1.9 358 2 Q835P8
188 Q17116 7 1.9 362 2 Q17116
189 Q9P723 7 1.9 363 1 PIT1_CHICK
190 Q9R6N1 7 1.9 364 2 Q9R6N1
191 Q65M11 7 1.9 364 2 Q65M11
192 Q8u685 7 1.9 364 2 Q8U685
193 Q82N00 7 1.9 365 2 Q82N00
194 Q40670 7 1.9 367 2 Q40670
195 Q8XP16 7 1.9 369 1 IDH2_YEAST
196 Q7V465 7 1.9 369 2 Q7V465
197 Q73947 7 1.9 370 2 Q73947
198 Q8K5K7 7 1.9 372 2 Q8K5K7
199 Q829U0 7 1.9 375 2 Q829U0
200 Q75FF8 7 1.9 379 2 Q75FF8
201 Q8EXB2 7 1.9 379 2 Q8EXB2
202 Q7WX06 7 1.9 379 2 Q7WX06
203 Q72UY5 7 1.9 380 2 Q72UY5
204 Q8EZY8 7 1.9 380 2 Q8EZY8
205 Q84LD1 7 1.9 383 2 Q84LD1
206 Q48980 7 1.9 384 2 Q48980
207 Q8G3K6 7 1.9 385 1 Y421_METTH
208 Q81L10 7 1.9 386 2 Q81L10
209 Q8AYG9 7 1.9 390 2 Q8AYG9
210 Q75LH4 7 1.9 390 2 Q75LH4
211 P2666 7 1.9 390 2 P2666
212 Q99XQ2 7 1.9 391 2 Q99XQ2
213 Q69780 7 1.9 393 2 Q69780
214 Q8KLH5 7 1.9 394 1 NADA_CORGL
215 Q9KXV2 7 1.9 394 1 NADA_STRCO
216 Q7BAA7 7 1.9 396 1 Q7BAA7
217 Q8U0U5 7 1.9 403 1 Q8U0U5
218 Q85J80 7 1.9 404 1 Q85J80
219 Q87PG9 7 1.9 404 2 Q87PG9
220 Q6NY19 7 1.9 409 2 Q6NY19
221 Q6TEN3 7 1.9 409 2 Q6TEN3
222 Q7ZTX1 7 1.9 410 1 Q7ZTX1
223 Q538G9 7 1.9 410 1 Q538G9
224 Q8F8Q3 7 1.9 415 2 Q8F8Q3
225 Q9H7A0 7 1.9 417 2 Q9H7A0
226 Q20844 7 1.9 420 2 Q20844
227 Q8SYJ3 7 1.9 420 2 Q8SYJ3
228 Q8EN25 7 1.9 421 2 Q8EN25
229 Q65MX4 7 1.9 421 2 Q65MX4
230 Q9ILR1 7 1.9 423 2 Q9ILR1
231 Q62YB6 7 1.9 423 2 Q62YB6
232 Q7VAR7 7 1.9 423 2 Q7VAR7
233 Q9XTY9 7 1.9 427 2 Q9XTY9
234 Q57599 7 1.9 436 1 Q57599
235 Q9UG89 7 1.9 436 1 Q9UG89
236 Q8S6X8 7 1.9 436 1 Q8S6X8
237 Q7XG76 7 1.9 436 1 Q7XG76
238 Q7XPU3 7 1.9 436 1 Q7XPU3
239 Q7VGA5 7 1.9 437 1 Q7VGA5
240 Q6NZ31 7 1.9 437 1 Q6NZ31
241 Q8ZSP5 7 1.9 439 1 Q8ZSP5
242 Q8BTR1 7 1.9 439 1 Q8BTR1
243 Q6BTR2 7 1.9 443 2 Q6BTR2
244 P20368 7 1.9 444 1 P20368
245 Q6Y8J4 7 1.9 446 1 Q6Y8J4
246 Q6T7F5 7 1.9 446 2 Q6T7F5
247 Q9D4G2 7 1.9 449 2 Q9D4G2
248 Q82FE3 7 1.9 453 2 Q82FE3
249 Q63XJ6 7 1.9 453 2 Q63XJ6
250 Q75H97 7 1.9 462 2 Q75H97

Q8nbp3 homo sapien
Q8ng15 homo sapien
Q96lb5 homo sapien
Q9h2p8 homo sapien
Q8ih84 arabidopsis
Q8xh8 arabidopsis
Q8h143 arabidopsis
Q75fz4 leptospira
Q8ey06 leptospira
Q85fq3 bacillus li
Q7qwb6 giardia lam
Q9ygl7 gallus gall
Q6mzm8 homo sapien
Q6n000 homo sapien
Q66i82 brachydanio
Q8d5ul erwinia car
Q8rc12 mycobacteri
P28211 saccharomyc
Q6cbz6 yarrowia li
Q91xb8 arabidopsis
Q91ua0 arabidopsis
Q8zt42 arabidopsis
Q8le24 arabidopsis
Q9maa1 arabidopsis
Q93hp3 streptomyce
Q8hm13 carapus ber
Q64hw4 oncorhynchu
Q8et70 oceanobacil
Q8tgu1 brachydanio
Q26521 methanobact
Q13901 schizosacch
Q75aw7 ashbya goss
Q8ix24 homo sapien
Q8mmf3 bdellovibri
Q9c0f1 homo sapien
Q91x79 arabidopsis
Q8nr10 corynebacte
Q9f364 streptomyce
P31211 rattus norv
CBG_RAT
P22324 cavia porce
P19496 methanobact
Q9fvq6 arabidopsis
Q82156 streptomyce
Q9ewg3 streptomyce
P22323 cavia porce
Q82al6 streptomyce
Q7r2j2 giardia lam
Q6rc07 mycobacteri
Q7xsj6 oryza sativ
Q9ssz5 oryza sativ
Q64bh3 uncultured
Q6cne2 kluyveromyc
Q9sw36 arabidopsis
Q8gp73 streptococc
Q9ah92 streptococc
Q9x0v7 thermotoga
Q9x0v7 thermotoga
Q8prg5 methanosarc
Q8tr28 methanosarc
Q50538 methanosarc
Q8tjc2 methanosarc
Q8c639 mus musculu
Q9c431 methanosarc
Q63673 rattus norv
Q89g6 taxus chine
Q8m6f0 taxus cupei
Q8em10 oceanobacil
Q84461 chlamydia t
P19541 saccharomyc
Q88pr9 pseudomonas
Q6v0k4 mycobacteri
Q8av91 oryza sativ
Q61561 mus musculu
Q6fjy2 candida gla

251	7	1.9	471	2	Q90577	Q90577 gallus gall	324	7	1.9	845	2	Q80Z08	Q80Z08 mus musculu
252	7	1.9	475	2	Q8KU28	Q8KU28 rhodococcus	325	7	1.9	852	2	Q35192	Q35192 mus musculu
253	7	1.9	477	2	Q7SBD7	Q7SBD7 neurospora	326	7	1.9	858	2	O18466	O18466 hiruod medi
254	7	1.9	482	2	Q72GE4	Q72GE4 thermus the	327	7	1.9	867	2	Q8IKI7	Q8IKI7 plasmodium
255	7	1.9	488	2	Q6CBY3	Q6CBY3 yarrowia li	328	7	1.9	869	2	Q9C744	Q9C744 arabidopsis
256	7	1.9	491	2	Q6CWP9	Q6CWP9 kluyveromyc	329	7	1.9	873	2	Q9I8E6	Q9I8E6 fugu rubrip
257	7	1.9	495	2	Q683K1	Q683K1 arabidopsis	330	7	1.9	876	1	EGL1_SACFI	P22506 saccharomyc
258	7	1.9	495	2	Q8GW36	Q8GW36 arabidopsis	331	7	1.9	885	1	FLSB_XANAC	Q8P80 xanthomonas
259	7	1.9	513	1	T160_HUMAN	Q92993 homo sapien	332	7	1.9	886	1	PLSB_XANCP	Q8P363 xanthomonas
260	7	1.9	513	1	T160_MOUSE	Q8CHK4 mus musculu	333	7	1.9	895	2	Q8CON3	Q8CON3 mus musculu
261	7	1.9	516	2	Q8C415	Q8C415 mus musculu	334	7	1.9	895	2	Q65CL1	Q65CL1 mus musculu
262	7	1.9	517	1	STG1_HUMAN	Q9N88 homo sapien	335	7	1.9	934	2	Q7UET9	Q7UET9 rhodopirell
263	7	1.9	517	1	STG1_MOUSE	Q925E1 mus musculu	336	7	1.9	951	2	Q9FVX8	Q9FVX8 oryza sativ
264	7	1.9	517	2	Q8NW66	Q8NW66 mus musculu	337	7	1.9	952	2	Q8X5G8	Q8X5G8 escherichia
265	7	1.9	519	2	Q7QSC6	Q7QSC6 giardia lam	338	7	1.9	960	2	Q7N7N1	Q7N7N1 photorhabdu
266	7	1.9	520	2	Q6H4F1	Q6H4F1 oryza sativ	339	7	1.9	969	2	Q8X3L3	Q8X3L3 escherichia
267	7	1.9	533	2	Q6Y3A2	Q6Y3A2 hordeum vul	340	7	1.9	982	2	Q7PGV3	Q7PGV3 anopheles g
268	7	1.9	544	1	BRH1_DROME	Q24255 drosophila	341	7	1.9	982	2	Q84VD8	Q84VD8 oryza sativ
269	7	1.9	544	2	Q7RXQ4	Q7RXQ4 neurospora	342	7	1.9	989	2	Q8NJU8	Q8NJU8 pichia past
270	7	1.9	550	2	Q97D46	Q97D46 clostridium	343	7	1.9	990	1	K6P1_PICPA	Q82448 pichia past
271	7	1.9	550	2	Q35270	Q35270 rattus norv	344	7	1.9	996	2	Q9S112	Q9S112 arabidopsis
272	7	1.9	556	2	Q9VFG2	Q9VFG2 drosophila	345	7	1.9	1006	2	Q9U360	Q9U360 caenorhabdi
273	7	1.9	560	2	Q14520	Q14520 homo sapien	346	7	1.9	1008	2	Q8H8Y7	Q8H8Y7 oryza sativ
274	7	1.9	570	2	Q8EJA7	Q8EJA7 shewanella	347	7	1.9	1011	2	Q7PIC1	Q7PIC1 anopheles g
275	7	1.9	573	2	Q9YDG3	Q9YDG3 aeropyrum p	348	7	1.9	1015	2	Q6ZQH7	Q6ZQH7 mus musculu
276	7	1.9	574	2	Q9VT95	Q9VT95 drosophila	349	7	1.9	1026	2	Q7AEP0	Q7AEP0 escherichia
277	7	1.9	592	2	Q90W59	Q90W59 brachydanio	350	7	1.9	1026	2	Q8X299	Q8X299 escherichia
278	7	1.9	593	2	Q98SM8	Q98SM8 brachydanio	351	7	1.9	1026	2	Q8XEJ2	Q8XEJ2 escherichia
279	7	1.9	593	2	Q8T6B7	Q8T6B7 dictyosteli	352	7	1.9	1035	2	Q6QI79	Q6QI79 rattus norv
280	7	1.9	594	1	NU5M_HIPAM	Q9ZZV1 hippopotamu	353	7	1.9	1045	1	SPS_BETVU	Q49031 beta vulgar
281	7	1.9	599	1	CAP4_ARATH	Q98A65 arabidopsis	354	7	1.9	1061	2	Q7R334	Q7R334 plasmodium
282	7	1.9	602	2	Q9UWT3	Q9UWT3 candida alb	355	7	1.9	1069	2	Q9JT46	Q9JT46 neisseria m
283	7	1.9	605	1	YS73_GEOSL	P61404 geobacter s	356	7	1.9	1080	2	Q8XAH7	Q8XAH7 escherichia
284	7	1.9	606	2	Q68GDO	Q68GDO bubalus bub	357	7	1.9	1080	2	Q6H9T7	Q6H9T7 phage phi 4
285	7	1.9	608	2	Q8SS67	Q8SS67 encephalito	358	7	1.9	1085	2	O53720	O53720 mycobacteri
286	7	1.9	611	1	CAP3_ARATH	Q8GX47 arabidopsis	359	7	1.9	1085	2	Q7U243	Q7U243 mycobacteri
287	7	1.9	633	1	RPOC_CYACA	O18897 cyanidium c	360	7	1.9	1092	2	Q7D9W9	Q7D9W9 mycobacteri
288	7	1.9	634	2	Q6FRC2	Q6FRC2 candida gla	361	7	1.9	1102	2	Q89D08	Q89D08 rhodobacter
289	7	1.9	635	2	Q8MKM9	Q8MKM9 drosophila	362	7	1.9	1117	2	Q6C316	Q6C316 yarrowia li
290	7	1.9	639	2	Q9SGH6	Q9SGH6 arabidopsis	363	7	1.9	1125	2	Q9VLE6	Q9VLE6 drosophila
291	7	1.9	663	2	Q9NV65	Q9NV65 homo sapien	364	7	1.9	1133	2	Q6MKG4	Q6MKG4 bdellovibri
292	7	1.9	668	2	Q8C0N1	Q8C0N1 mus musculu	365	7	1.9	1165	2	Q72TU4	Q72TU4 leptospira
293	7	1.9	670	2	Q81762	Q81762 arabidopsis	366	7	1.9	1185	2	Q8FIC9	Q8FIC9 leptospira
294	7	1.9	685	1	STM1_MOUSE	P70302 mus musculu	367	7	1.9	1187	2	Q8K0C0	Q8K0C0 mus musculu
295	7	1.9	685	2	Q8K1E1	Q8K1E1 mus musculu	368	7	1.9	1190	2	Q9HS95	Q9HS95 halobacteri
296	7	1.9	689	2	Q9FWE0	Q9FWE0 arabidopsis	369	7	1.9	1216	1	AEGP_RAT	Q63191 rattus norv
297	7	1.9	691	2	Q80YB4	Q80YB4 mus musculu	370	7	1.9	1221	2	Q9BIW9	Q9BIW9 caenorhabdi
298	7	1.9	695	2	Q35272	Q35272 rattus norv	371	7	1.9	1221	2	Q9N5Z3	Q9N5Z3 caenorhabdi
299	7	1.9	695	2	Q80X11	Q80X11 mus musculu	372	7	1.9	1228	1	MRN1_HUMAN	Q13201 homo sapien
300	7	1.9	696	2	Q7PV95	Q7PV95 anopheles g	373	7	1.9	1228	2	Q6P3T8	Q6P3T8 homo sapien
301	7	1.9	696	2	Q8JKI5	Q8JKI5 heliothis z	374	7	1.9	1265	2	Q9MIT3	Q9MIT3 arabidopsis
302	7	1.9	697	2	Q8I3Q9	Q8I3Q9 plasmodium	375	7	1.9	1389	2	Q6WG27	Q6WG27 mycobacteri
303	7	1.9	699	2	Q8BMX6	Q8BMX6 mus musculu	376	7	1.9	1402	2	Q96668	Q96668 dictyosteli
304	7	1.9	709	2	Q49733	Q49733 arabidopsis	377	7	1.9	1411	2	Q8JKS5	Q8JKS5 heliothis z
305	7	1.9	723	2	Q8EVP3	Q8EVP3 mycoplasma	378	7	1.9	1443	2	Q80TN2	Q80TN2 mus musculu
306	7	1.9	723	2	Q35193	Q35193 mus musculu	379	7	1.9	1452	2	Q6WG26	Q6WG26 mycobacteri
307	7	1.9	730	2	Q64760	Q64760 arabidopsis	380	7	1.9	1534	2	Q7PIC2	Q7PIC2 anopheles g
308	7	1.9	733	2	Q6T1W9	Q6T1W9 aneurinibac	381	7	1.9	1554	2	Q8KZL5	Q8KZL5 streptococc
309	7	1.9	737	2	Q7F9L4	Q7F9L4 oryza sativ	382	7	1.9	1557	2	Q7PX40	Q7PX40 anopheles g
310	7	1.9	743	1	COG8_CAEEL	Q44502 caenorhabdi	383	7	1.9	1605	2	Q89ZN3	Q89ZN3 bacteroides
311	7	1.9	746	2	Q9D230	Q9D230 mus musculu	384	7	1.9	1748	2	Q6CYG5	Q6CYG5 kluyveromyc
312	7	1.9	758	2	Q9I2M9	Q9I2M9 pseudomonas	385	7	1.9	1818	2	Q8EVP1	Q8EVP1 mycoplasma
313	7	1.9	770	2	Q8YMK4	Q8YMK4 anabaena sp	386	7	1.9	1840	2	Q9HED6	Q9HED6 neurospora
314	7	1.9	789	2	Q39548	Q39548 cucurbita m	387	7	1.9	1920	2	Q94ZJ8	Q94ZJ8 oryza sativ
315	7	1.9	797	2	Q9QWK0	Q9QWK0 rattus norv	388	7	1.9	1928	2	Q6VZT3	Q6VZT3 canarypox v
316	7	1.9	802	2	Q35271	Q35271 rattus norv	389	7	1.9	1964	2	Q8SMQ7	Q8SMQ7 loligo peal
317	7	1.9	804	2	Q35202	Q35202 mus musculu	390	7	1.9	2153	2	Q6LFD0	Q6LFD0 plasmodium
318	7	1.9	807	2	Q8ZLJ2	Q8ZLJ2 salmoneilla	391	7	1.9	2410	2	Q6MZA5	Q6MZA5 mycobacteri
319	7	1.9	822	2	Q7KUX2	Q7KUX2 drosophila	392	7	1.9	2474	2	Q6RT24	Q6RT24 mus musculu
320	7	1.9	823	2	Q6SJRO	Q6SJRO arabidopsis	393	7	1.9	3298	2	Q9VB11	Q9VB11 drosophila
321	7	1.9	823	2	Q6PD00	Q6PD00 mus musculu	394	7	1.9	4315	2	Q6RKJ3	Q6RKJ3 botrytis ci
322	7	1.9	826	2	Q80XK5	Q80XK5 mus musculu	395	7	1.9	5020	2	Q8E9W3	Q8E9W3 shewanella
323	7	1.9	841	2	Q92RX8	Q92RX8 rhizobium m	396	7	1.9	7756	2	Q70LM5	Q70LM5 bacillus br

397 1-9 14130 2 Q6MZ72 O6mz72 mycobacteri
398 1-9 16990 2 Q6MZA4 O6mza4 mycobacteri
399 1-9 13 Q47607 Q47607 escherichia
400 1-9 31 Q81G64 Q81g64 bacillus ce
401 1-9 36 Q8DWG4 Q8dwg4 streptococc
402 1-9 39 Q6BR23 Q6br23 debaryomyce
403 1-9 42 Q81NB8 Q81nb8 bacillus an
404 1-9 41 Q9LE12 Q9le12 equisetum s
405 1-9 42 Q9EW7 Q9ew7 streptomyc
406 1-9 45 Q81F15 Q81f15 trypanosoma
407 1-9 53 1 LHA2 RHOAC P35090 rhodopsu
408 1-9 53 Q8DUB8 Q8dub8 streptococc
409 1-9 56 Q76N70 Q76n70 glycine max
410 1-9 58 Q8S5W8 Q8s5w8 oryza sativ
411 1-9 59 Q72ZA6 Q72za6 bacillus ce
412 1-9 59 Q8IKW0 Q8ikw0 bacillus an
413 1-9 60 Q52650 Q52650 rhodopsu
414 1-9 60 Q52652 Q52652 rhodopsu
415 1-9 60 Q8X4F9 Q8x4f9 escherichia
416 1-9 61 Q98A74 Q98a74 rhizobium l
417 1-9 61 Q8G115 Q8g115 brucella su
418 1-9 62 Q93IL5 Q93il5 thermus the
419 1-9 62 Q6AXY5 Q6axy5 rattus norv
420 1-9 63 Q94CJ7 Q94cj7 arabidopsis
421 1-9 63 Q65QW3 Q65qw3 manheimia
422 1-9 64 Q7PA35 Q7pa35 rickettsia
423 1-9 64 Q92G32 Q92g32 rickettsia
424 1-9 65 1 RPR DROME Q24475 drosophila
425 1-9 65 Q82AP8 Q82ap8 streptomyc
426 1-9 66 Q81S33 Q81s33 bacillus ce
427 1-9 66 Q8DVA6 Q8dva6 streptococc
428 1-9 66 Q8QIA5 Q8qia5 hepatitis c
429 1-9 66 Q91JF9 Q91jf9 hepatitis c
430 1-9 67 Q10735 Q10735 sus scrofa
431 1-9 67 Q8HSB6 Q8hsb6 bacillus an
432 1-9 67 Q633G7 Q633g7 bacillus ce
433 1-9 67 Q817C9 Q817c9 bacillus ce
434 1-9 67 Q6HC00 Q6hcq0 bacillus th
435 1-9 67 Q6V5X9 Q6v5x9 human immun
436 1-9 68 Q8VAR4 Q8var4 white spot
437 1-9 68 Q913B6 Q913b6 white spot
438 1-9 69 Q9FLN2 Q9fln2 arabidopsis
439 1-9 69 Q71109 Q71109 bovine aden
440 1-9 70 1 MEL POLHE P59261 polistes he
441 1-9 70 Q97S32 Q97s32 streptococc
442 1-9 70 Q6AIW6 Q6aiw6 desulfatole
443 1-9 71 Q82950 Q82950 bacillus su
444 1-9 71 Q80XY2 Q80xy2 mus musculu
445 1-9 72 Q81F00 Q81f00 trypanosoma
446 1-9 72 Q7MQA0 Q7mqao vibrio vuln
447 1-9 73 1 YAL3 CANBF Q7vqv2 candidatus
448 1-9 74 Q9UZE1 Q9uzel pyrococcus
449 1-9 74 Q8W261 Q8w261 arabidopsis
450 1-9 75 Q8Y180 Q8y180 raietonia s
451 1-9 76 Q93T61 Q93t61 corynebacte
452 1-9 78 Q7VAB7 Q7vab7 prochloroco
453 1-9 78 Q878T6 Q878t6 streptococc
454 1-9 79 Q8GMD6 Q8gmd6 cucurbit ye
455 1-9 79 Q808I4 Q808i4 cucurbit ye
456 1-9 80 Q14820 Q14820 homo sapien
457 1-9 80 Q6JHS2 Q6jhs2 vibrio fisc
458 1-9 81 Q18915 Q18915 bos taurus
459 1-9 81 Q8HYZ3 Q8hyz3 bos taurus
460 1-9 81 Q93RZ1 Q93rz1 streptomyc
461 1-9 81 Q8QL41 Q8ql41 sulfolobus
462 1-9 82 Q7Q348 Q7q348 anopheles g
463 1-9 82 Q7QG02 Q7qg02 anopheles g
464 1-9 83 Q82FW9 Q82fw9 streptomyc
465 1-9 83 Q7TM54 Q7tm54 uncultured
466 1-9 83 Q8BCV7 Q8bcv7 mirafiori l
467 1-9 84 Q7CFY7 Q7cfy7 anopheles g
468 1-9 84 Q88SL5 Q88sl5 lactobacilli
469 1-9 84 Q9RKJ8 Q9rkj8 streptomyc

470 1-6 6 Q8V9P8 2 Q8V9P8 84 2 1-6 6
471 1-6 6 1 YME3 THIFE 85 1 1-6 6
472 1-6 6 Q38673 85 2 1-6 6
473 1-6 6 Q8SOW2 85 2 1-6 6
474 1-6 6 Q728E9 85 2 1-6 6
475 1-6 6 Q80844 85 2 1-6 6
476 1-6 6 Q8BN41 86 2 1-6 6
477 1-6 6 Q9YY98 86 2 1-6 6
478 1-6 6 1 BC10 BOVIN 87 1 1-6 6
479 1-6 6 1 BC10_FELCA 87 1 1-6 6
480 1-6 6 1 BC10_MOUSE 87 1 1-6 6
481 1-6 6 1 BC10_RAT 87 1 1-6 6
482 1-6 6 Q90WT7 87 2 1-6 6
483 1-6 6 Q91B61 87 2 1-6 6
484 1-6 6 Q938K9 88 2 1-6 6
485 1-6 6 Q79XU2 88 2 1-6 6
486 1-6 6 Q8K780 88 2 1-6 6
487 1-6 6 Q8POA0 88 2 1-6 6
488 1-6 6 Q9A0P0 88 2 1-6 6
489 1-6 6 Q734G6 88 2 1-6 6
490 1-6 6 Q7CWM8 88 2 1-6 6
491 1-6 6 Q7CN26 88 2 1-6 6
492 1-6 6 Q82VJ2 88 2 1-6 6
493 1-6 6 Q8DQT3 88 2 1-6 6
494 1-6 6 P89505 88 2 1-6 6
495 1-6 6 Q8WZ11 90 2 1-6 6
496 1-6 6 Q7MQJ9 90 2 1-6 6
497 1-6 6 Q7TXY0 90 2 1-6 6
498 1-6 6 Q638E6 90 2 1-6 6
499 1-6 6 Q81AX4 91 2 1-6 6
500 1-6 6 Q81YQ9 91 2 1-6 6
501 1-6 6 Q83BK5 91 2 1-6 6
502 1-6 6 Q83G02 91 2 1-6 6
503 1-6 6 1 PHAF RHIME 92 1 1-6 6
504 1-6 6 Q658A0 92 2 1-6 6
505 1-6 6 Q6J2A9 92 2 1-6 6
506 1-6 6 Q7U6Q0 92 2 1-6 6
507 1-6 6 Q9RJB2 92 2 1-6 6
508 1-6 6 Q7TW51 92 2 1-6 6
509 1-6 6 Q9W5C8 92 2 1-6 6
510 1-6 6 P74056 93 2 1-6 6
511 1-6 6 Q6N625 93 2 1-6 6
512 1-6 6 Q8TFH9 93 2 1-6 6
513 1-6 6 Q8TFH9 93 2 1-6 6
514 1-6 6 Q6N7U0 94 2 1-6 6
515 1-6 6 Q7U8T3 94 2 1-6 6
516 1-6 6 Q7TL25 94 2 1-6 6
517 1-6 6 Q9NZW7 95 2 1-6 6
518 1-6 6 Q9ZE65 95 2 1-6 6
519 1-6 6 Q89IL0 95 2 1-6 6
520 1-6 6 Q84029 95 2 1-6 6
521 1-6 6 Q61692 96 2 1-6 6
522 1-6 6 Q6AY00 96 2 1-6 6
523 1-6 6 Q7RDA7 97 2 1-6 6
524 1-6 6 Q9LJP9 97 2 1-6 6
525 1-6 6 Q7X2K5 97 2 1-6 6
526 1-6 6 Q8UFY0 97 2 1-6 6
527 1-6 6 Q97Q06 97 2 1-6 6
528 1-6 6 Q9H4C2 98 2 1-6 6
529 1-6 6 Q644Y9 98 2 1-6 6
530 1-6 6 Q6K2J0 98 2 1-6 6
531 1-6 6 Q7X2K3 98 2 1-6 6
532 1-6 6 Q98JTB 98 2 1-6 6
533 1-6 6 Q8U8A0 98 2 1-6 6
534 1-6 6 1 RL36 CANAL 99 1 1-6 6
535 1-6 6 Q6ERT5 99 2 1-6 6
536 1-6 6 Q7X2K7 99 2 1-6 6
537 1-6 6 Q7N4G6 99 2 1-6 6
538 1-6 6 Q6I743 99 2 1-6 6
539 1-6 6 100 2 O58804 100 2 1-6 6
540 1-6 6 Q6TBQ7 100 2 1-6 6
541 1-6 6 Q67UW1 101 2 1-6 6
542 1-6 6 Q67T43 101 2 1-6 6

Q8v9p8 sulfolobus
P22304 thiobacillu
Q38673 bacterioph
Q8sow2 oryza sativ
Q728e9 desulfovibr
Q80844 hantavirus
Q8bn41 mus musculu
Q9yy98 human immun
P62954 bos taurus
P62953 felis silve
P62952 homo sapien
P62951 mus musculu
P62950 rattus norv
Q90wt7 carassius a
Q91b61 brachydanio
Q938k9 temperate p
Q79xu2 streptococc
Q8k780 streptococc
Q8pua0 streptococc
Q9a0p0 streptococc
Q734g6 bacillus ce
Q7cmw8 streptococc
Q7cn26 streptococc
Q82vj2 nitrosomona
Q8dqt3 streptococc
P89505 saccharomyc
Q8wz11 homo sapien
Q7mqj9 vibrio vuln
Q7txy0 mycobacteri
Q638e6 bacillus ce
Q81ax4 bacillus ce
Q81yq9 bacillus an
Q83bk5 coxiella th
Q6hg02 bacillus th
Q52983 rhizobium m
Q658a0 oryza sativ
Q6j2a9 pseudomonas
Q7u6q0 synecococc
Q9rjb2 streptomyc
Q7tm51 uncultured
Q9w5c8 drosophila
P74056 rhynchocyst
Q6n625 rhodopsu
Q8tfh9 schizosacch
Q6n7u0 rhodopsu
Q7u8t3 synecococc
Q7tl25 uncultured
Q9nzw7 homo sapien
Q9ze65 carnobacter
Q89il0 bradyrhizob
Q84029 influenza a
Q61692 drosophila
Q6ay00 rattus norv
Q7rda7 plasmodium
Q9ljp9 arabidopsis
Q7x2k5 helicobacte
Q8ufy0 agrobacteri
Q97qg6 streptococc
Q9h4c2 homo sapien
Q644y9 eurycea bis
Q8k2j0 oryza sativ
Q7x2k3 helicobacte
Q98jtb rhizobium l
Q8u8a0 agrobacteri
P47834 candida alb
Q6ert5 oryza sativ
Q7x2k7 helicobacte
Q7n4g6 photorhabdu
Q58804 pyrococcus
Q6tbq7 stellier sea
Q67uw1 oryza sativ
Q67t43 symbiobacte

543	6	1.6	101	2	Q72D05	Q72d05 desulfovibr	616	2	Q84060	Q84060 influenza a
544	6	1.6	101	2	Q9CT33	Q9ct33 mus musculu	617	1	YG4U_YEAST	P53308 saccharomyc
545	6	1.6	102	2	Q6I114	Q6i114 drosophila	618	2	Q74MW7	Q74mw7 nanoarchaeu
546	6	1.6	102	2	Q746T6	Q746t6 geobacter s	619	2	Q7RY92	Q7ry92 neurospora
547	6	1.6	102	2	Q8C2B7	Q8c2b7 mus musculu	620	2	Q8L3S7	Q8l3s7 arabidopsis
548	6	1.6	102	2	Q9D8U9	Q9d8u9 m mus muscu	621	2	Q9SLC8	Q9slc8 arabidopsis
549	6	1.6	102	2	Q6Y8W2	Q6y8w2 human immun	622	2	Q72C35	Q72c35 desulfovibr
550	6	1.6	103	2	Q8Z7S8	Q8z7s8 oryza sativ	623	2	Q83R32	Q83r32 shigella fl
551	6	1.6	103	2	Q8KK27	Q8kk27 proteus vul	624	2	Q9ANL7	Q9anl7 bradyrhizob
552	6	1.6	103	2	Q6D912	Q6d912 erwinia car	625	1	HV44_MOUSE	P01820 mus musculu
553	6	1.6	103	2	Q07664	Q07664 influenza a	626	2	Q8ZV94	Q8zv94 pyrobaculum
554	6	1.6	103	2	Q07665	Q07665 influenza a	627	2	P87272	P87272 saccharomyc
555	6	1.6	103	2	Q5LED5	Q5led5 influenza a	628	2	Q6XFP0	Q6xfp0 nectarinia
556	6	1.6	103	2	Q9YVP9	Q9yvp9 melanoplus	629	2	Q6ES28	Q6es28 oryza sativ
557	6	1.6	104	1	RL24_PSEAB	Q9hwe6 pseudomonas	630	2	Q8VTC5	Q8vts5 helicobacte
558	6	1.6	104	1	RL24_PSEPK	Q88qm4 pseudomonas	631	2	Q8YKB1	Q8ykb1 anabaena sp
559	6	1.6	104	1	RL24_PSSSM	Q889w0 pseudomonas	632	2	Q9RWK4	Q9rww4 deinococcus
560	6	1.6	104	2	Q9YGE2	Q9yge2 aeropyrum p	633	2	HV45_MOUSE	P01821 mus musculu
561	6	1.6	104	2	Q8NV76	Q8nv76 staphylococ	634	2	Q9XZE8	Q9xze8 oxytricha t
562	6	1.6	104	2	Q72XS2	Q72xs2 bacillus ce	635	2	Q6XFE4	Q6xfe4 nectarinia
563	6	1.6	104	2	Q815G2	Q815g2 bacillus ce	636	2	Q6XFE5	Q6xfe5 nectarinia
564	6	1.6	104	2	Q81X21	Q81x21 bacillus an	637	2	Q6XFE7	Q6xfe7 nectarinia
565	6	1.6	105	2	Q96YV4	Q96yv4 sulfobolus	638	2	Q6XFE9	Q6xfe9 nectarinia
566	6	1.6	105	2	Q44813	Q44813 caenorhabdi	639	2	Q6XFX0	Q6xfx0 nectarinia
567	6	1.6	105	2	Q7M0S1	Q7m0s1 myxococcus	640	2	Q6XFX2	Q6xfx2 nectarinia
568	6	1.6	106	2	Q8X3P5	Q8x3p5 escherichia	641	2	Q6XFX5	Q6xfx5 nectarinia
569	6	1.6	107	2	Q6YV07	Q6yv07 oryza sativ	642	2	Q6XFX9	Q6xfx9 nectarinia
570	6	1.6	107	2	Q6HQV5	Q6hqv5 bacillus an	643	2	Q6XFY0	Q6xfy0 nectarinia
571	6	1.6	107	2	Q631F8	Q631f8 bacillus ce	644	2	Q6XFY1	Q6xfy1 nectarinia
572	6	1.6	107	2	Q6HB93	Q6hb93 bacillus th	645	2	Q8SB17	Q8sb17 oryza sativ
573	6	1.6	107	2	Q7LZ26	Q7lzz6 influenza a	646	2	Q9LGI1	Q9lgi1 oryza sativ
574	6	1.6	108	2	Q9H2R1	Q9h2r1 homo sapien	647	2	Q67R66	Q67r66 symbiobacte
575	6	1.6	109	1	ATPL_UREPA	Q9pro8 ureaplasma	648	1	RL18_BUCAK	P46182 buchnera ap
576	6	1.6	109	1	Y4J7_METAC	Q8tip5 methanosaar	649	2	Q8LEM9	Q8lem9 arabidopsis
577	6	1.6	109	2	Q6PR10	Q6pr10 xanthomonas	650	2	Q9ZTH7	Q9zth7 physalis ci
578	6	1.6	109	2	Q6F792	Q6f792 acinetobact	651	2	Q65SD3	Q65sd3 oryza sativ
579	6	1.6	109	2	Q81246	Q81246 hepatitis c	652	2	Q6H088	Q6h088 fremyella d
580	6	1.6	109	2	Q81300	Q81300 hepatitis c	653	2	Q8XY03	Q8xy03 raietonia s
581	6	1.6	109	2	Q81482	Q81482 hepatitis c	654	2	Q8Y802	Q8y802 listeria mo
582	6	1.6	110	2	Q95SE7	Q95se7 drosophila	655	2	Q720W6	Q720w6 listeria mo
583	6	1.6	110	2	Q7D4T5	Q7d4t5 mycobacteri	656	2	HIS3_RHOSH	Q3158 rhodobacter
584	6	1.6	110	2	Q7NVA5	Q7nva5 chronobacte	657	2	Q9ME52	Q9me92 oenothera h
585	6	1.6	110	2	Q831I9	Q831i9 shigella fl	658	2	Q9L3V9	Q9l3v9 bacillus ci
586	6	1.6	110	2	Q808E5	Q808e5 hepatitis c	659	2	Q63105	Q63105 rattus norv
587	6	1.6	110	2	Q808B6	Q808e6 hepatitis c	660	2	Q7YVG8	Q7yvg8 trypanosoma
588	6	1.6	110	2	Q808E7	Q808e7 hepatitis c	661	2	Q9A7K6	Q9a7k6 caulobacter
589	6	1.6	111	1	Y518_METTH	Q26618 methanobact	662	2	RL22_SYNY3	P73315 synechocyst
590	6	1.6	111	2	Q6DY61	Q6dy61 nectarinia	663	2	Q01445	Q01445 caenorhabdi
591	6	1.6	111	2	Q6DY62	Q6dy62 nectarinia.	664	2	Q815P1	Q815p1 bacillus ce
592	6	1.6	111	2	Q6DY64	Q6dy64 nectarinia	665	2	Q99NG4	Q99ng4 mus musculu
593	6	1.6	111	2	Q6DY65	Q6dy65 nectarinia	666	2	Q8K3C1	Q8k3c1 mus musculu
594	6	1.6	111	2	Q6DY66	Q6dy66 nectarinia	667	2	Q66897	Q66897 four corner
595	6	1.6	111	2	Q6DY98	Q6dy98 nectarinia	668	2	Q87WR7	Q87wr7 pseudomonas
596	6	1.6	111	2	Q6DYA1	Q6dyal nectarinia	669	2	Q9Z749	Q9z749 chlamydia p
597	6	1.6	111	2	Q6DYA2	Q6dy2 nectarinia	670	2	Q6ARF8	Q6arf8 desulfotale
598	6	1.6	111	2	Q6DYA5	Q6dya5 nectarinia	671	2	Q8B5J6	Q8b5j5 dengue viru
599	6	1.6	111	2	Q8LKE8	Q8lke8 malus domes	672	2	Q8B5J7	Q8b5j6 dengue viru
600	6	1.6	111	2	Q9SNR9	Q9snr9 oryza sativ	673	2	Q8B5J7	Q8b5j7 dengue viru
601	6	1.6	111	2	Q07804	Q07804 mycobacteri	674	2	Q8B5J8	Q8b5j8 dengue viru
602	6	1.6	111	2	Q8MI86	Q8mie6 bdellovibri	675	2	Q8B5J9	Q8b5j9 dengue viru
603	6	1.6	111	2	Q735D6	Q735d6 bacillus ce	676	2	Q8B5K0	Q8b5k0 dengue viru
604	6	1.6	111	2	Q7TV14	Q7tv14 mycobacteri	677	2	Q8B5K1	Q8b5k1 dengue viru
605	6	1.6	111	2	Q82QM5	Q82qm5 streptomyce	678	2	Q8B5K2	Q8b5k2 dengue viru
606	6	1.6	112	2	Q75JB5	Q75jb5 dictyosteli	679	2	Q8B5K3	Q8b5k3 dengue viru
607	6	1.6	112	2	Q81672	Q81672 hepatitis c	680	2	Q8B5K4	Q8b5k4 dengue viru
608	6	1.6	113	1	ASG1_MOUSE	Q82407 mus musculu	681	2	Q8B5K5	Q8b5k5 dengue viru
609	6	1.6	113	2	Q9Y9K8	Q9y9k8 aeropyrum p	682	2	Q8B5K6	Q8b5k6 dengue viru
610	6	1.6	113	2	Q9JZP9	Q9jzp9 neisseria m	683	2	Q8B5K7	Q8b5k7 dengue viru
611	6	1.6	113	2	Q71179	Q71179 hepatitis c	684	2	Q8B5K8	Q8b5k8 dengue viru
612	6	1.6	113	2	Q80N59	Q80n59 hepatitis c	685	2	Q8B5K9	Q8b5k9 dengue viru
613	6	1.6	113	2	Q80NA2	Q80na2 hepatitis c	686	2	Q8B5L0	Q8b5l0 dengue viru
614	6	1.6	113	2	Q80NA3	Q80na3 hepatitis c	687	2	Q8B5L1	Q8b5l1 dengue viru
615	6	1.6	113	2	Q84030	Q84030 influenza a	688	2	Q8B5L2	Q8b5l2 dengue viru

689	6	1.6	123	2	Q6IAD3	Q6iad3 homo sapien	762	6	1.6	139	2	Q9AK85	Q9ak85 streptomyc
690	6	1.6	123	2	Q9NXX1	Q9nxx1 homo sapien	763	6	1.6	139	2	Q9YWL0	Q9ywl0 melanoplus
691	6	1.6	123	2	Q8VPC3	Q8vpc3 micrococ	764	6	1.6	140	2	Q756H3	Q756h3 ashbya goss
692	6	1.6	123	2	Q8L242	Q8l242 streptomyc	765	6	1.6	140	2	Q716E1	Q716e1 bacterioph
693	6	1.6	123	2	Q7T9V0	Q7t9v0 adoxophyes	766	6	1.6	140	2	Q9ARP0	Q9arp0 oryza sativ
694	6	1.6	123	2	Q86997	Q86997 sugarcane b	767	6	1.6	140	2	Q68252	Q68252 hepatitis c
695	6	1.6	124	1	ZWIA_HUMAN	Zwia human	768	6	1.6	141	1	USPA_PASMU	Q9c1e9 pasteurella
696	6	1.6	124	2	Q8U6H5	Q8u6h5 agrobacteri	769	6	1.6	141	2	Q8YPI81	Q8ypi81 anopheles g
697	6	1.6	124	2	Q8LJR5	Q8ljr5 photobacter	770	6	1.6	141	2	Q8Y2R3	Q8y2r3 ralstonia s
698	6	1.6	125	2	Q8A2N6	Q8a2n6 caulobacter	771	6	1.6	141	2	Q81G1	Q81g1 rhizobium l
699	6	1.6	126	2	Q8ZU12	Q8zu12 homo sapien	772	6	1.6	141	2	Q9KSI4	Q9ksi4 vibrio chol
700	6	1.6	126	2	Q9H354	Q9h354 homo sapien	773	6	1.6	142	2	Q7Y262	Q7y262 cyanophage
701	6	1.6	126	2	Q9BE92	Q9be92 macaca fasc	774	6	1.6	142	2	Q7Y481	Q7y481 cyanophage
702	6	1.6	126	2	Q51511	Q51511 pseudomonas	775	6	1.6	142	2	Q7Y4A5	Q7y4a5 cyanophyta h
703	6	1.6	126	2	Q65VH6	Q65vh6 manheimia	776	6	1.6	142	2	Q6J9F4	Q6j9f4 xerophyta h
704	6	1.6	127	2	Q74N98	Q74n98 nanoarchaeu	777	6	1.6	142	2	Q8XJG1	Q8xjg1 clostridium
705	6	1.6	127	2	Q21039	Q21039 dictyosteli	778	6	1.6	142	2	Q87I31	Q87i31 vibrio para
706	6	1.6	127	2	Q6H4P1	Q6h4p1 oryza sativ	779	6	1.6	142	2	Q9CMK2	Q9cmk2 pasteurella
707	6	1.6	128	2	Q6LTT5	Q6lts5 photobacter	780	6	1.6	142	2	Q9Z4W4	Q9z4w4 streptomyc
708	6	1.6	128	1	CRB2_LISIN	Q929t6 listeria in	781	6	1.6	142	2	Q91HJ4	Q91hj4 avian param
709	6	1.6	129	2	Q96ZR1	Q96zr1 sulfolobus	782	6	1.6	143	1	PONA_DICDI	P54660 dictyosteli
710	6	1.6	129	2	Q7UEB1	Q7ueb1 rhodopirell	783	6	1.6	143	1	YIFN_HAEIN	P43936 haemophilus
711	6	1.6	129	2	Q8ZSN3	Q8zsn3 nitrosonoma	784	6	1.6	143	2	Q7QYR8	Q7qyr8 giardia lam
712	6	1.6	129	2	Q91C23	Q91cz3 tt virus. o	785	6	1.6	143	2	Q9BE32	Q9be32 macaca fasc
713	6	1.6	130	2	Q9H4C3	Q9h4c3 homo sapien	786	6	1.6	143	2	Q7Y496	Q7y496 cyanophage
714	6	1.6	130	2	Q7YV79	Q7yvf9 trypanosoma	787	6	1.6	143	2	Q6K222	Q6k222 oryza sativ
715	6	1.6	130	2	Q8SD59	Q8sd59 pseudomonas	788	6	1.6	143	2	Q6Y2G3	Q6y2g3 oryza sativ
716	6	1.6	130	2	Q8K4C6	Q8k4c6 oryza sativ	789	6	1.6	143	2	Q6Y2G3	Q6y2g3 coxiella bu
717	6	1.6	130	2	Q99RE3	Q99re3 staphylococ	790	6	1.6	143	2	Q8RIH6	Q8rih6 mus musculu
718	6	1.6	130	2	Q7A007	Q7a007 staphylococ	791	6	1.6	143	2	Q6U390	Q6u390 human herpe
719	6	1.6	130	2	Q7A3K8	Q7a3k8 staphylococ	792	6	1.6	143	2	Q6U391	Q6u391 human herpe
720	6	1.6	130	2	Q6G614	Q6g614 staphylococ	793	6	1.6	143	2	Q9UYT5	Q9uyn5 pyrococcus
721	6	1.6	130	2	Q6GDV0	Q6gdv0 staphylococ	794	6	1.6	144	2	Q96NC1	Q96nc1 homo sapien
722	6	1.6	131	2	Q970U1	Q970u1 sulfolobus	795	6	1.6	144	2	Q96NC1	Q96nc1 homo sapien
723	6	1.6	131	2	Q8TFH6	Q8tfh6 schizosacch	796	6	1.6	145	1	HINL_HUMAN	Q01804 homo sapien
724	6	1.6	131	2	Q818903	Q818903 caenorhabdi	797	6	1.6	145	2	Q81EB8	Q8ieb8 plasmodium
725	6	1.6	131	2	Q6B7D4	Q6b7d4 legionella	798	6	1.6	145	2	Q8LID3	Q8lid3 streptomyc
726	6	1.6	131	2	Q7UT01	Q7ut01 rhodopirell	799	6	1.6	145	2	Q6H063	Q6h063 fremyella d
727	6	1.6	131	2	Q997Q5	Q997q5 clostridium	800	6	1.6	145	2	Q7AXX9	Q7axx9 salmonella
728	6	1.6	131	2	Q8CZ68	Q8cz68 erwinia car	801	6	1.6	145	2	Q93IQ8	Q93iq8 salmonella
729	6	1.6	132	1	RNPA_MICLU	P21172 micrococ	802	6	1.6	146	2	Q9UKT0	Q9ukt0 homo sapien
730	6	1.6	132	2	Q7OKC0	Q7okc0 gondonia we	803	6	1.6	146	2	Q9UMQ0	Q9umo0 homo sapien
731	6	1.6	132	2	Q835A7	Q835a7 enterococcu	804	6	1.6	146	2	Q6L7I9	Q6l7i9 canis famil
732	6	1.6	132	2	Q83GC1	Q83gc1 tropheryma	805	6	1.6	146	2	Q8GT54	Q8gt54 hordeum vul
733	6	1.6	132	2	Q83HV8	Q83hv8 tropheryma	806	6	1.6	146	2	Q98NF2	Q98nf2 rhizobium l
734	6	1.6	134	2	Q6H4E5	Q6h4e5 oryza sativ	807	6	1.6	146	2	Q98NF2	Q98nf2 bdellovibri
735	6	1.6	134	2	Q6H4G1	Q6h4g1 oryza sativ	808	6	1.6	146	2	Q6MNI1	Q6mni1 bdellovibri
736	6	1.6	134	2	Q44672	Q44672 borrelia af	809	6	1.6	146	2	Q7VFX3	Q7vfx3 helicobacte
737	6	1.6	134	2	Q64UX9	Q64ux9 bacteroides	810	6	1.6	147	2	Q61PW1	Q6ipw1 homo sapien
738	6	1.6	134	2	Q6D168	Q6d168 erwinia un	811	6	1.6	147	2	Q842F2	Q842f2 streptococ
739	6	1.6	134	2	Q99MD4	Q99md4 meriones un	812	6	1.6	147	2	Q8PRM2	Q8prm2 xanthomonas
740	6	1.6	135	1	Y886_METKA	Q8tva6 methanopyru	813	6	1.6	147	2	Q7MP01	Q7mp01 vibrio vuln
741	6	1.6	135	2	Q8PTW9	Q8ptw9 methanosarc	814	6	1.6	147	2	Q87SL6	Q87sl6 vibrio para
742	6	1.6	135	2	Q8ZXQ8	Q8zxq8 pyrobaculum	815	6	1.6	147	2	Q8CPK3	Q8cpk3 staphylococ
743	6	1.6	135	2	Q67LB2	Q67lb2 symbiobacte	816	6	1.6	147	2	Q8DEG3	Q8deg3 vibrio vuln
744	6	1.6	136	2	Q96N35	Q96n35 homo sapien	817	6	1.6	147	2	Q8DKZ9	Q8dkz9 synecococ
745	6	1.6	136	2	Q9H7X8	Q9h7x8 homo sapien	818	6	1.6	147	2	Q8FGK6	Q8fgk6 escherichia
746	6	1.6	136	2	Q6LJB8	Q6ljb8 photobacter	819	6	1.6	147	2	Q8XBA8	Q8xba8 escherichia
747	6	1.6	136	2	Q6NAI8	Q6nai8 rhodospseudo	820	6	1.6	148	2	Q6K2J8	Q6k2j8 oryza sativ
748	6	1.6	136	2	Q7MQ89	Q7mq89 vibrio vuln	821	6	1.6	148	2	Q6B7C0	Q6b7c0 legionella
749	6	1.6	136	2	Q7VX17	Q7vx17 bordetella	822	6	1.6	148	2	Q6B7C1	Q6b7c1 legionella
750	6	1.6	136	2	Q7W7X0	Q7w7x0 bordetella	823	6	1.6	148	2	Q6B7C2	Q6b7c2 legionella
751	6	1.6	136	2	Q7WLB0	Q7wlb0 bordetella	824	6	1.6	148	2	Q6B7C3	Q6b7c3 legionella
752	6	1.6	136	2	Q8DD51	Q8dd51 vibrio vuln	825	6	1.6	148	2	Q6B7C4	Q6b7c4 legionella
753	6	1.6	136	2	Q8JDY2	Q8jdy2 human immun	826	6	1.6	148	2	Q6B7C5	Q6b7c5 legionella
754	6	1.6	138	2	Q9NE26	Q9ne26 leishmania	827	6	1.6	148	2	Q6B7C6	Q6b7c6 legionella
755	6	1.6	138	2	Q8ERQ6	Q8erq6 oceanobacil	828	6	1.6	148	2	Q6B7C7	Q6b7c7 legionella
756	6	1.6	139	1	ARSC_BACHD	Q9k8k8 bacillus ha	829	6	1.6	148	2	Q6B7C8	Q6b7c8 legionella
757	6	1.6	139	2	Q58363	Q58363 pyrococcus	830	6	1.6	148	2	Q6B7C9	Q6b7c9 legionella
758	6	1.6	139	2	Q33304	Q33304 mycobacteri	831	6	1.6	148	2	Q6B7D0	Q6b7d0 legionella
759	6	1.6	139	2	Q87LT8	Q87lt8 vibrio para	832	6	1.6	148	2	Q6B7D1	Q6b7d1 legionella
760	6	1.6	139	2	Q89KM2	Q89km2 bradyrhizob	833	6	1.6	148	2	Q6B7D2	Q6b7d2 legionella
761	6	1.6	139	2	Q8F6L3	Q8f6l3 leptospira	834	6	1.6	148	2	Q6B7D3	Q6b7d3 legionella

835	6	1.6	148	2	Q6B7D5	Q6b7d5 legionella	908	1.6	159	2	Q7PNH2	Q7pnh2 anopheles g
836	6	1.6	148	2	Q6B7D6	Q6b7d6 legionella	909	1.6	159	2	Q72PP4	Q72pp4 leptospira
837	6	1.6	148	2	Q92RW8	Q92rw8 rhizobium m	910	1.6	159	2	Q749V4	Q749v4 geobacter s
838	6	1.6	148	2	Q93246	Q93246 cyprinus ca	911	1.6	159	2	Q7POT7	Q7pot7 chromobacte
839	6	1.6	149	2	Q9LY57	Q9ly57 arabidopsis	912	1.6	159	2	Q8BXD9	Q8bx9 mus muscucu
840	6	1.6	149	2	Q73048	P73048 synechocyst	913	1.6	160	2	Q62357	Q62357 caenorhabdi
841	6	1.6	149	2	Q9JWE1	Q9jwe1 neisseria m	914	1.6	160	2	Q7QA10	Q7qa10 anopheles g
842	6	1.6	149	2	Q9JXJ2	Q9jxj2 neisseria m	915	1.6	160	2	Q8KZ46	Q8kz46 uncultured
843	6	1.6	150	1	RP21 MOUSE	Q8r040 mus musculu	916	1.6	160	2	Q92KK5	Q92kk5 thizobium m
844	6	1.6	150	2	Q9USE0	Q9use0 schizosacch	917	1.6	160	2	Q6ADH9	Q6adh9 leifsonia x
845	6	1.6	150	2	Q8NP75	Q8nf75 homo sapien	918	1.6	160	2	Q8AXA8	Q8axa8 gallus gall
846	6	1.6	150	2	Q48865	Q48865 agrostis st	919	1.6	160	2	Q8AED9	Q8aed9 human immun
847	6	1.6	150	2	Q05989	Q05989 brassica ol	920	1.6	161	2	Q64R54	Q64r54 uncultured
848	6	1.6	150	2	Q8RVJ5	Q8rvj5 pinus pinas	921	1.6	161	2	Q64ED7	Q64ed7 uncultured
849	6	1.6	150	2	Q70AJ3	Q70aj3 triticum ae	922	1.6	161	2	Q92229	Q92229 emericella
850	6	1.6	150	2	Q83299	Q83299 escherichia	923	1.6	161	2	Q96D98	Q96d98 homo sapien
851	6	1.6	150	2	Q832A6	Q832a6 escherichia	924	1.6	161	2	Q6ZQV2	Q6zqv2 homo sapien
852	6	1.6	150	2	Q97HB5	Q97hb5 clostridium	925	1.6	161	2	Q7PS22	Q7ps22 anopheles g
853	6	1.6	150	2	Q89LZ4	Q89lz4 bradyrhizob	926	1.6	161	2	Q69K10	Q69k10 oryza sativ
854	6	1.6	150	2	Q8F1X8	Q8f1x8 escherichia	927	1.6	161	2	Q9D7K2	Q9d7k2 mus musculu
855	6	1.6	151	1	CT78 HUMAN	Q9br46 homo sapien	928	1.6	162	2	Q8SWG5	Q8swg5 encephalito
856	6	1.6	151	2	Q26932	Q26932 methanobact	929	1.6	162	2	Q94X57	Q94x57 dendropoma
857	6	1.6	151	2	Q9H4C4	Q9h4c4 homo sapien	930	1.6	162	2	Q853J5	Q853j5 mycobacteri
858	6	1.6	151	2	Q84W91	Q84w91 arabidopsis	931	1.6	162	2	Q93F91	Q93f91 streptomyce
859	6	1.6	151	2	Q93GC1	Q93gc1 xanthomonas	932	1.6	162	2	Q7P340	Q7p340 fusobacteri
860	6	1.6	152	1	RL30 ARCFU	Q28375 archaeoglob	933	1.6	162	2	Q8RDM2	Q8rdm2 fusobacteri
861	6	1.6	152	1	RL30 METHH	Q26132 methanobact	934	1.6	162	2	Q98L95	Q98l95 thizobium l
862	6	1.6	152	2	Q648R1	Q648r1 uncultured	935	1.6	162	2	Q7VXL2	Q7vxl2 bordetella
863	6	1.6	152	2	Q7VK74	Q7vk74 helicobacte	936	1.6	162	2	Q7W5V5	Q7w5v5 bordetella
864	6	1.6	153	2	Q8PV29	Q8pv29 methanosarc	937	1.6	162	2	Q8FGH4	Q8fgh4 escherichia
865	6	1.6	153	2	Q8TR36	Q8tr36 methanosarc	938	1.6	162	2	Q9X930	Q9x930 streptomyce
866	6	1.6	153	2	Q7SG14	Q7sg14 neurospora	939	1.6	162	2	Q6MDE5	Q6mde5 parachlamyd
867	6	1.6	153	2	Q84J58	Q84j58 oryza sativ	940	1.6	163	2	Q6T9Q5	Q6t9q5 vitis ripar
868	6	1.6	153	2	Q66792	Q66792 aquifex aeo	941	1.6	163	2	Q9STI9	Q9st19 arabidopsis
869	6	1.6	153	2	Q89H71	Q89h71 bradyrhizob	942	1.6	163	2	Q93GK3	Q93gk3 klebsiella
870	6	1.6	153	2	P79919	P79919 xenopus lae	943	1.6	163	2	Q639X1	Q639x1 bacillus ce
871	6	1.6	154	1	RL30 METJA	P54046 methanococc	944	1.6	164	2	Q6J7Y5	Q6j7y5 actinoplane
872	6	1.6	154	1	RL30 METVA	P14035 methanococc	945	1.6	164	2	Q8E221	Q8e221 streptococc
873	6	1.6	154	1	SSRP TREPA	Q83214 treponema p	946	1.6	164	2	Q8EA02	Q8ea02 shewanella
874	6	1.6	154	2	Q61XD2	Q61xd2 methanococc	947	1.6	164	2	Q9CVR8	Q9cvr8 mus musculu
875	6	1.6	154	2	Q6M0J3	Q6m0j3 methanococc	948	1.6	164	2	Q9EP94	Q9ep94 mus musculu
876	6	1.6	154	2	Q8RQ15	Q8rq15 bacillus ce	949	1.6	165	1	FTN2 HARIN	P43708 haemophilus
877	6	1.6	154	2	Q85G82	Q85g82 bacillus li	950	1.6	165	1	YAJ5_SCHPO	P99905 schizosacch
878	6	1.6	154	2	Q73MP4	Q73mp4 treponema d	951	1.6	165	2	Q8HQV4	Q8hqv4 tropidola ef
879	6	1.6	154	2	Q7MIX6	Q7mix6 vibrio vuln	952	1.6	165	2	Q6IWI6	Q6iwi6 escherichia
880	6	1.6	154	2	Q8DAY0	Q8day0 vibrio vuln	953	1.6	165	2	Q97RF8	Q97rf8 streptococc
881	6	1.6	155	1	RL30 PYRAB	Q9vlv6 pyrococcus	954	1.6	165	2	Q87Y87	Q87y87 pseudomonas
882	6	1.6	155	1	RL30 PYRHO	Q59440 pyrococcus	955	1.6	165	2	Q8DQ46	Q8dqa6 streptococc
883	6	1.6	155	2	Q849M4	Q849m4 uncultured	956	1.6	165	2	Q9CMY3	Q9cm3 pasteurella
884	6	1.6	155	2	Q97CN4	Q97cn4 thermoplasma	957	1.6	166	1	Q9YI27	Q9y127 carassius a
885	6	1.6	155	2	Q9HY78	Q9hy78 pyrococcus	958	1.6	166	1	IL3 RAT	P04823 rattus norv
886	6	1.6	155	2	Q7QLU3	Q7qlu3 anopheles g	959	1.6	166	1	SSB MYCPN	P75542 mycoplasma
887	6	1.6	155	2	Q6WH24	Q6wh24 bacterioph	960	1.6	166	2	Q8RAG3	Q8rag3 thermoplasma
888	6	1.6	155	2	Q7Y3W5	Q7y3w5 bacterioph	961	1.6	166	2	Q6D1N1	Q6d1n1 erwinia car
889	6	1.6	155	2	Q72UC3	Q72uc3 leptospira	962	1.6	166	2	Q8V3I5	Q8v3i5 swinepox vi
890	6	1.6	155	2	Q82VX9	Q82vx9 nitrosomona	963	1.6	167	1	PLMP GRIFR	P81054 grifolia fro
891	6	1.6	155	2	Q8F005	Q8f0g5 leptospira	964	1.6	167	1	Y199 MYCGE	P47441 mycoplasma
892	6	1.6	155	2	Q9DH98	Q9dh98 gallid herp	965	1.6	167	1	Y005_BPHP1	P51706 bacterioph
893	6	1.6	156	1	PYR1 METHH	Q26938 methanobact	966	1.6	167	2	Q467I3	Q467i3 bos taurus
894	6	1.6	156	1	SSB1_STRCO	Q9ky19 streptomyce	967	1.6	167	2	Q46753	Q46753 bos taurus
895	6	1.6	156	2	Q7WGR7	Q7wgr7 bordetella	968	1.6	167	2	Q46763	Q46763 bos taurus
896	6	1.6	156	2	Q88E81	Q88e81 pseudomonas	969	1.6	167	2	Q46782	Q46782 bos taurus
897	6	1.6	156	2	Q9D8L9	Q9d8l9 mus musculu	970	1.6	167	2	Q6LBC7	Q6lbc7 oligotropha
898	6	1.6	157	2	Q8TXR0	Q8txr0 methanopyru	971	1.6	168	1	RL10 MYCPU	Q98qel mycoplasma
899	6	1.6	157	2	Q6CHV5	Q6chv5 varrowia li	972	1.6	168	2	Q7EZX8	Q7ezx8 oryza sativ
900	6	1.6	157	2	Q7KRA1	Q7kral drosophila	973	1.6	168	2	Q8VQZ1	Q8vqz1 myxococcus
901	6	1.6	157	2	Q6LS75	Q6ls75 photobacter	974	1.6	168	2	Q98K83	Q98k83 rhizobium l
902	6	1.6	158	1	P1GP HUMAN	P57054 h phosphate	975	1.6	168	2	Q8UCX8	Q8ucx8 agrobacteri
903	6	1.6	158	2	Q57824	Q57824 pyrococcus	976	1.6	168	2	Q8QS78	Q8qs78 pongine her
904	6	1.6	158	2	Q84HN3	Q84hn3 kitaatoapo	977	1.6	169	2	Q84Y41	Q84y41 ranunculus
905	6	1.6	158	2	Q8CTC6	Q8ctc6 rhizobium l	978	1.6	169	2	Q92VT0	Q92vt0 rhizobium m
906	6	1.6	159	2	Q6UY33	Q6uy33 homo sapien	979	1.6	169	2	Q9K962	Q9k962 bacillus ha
907	6	1.6	159	2	Q6ZNY8	Q6zny8 homo sapien	980	1.6	169	2	P97688	P97688 rattus norv

981 Q919p8 brachydanio
 982 Q58033 pyrococcus
 983 Q86u37 homo sapien
 984 Q8h912 homo sapien
 985 Q8uq13 smithiantha
 986 Q72uc4 leptospira
 987 Q8f0q4 leptospira
 988 Q96na0 homo sapien
 989 Q95rf6 drosophila
 990 Q81r45 oryza sativ
 991 Q8xuv7 raistonia s
 992 Q8ner8 corynebacte
 993 Q7nmf7 gloebacter
 994 Q7vbg6 parachloroc
 995 Q6mcs2 parachlamyd
 996 Q6lca0 mus musculu
 997 Q79f75 brevibacter
 998 Q79vg4 corynebacte
 999 Q7uqy7 rhodopirell
 1000 Q8fpx2 corynebacte

ALIGNMENTS

RESULT 1
 CYCIN HUMAN
 ID CYCIN HUMAN STANDARD; PRT; 377 AA.
 AC Q14094;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclin I.
 GN Name=CCNI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Forebrain cortex;
 RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
 RA Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
 RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
 RL Exp. Cell Res. 221:534-542(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
 RA Qiang B.Q.;
 RT "Isolating a new cDNA coding for human cyclin protein.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.; AND VARIANT ILE-207.
 RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrat L.A., Nickerson D.A.;
 RT "NIHES-SNPs, environmental genome project, NIHES RS15478, Department
 of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore I., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-178 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98381026; PubMed=9705891; DOI=10.1006/bbrc.1998.9052;
 RA Zhu X., Naz R.K.;
 RT "Expression of a novel isoform of cyclin I in human testis.";
 RL Biochem. Biophys. Res. Commun. 249:56-60(1998).
 CC -I- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
 skeletal muscle. Lower levels in fetal placenta, lung, kidney and
 pancreas. Also high levels in fetal brain and lower levels in
 fetal lung, liver and kidney. Also abundant in testis and thyroid.
 CC -I- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
 in lung fibroblasts.
 CC -I- SIMILARITY: Belongs to the cyclin family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; D50310; BAA08849.1; -;
 CC EMBL; AY207372; AAO13492.1; -;
 CC EMBL; BC000420; AAH00420.1; -;
 CC EMBL; BC004975; AAH04975.1; -;
 CC EMBL; AF135162; AAF43786.1; -;
 CC PIR; JEO264; JEO264.
 CC H-InvDB; HGNC:1595; CCNI.
 CC GO; GO:0007283; P: spermatogenesis; NAS.
 CC InterPro; IPR006670; Cyclin.
 CC InterPro; IPR011028; Cyclin_like.
 CC InterPro; IPR006671; Cyclin_N.
 CC Pfam; PF00134; Cyclin_N; 1.
 CC SMART; SM00385; CYCLIN; 1.
 CC PROSITE; PS00292; CYCLINS; FALSE_NEG.
 CC Cyclin; Polymorphism.
 KW VARIANT 207 207 V->I (in dbSNP:4252903).
 FT CONFLICT 9 9 N->D (in Ref. 5).
 FT CONFLICT 58 58 Q->R (in Ref. 5).
 FT CONFLICT 75 75 R->G (in Ref. 5).
 SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA74698F6C CRC64;
 Query Match 100.0%; Score 377; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQLSFLLEKAITREAOQWKNVVRKMPNSQNVSPQRDEVIOWLAKLYQFN 60
 DB 1 MKFPGPLENQLSFLLEKAITREAOQWKNVVRKMPNSQNVSPQRDEVIOWLAKLYQFN 60
 QY 61 LYPFTFALASLLDRFLATVKAKHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
 DB 61 LYPFTFALASLLDRFLATVKAKHPKYLSCIAISCFLLAAKTVEDEIPVLKVLARDSFC 120
 QY 121 GCSSEILMERIILDKLNWDLHTATPDLFLHIFAHAVSTRPOLLPLKLSPSQHLAV 180
 DB 121 GCSSEILMERIILDKLNWDLHTATPDLFLHIFAHAVSTRPOLLPLKLSPSQHLAV 180
 QY 181 LTKQLLHCMAQNQLQFGSGMLALANVLEMEKLPDLWLSLTIELLQKQAMDSQLIHCR 240

```
Db 181 LTKQLLHMACNQLLQFRGSLAMLVSEMEKLIIPDWLSLTIELLOQAQMDSSQLHCR 240
Qy 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDPFSDKNSKPEVPV 300
Db 241 ELVAHLSTLQSSPLNSVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDPFSDKNSKPEVPV 300
Qy 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLR 360
Db 301 RGTAAFYHLLPAASGCKQTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLR 360
Qy 361 QEGHASPCCPPLQPVSV 377
Db 361 QEGHASPCCPPLQPVSV 377

RESULT 2
ID Q6FHHO PRELIMINARY; PRT; 377 AA.
AC Q6FHHO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE CCNI protein (Fragment).
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Mkundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schattner R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; CR541783; CAG46582.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
FT NON-TER 377 377
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;

Query Match 63.7%; Score 240; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 2.2e-241;
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 138 LNWDLHTATPLDLFIHFAIAVSTRPQLLSPLKSPSHLAVLTQLLHMACNQLLQF 197
Db 138 LNWDLHTATPLDLFIHFAIAVSTRPQLLSPLKSPSHLAVLTQLLHMACNQLLQF 197
Qy 198 RGSMLAMVSEMEKLIIPDWLSLTIELLOQAQMDSSQLHCRELVHHLSTLQSSPLN 257
Db 198 RGSMLAMVSEMEKLIIPDWLSLTIELLOQAQMDSSQLHCRELVHHLSTLQSSPLN 257
Qy 258 SVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDPFSDKNSKPEVPVGTAAFYHLLPAASGCK 317
Db 258 SVYVYRPLKHTLVCTDKGVFLRLHPSSVPGDPFSDKNSKPEVPVGTAAFYHLLPAASGCK 317
Qy 318 QTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLRSRQEGHASPCCPPLQPVSV 377
Db 318 QTSTKRKVEEMEVDDFDGIGKRLYNEDNVSENVSGVCGTDLRSRQEGHASPCCPPLQPVSV 377

RESULT 3
ID Q99LF2 PRELIMINARY; PRT; 377 AA.
AC Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
```

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RA MEDLINE=22308257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skaleka U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AA03290.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match 23.9%; Score 90; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1e-84;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 IPVLUKLARDFSCSSSEILRMERITLDKLNWDLHTATPLDLFIHFAIAVSTRPQLLF 167
Db 108 IPVLUKLARDFSCSSSEILRMERITLDKLNWDLHTATPLDLFIHFAIAVSTRPQLLF 167
Qy 168 SLPKSPSHLAVLTQLLHMACNQLLQF 197
Db 168 SLPKSPSHLAVLTQLLHMACNQLLQF 197

RESULT 4
ID Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone: C820001G04 product: cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
```


ID AC Q6DJQ8 PRELIMINARY; PRT; 382 AA.
AC Q6DJQ8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cname=cnpi-prov;
DE Cname=cnpi-prov;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OC NCBI_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC075116; AAH75116.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR Cyclin.
KW SMART; SM00385; CYCLIN; 1.
SQ SEQUENCE 382 AA; 42919 MW; E1F28D13AFB42CEA CRC64;
Query Match 7.7%; Score 29; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.2e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 128 LRMERIILDKLNDLHTATPLDPLHIFHA 156
Db 130 LRMERIILDKLNDLHTATPLDPLHIFHA 158
RESULT 7
ID Q6P7H3 PRELIMINARY; PRT; 382 AA.
AC Q6P7H3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MG68660 protein.
DE Name=MG68660;
GN Xenopus laevis (African clawed frog).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC061670; AAH61670.1; -.
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLIN; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 42913 MW; E19D7C5D8FEC626A CRC64;
Query Match 7.7%; Score 29; DB 2; Length 382;
Best Local Similarity 100.0%; Pred. No. 5.2e-21;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 128 LRMERIILDKLNDLHTATPLDPLHIFHA 156
Db 130 LRMERIILDKLNDLHTATPLDPLHIFHA 158
RESULT 8
ID Q6NUZ7 PRELIMINARY; PRT; 355 AA.
AC Q6NUZ7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cyclin I.
DE Name=ccni;
GN Brachydanio rerio (Zebrafish) (Danio rerio).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;

RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Donald M.F., Casavani T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters K.G., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RL	[2]
RP	SEQUENCE FROM N.A.
RP	STRAIN=AB; TISSUE=Whole body;
RC	Strausberg R.;
RC	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
RL	-!- SIMILARITY: Belongs to the cyclin family.
CC	EMBL; BC044400; AAH4400.1; -.
DR	HSSP; P30274; 1VIN.
DR	ZFIN; ZDB-GENE-040426-2898; ccml.
DR	InterPro; IPR006670; Cyclin.
DR	InterPro; IPR011028; Cyclin like.
DR	InterPro; IPR006671; Cyclin_N.
DR	Pfam; PF00134; Cyclin_N; 1.
DR	SMART; SM00385; CYCLIN; 1.
DR	PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW	Cyclin.
QY	SEQUENCE 355 AA; 39517 MW; D2999F2E9812C880 CRC64;
DB	Query Match 3.4%; Score 13; DB 2; Length 355;
	Best Local Similarity 100.0%; Pred. No. 0.00025;
	Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	89 CIAISCFFLAAKT 101
DB	91 CIAISCFFLAAKT 103
RESULT 10	
Q9XFC9	
ID	PRELIMINARY; PRT; 462 AA.
AC	Q9XFC9;
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	No factor binding lectin-nucleotide phosphohydrolase.
GN	Name=LNP;
OS	Dolichos biflorus (Horse gram).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC	eurosid 1; Fabales; Fabaceae; Papilionoideae; Phasoleae; Dolichos.
OX	NCBI_TaxId=3840;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Root;
RX	MEDLINE=99254131; PubMed=10318974; DOI=10.1073/pnas.96.10.5856;
RA	Etzler M.E., Kalsi G., Ewing N.N., Roberts N.J., Day R.B.,
RA	Murphy J.B.;
RT	"A nod factor binding lectin with apyrase activity from legume
RT	roots.";
RL	Proc. Natl. Acad. Sci. U.S.A. 96:5856-5861(1999).
DR	EMBL; AF139807; AAD31285.1; -.
DR	GO; GO:0016787; F:hydrolase activity; IEA.
DR	GO; GO:0005529; F:sugar binding; IEA.
DR	InterPro; IPR000407; GDAL_CD39_NTPase.
DR	Pfam; PF01150; GDAL CD39; 1.
DR	PROSITE; PS01238; GDAL CD39_NTPASE; 1.
KW	Hydrolase; Lectin.


```
SQ SEQUENCE 462 AA; 51183 MW; 59F865A9D4CC44B CRC64;
Query Match 2.4%; Score 9; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 165 LLFSLPKLS 173
Db 20 LLFSLPKLS 28

RESULT 11
Q83YJ9 PRELIMINARY; PRT; 227 AA.
AC Q83YJ9;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Bifidobacterium longum.
OG Plasmid pNAC3.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RW041;
RX PubMed=15003705; DOI=10.1016/j.plasmid.2003.12.003;
RA Corneau N., Emond E., LaPointe G.;
RT "Molecular characterization of three plasmids from Bifidobacterium longum.";
RL Plasmid 51:87-100(2004).
DR EMBL; AY112722; AAC66779.1; -.
DR InterPro; IPR006025; Pept M Zn BS.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 227 AA; 24946 MW; 4DFF32A39C7F9A41 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 297 EYVVRGTA 304
Db 7 EYVVRGTA 14

RESULT 12
Q86F16 PRELIMINARY; PRT; 231 AA.
AC Q86F16;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Clone ZD120 mRNA sequence.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22879925; PubMed=12973349; DOI=10.1038/ng1236;
RA Hu W., Yan Q., Shen D.K., Liu F., Zhu Z.D., Song H.D., Xu X.R.,
RA Wang Z.J., Rong Y.P., Zeng L.C., Wu J., Zhang X., Wang J.J., Xu X.N.,
RA Wang S.Y., Fu G., Zhang X.L., Wang Z.Q., Brindley P.J., McManus D.P.,
RA Xue C.L., Feng Z., Chen Z., Han Z.G.;
RT "Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource.";
RL Nat. Genet. 35:139-147(2003).
DR EMBL; AY221048; AAP06071.1; -.
DR InterPro; IPR002893; ZnF MYND.
DR Pfam; PF01753; ZF-MYND; 1.
DR PROSITE; PS01360; ZF_MYND_1; UNKNOWN_1.
```

```
DR PROSITE; PS0865; ZF_MYND_2; 1.
SQ SEQUENCE 231 AA; 27255 MW; D629D635C439D0FD CRC64;
Query Match 2.1%; Score 8; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 125 SEILRMER 132
Db 4 SEILRMER 11

RESULT 13
Q6NWA8 PRELIMINARY; PRT; 332 AA.
AC Q6NWA8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE SPT3-associated factor 42.
GN Name=STAF42; ORFNames=zgc:85851;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RT TISSUE=Kidney marrow;
RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC067660; AAH67660.1; -.
DR EMBL; AY423005; AAQ97981.1; -.
DR ZFIN; ZDB-GENE-040426-58; zgc:85851.
SQ SEQUENCE 332 AA; 36961 MW; 72E41538D8FDC638 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 332;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 369 PPIQPSV 376
Db 11
```


Db 268 PPLQPVSV 275

RESULT 14

Q661Z0 PRELIMINARY; PRT; 359 AA.

AC Q661Z0, 25-OCT-2004 (TREMELrel. 28, Created)

DT 25-OCT-2004 (TREMELrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)

DE MGC83953 protein.

GN Name=MGC83953;

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative."

RL Dev. Dyn. 225:384-391 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RX PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;

RA Klein S., Gerhard D.S.;

RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the cyclin family.

DR EMBL: BC081135; AAH81135.1; -

DR InterPro: IPR006670; Cyclin.

DR InterPro: IPR011028; Cyclin like.

DR InterPro: IPR006671; Cyclin N.

DR Pfam: PF00134; Cyclin N; 1.

DR SMART: SM00385; CYCLIN; 1.

KW Cyclin.

SQ SEQUENCE 359 AA; 40577 MW; 230B61BE382A6BC7 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 359;

Best Local Similarity 100.0%; Pred. No. 42;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 126 EILRMERI 133

Db 128 EILRMERI 135

RESULT 15

Q947Z5 PRELIMINARY; PRT; 364 AA.

AC Q947Z5;

DT 01-DEC-2001 (TREMELrel. 19, Created)

DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Hypothetical protein OSJNBa0067N01.1.

GN Name=OSJNBa0067N01.1;

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Ehrhartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Nipponbare;

RA de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,

RA Nascimben L., Baker J., Vil M.D., Zutavern T., Santos L., Miller B.,

RA Kuit K., Cunnius D.M., Rodriguez S., Balija V., Shah R., Bahret A.,

RA Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedhia N.,

RA McCombie W.R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

RL EMBL: AC090485; AAK98722.1; -

DR Gramene; Q947Z5; -

DR InterPro: IPR007749; DUF677.

DR Pfam: PF05055; DUF677; 1.

KW Hypothetical protein.

SQ SEQUENCE 364 AA; 39894 MW; 5E0497ACCA3A3F36 CRC64;

Query Match 2.1%; Score 8; DB 2; Length 364;

Best Local Similarity 100.0%; Pred. No. 43;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 262 YRPLKHTL 269

Db 133 YRPLKHTL 140

Search completed: February 11, 2005, 03:18:19

Job time : 145.276 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:00:19 ; Search time 31.8184 Seconds
(without alignments)
884.478 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPPLENQRLSFLEKAI.....LSRQEGHASPDPPIQPVSM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pdp.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	2	US-08-969-106-6
2	1962	100.0	377	3	US-09-054-492B-1
3	1962	100.0	377	4	US-09-338-125-6
4	1309	66.7	254	4	US-09-796-149B-4
5	667	34.0	131	4	US-09-513-999C-5984
6	326.5	16.6	389	4	US-09-949-016-7723
7	271.5	13.8	249	4	US-09-796-149B-3
8	271.5	13.8	295	4	US-09-949-016-6449
9	271.5	13.8	302	4	US-09-949-016-10213
10	265.5	13.5	249	4	US-09-796-149B-7
11	265.5	13.5	253	4	US-09-796-149B-8
12	204	10.4	404	2	US-09-092-770-3
13	204	10.4	404	3	US-09-222-851-3
14	204	10.4	407	4	US-09-949-016-11184
15	202	10.3	403	2	US-09-092-770-4
16	202	10.3	403	3	US-09-222-851-4
17	192	9.8	357	4	US-09-404-296B-10
18	188.5	9.6	373	4	US-09-404-296B-4
19	187.5	9.6	367	3	US-08-895-707-6
20	187.5	9.6	386	3	US-08-895-707-7
21	187.5	9.6	392	1	US-08-706-539-9
22	187.5	9.6	392	3	US-09-027-007-9
23	187.5	9.6	395	1	US-08-485-859-2
24	187.5	9.6	395	1	US-08-706-539-11
25	187.5	9.6	395	1	US-08-522-166-2
26	187.5	9.6	395	1	US-08-488-382A-2
27	187.5	9.6	395	2	US-08-480-912-2

28 187.5 9.6 395 3 US-09-027-007-11 Sequence 11, Appli
29 187.5 9.6 616 3 US-08-895-707-2 Sequence 2, Appli
30 176 9.0 471 4 US-09-538-092-344 Sequence 344, Appl
31 171.5 8.7 436 1 US-08-706-539-10 Sequence 10, Appli
32 171.5 8.7 436 3 US-09-027-007-10 Sequence 10, Appli
33 169 8.6 289 2 US-08-246-361A-4 Sequence 4, Appli
34 169 8.6 289 4 US-09-919-497-54 Sequence 54, Appli
35 169 8.6 289 4 US-09-949-016-6127 Sequence 6127, Ap
36 169 8.6 289 5 PCT-US93-05000-4 Sequence 4, Appli
37 169 8.6 378 4 US-09-949-016-8020 Sequence 8020, Ap
38 168.5 8.6 428 4 US-09-684-169-2 Sequence 2, Appli
39 167 8.5 174 1 US-08-193-977-8 Sequence 8, Appli
40 167 8.5 491 4 US-09-538-092-813 Sequence 813, App
41 166 8.5 236 2 US-08-464-517-22 Sequence 22, Appli
42 166 8.5 236 2 US-08-246-361A-22 Sequence 22, Appli
43 166 8.5 236 3 US-08-463-772-22 Sequence 22, Appli
44 166 8.5 236 5 PCT-US93-05000-22 Sequence 22, Appli
45 166 8.5 309 2 US-08-464-517-4 Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6

Query Match 100.0%; Score 1962; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 1.9e-213;

Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKFPPLENQRLSFLEKAITREAQMKVNRKMPNSQNVSPORDEVIOMLAKLYQFN 60

Db 1 MKFPPLENQRLSFLEKAITREAQMKVNRKMPNSQNVSPORDEVIOMLAKLYQFN 60

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLSPKLSPOHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLSPKLSPOHLAV 180
QY 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQWDSOQLIHC 240
DB 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQWDSOQLIHC 240
QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
DB 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIRKRLYNEDNVSNVSGVCGTDLR 360
DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIRKRLYNEDNVSNVSGVCGTDLR 360
QY 361 QEGHASPCCPPLQPVSV 377
DB 361 QEGHASPCCPPLQPVSV 377

RESULT 2

US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054.492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match 100.0%; Score 1962; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.9e-213;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENORLSFLEKAITREAOQWKVNRKMPNSQNSVPSORDEVIOWLAKLYQFN 60
DB 1 MKFPGPLENORLSFLEKAITREAOQWKVNRKMPNSQNSVPSORDEVIOWLAKLYQFN 60

QY 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
DB 61 LYPETFALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLSPKLSPOHLAV 180
DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLLSPKLSPOHLAV 180
QY 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQWDSOQLIHC 240
DB 181 LTKQLLHCWACNQLLOFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQWDSOQLIHC 240
QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
DB 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDNSKPEVPV 300
QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIRKRLYNEDNVSNVSGVCGTDLR 360
DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMEVDDFYDGIRKRLYNEDNVSNVSGVCGTDLR 360
QY 361 QEGHASPCCPPLQPVSV 377
DB 361 QEGHASPCCPPLQPVSV 377

RESULT 3

US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338.125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969.106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-338-125-6

Query Match 100.0%; Score 1962; DB 4; Length 377;

```

RESULT 4
US-09-796-149B-4
; Sequence 4, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-4

Query Match          66.7%; Score 1309; DB 4; Length 254;
Best Local Similarity 100.0%; Pred. No. 1.1e-139;
Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 VSPQRDEVIQWLAKKYQFNLYPETETALASSLLDRFLATVKAKPKYLSCIAISCFFLAA 99
DB 1 VSPQRDEVIQWLAKKYQFNLYPETETALASSLLDRFLATVKAKPKYLSCIAISCFFLAA 60

QY 100 KTVVEDEIRIPVLKVLARDSPFCGSSSSBILRMERIIIDKLNWDLHTATPLDPLHIFHAIV 159
DB 61 KTVVEDEIRIPVLKVLARDSPFCGSSSSBILRMERIIIDKLNWDLHTATPLDPLHIFHAIV 120

QY 160 STRPQLLFSLPKLSPSOHLAVLTQOLLHCACNQLQFRGSMALAMVSLMEKLIIPDWL 219
DB 121 STRPQLLFSLPKLSPSOHLAVLTQOLLHCACNQLQFRGSMALAMVSLMEKLIIPDWL 180

QY 220 SLRIELQKQAMDSQLIHCRELVAHLSLTQSSPLNSVVVYRPLKHTLVTCDKGVRL 279
DB 181 SLRIELQKQAMDSQLIHCRELVAHLSLTQSSPLNSVVVYRPLKHTLVTCDKGVRL 240

QY 280 HPSSVPGPDFSKDN 293
DB 241 HPSSVPGPDFSKDN 254

```

```
Db 86 IEATPNDNTLCGLRNAKVEDLRSANFGSGCTETVFLAVNILDRLFLAMKVKPKHLS 145
QY 90 IAISCFEFLAAKTVEEDERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLD 149
Db 146 IGVCSELLAARIVEEDCNIPSTHDVIRISQCKTASDIKMEKIISEKHYELEATTALN 205
QY 150 FLHIFHAIIV---STPQLLFSLPKLPSPQHLAVLTKQLLHCWACNQLLOF---RGSMLA 203
Db 206 FLHLYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRILFSKAKPSVLA 252
QY 204 LAMVLEMEKLIIDWLSLTIQLQ-----KAQDSSQLIHCRELVAHHLSTLQS 252
Db 253 LCLINLEVTL-----KSVLELLEILLVKKHSKINDTEFFWRELVSKLAEYSS 302
```

RESULT 7

```
US-09-796-149B-3
; Sequence 3, Application US/09796149B
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149B
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149B-3
```

```
Query Match 13.8%; Score 271.5; DB 4; Length 249;
Best Local Similarity 32.6%; Pred. No. 4.7e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;

QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 6 RDEVKDLSSLTQFFGFDFTETSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 65

QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 66 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVKATTAFQFLQLYYSL----- 118

QY 165 LFLSLP-KLSPSQHLAVLTKQLLHCWACNQLLOFRGSMALAMVLSLEMEKLIIDWLSLTI 223
Db 119 LQENLPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIQAKCVLGTGI 178

QY 224 ELLOK-AQMDSSQLIHCRELVAHHLSTLQS---SLP-----LNSVYVYRPLKHT 268
Db 179 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 234
```

RESULT 8

```
US-09-949-016-6449
; Sequence 6449, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 6449
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6449
```

```
Query Match 13.8%; Score 271.5; DB 4; Length 295;
Best Local Similarity 32.6%; Pred. No. 6.1e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;
```

```
QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 52 RDEVKDLSSLTQFFGFDFTETSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 111

QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 112 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVKATTAFQFLQLYYSL----- 164

QY 165 LFLSLP-KLSPSQHLAVLTKQLLHCWACNQLLOFRGSMALAMVLSLEMEKLIIDWLSLTI 223
Db 165 LQENLPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIQAKCVLGTGI 224

QY 224 ELLOK-AQMDSSQLIHCRELVAHHLSTLQS---SLP-----LNSVYVYRPLKHT 268
Db 225 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 280
```

RESULT 9

```
US-09-949-016-10213
; Sequence 10213, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10213
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10213
```

```
Query Match 13.8%; Score 271.5; DB 4; Length 302;
Best Local Similarity 32.6%; Pred. No. 6.4e-22;
Matches 77; Conservative 51; Mismatches 89; Indels 19; Gaps 5;
```

```
QY 45 RDEVQWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 59 RDEVKDLSSLTQFFGFDFTETSLAVNLLDRFLSKMKVQPKHLGCVGLSCFYLAVKSTEE 118

QY 105 DERIPVLKVLARDSCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 119 ERNVPLATDLIRISQYRFTVSDLMRMEKIVLEKVCWKVKATTAFQFLQLYYSL----- 171

QY 165 LFLSLP-KLSPSQHLAVLTKQLLHCWACNQLLOFRGSMALAMVLSLEMEKLIIDWLSLTI 223
Db 172 LQENLPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIQAKCVLGTGI 231

QY 224 ELLOK-AQMDSSQLIHCRELVAHHLSTLQS---SLP-----LNSVYVYRPLKHT 268
Db 232 ECLQKHSKINGRDLTFWQELVSKCLTEYSSNCKSPNVQKLKWIIVSGRTARQLKHS 287
```

```
RESULT 10
US-09-796-1498-7
; Sequence 7, Application US/097961498
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796.1498
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-1498-7

Query Match      13.5%; Score 265.5; DB 4; Length 249;
Best Local Similarity 32.2%; Pred. No. 2.2e-21;
Matches 76; Conservative 51; Mismatches 90; Indels 19; Gaps 5;

Qy 45 RDEVIQWLAKYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 6 RDEVKDLSLTQFFGDTETFSIAVNLDRFLSKMKVQPKHLCVGLSCFYLAVASIEE 65

Qy 105 DERIPVLKVLARDSCGSSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 66 ERNVPLATDLIRISQYRFTVSDLRMEKIVLEKVCWKVATTAFQFLQLYYSL----- 118

Qy 165 LLFSLP-KLSPSOHLAVITKQLLHMACNQLQFRGSMALAMVLSLEMEKLIPOWLSLTI 223
Db 119 LQENPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIOAKCVELTEGI 178

Qy 224 ELLOK-AQMDSSQLIHCHRELVAAHLSTLOS---SLP-----LNSVVVRPLKHT 268
Db 179 ECLQKSKINGRDLTFWQELVSKCLTEYSSNCKSKPNVQKLKWIIVSGRTARQLKHS 234

RESULT 11
US-09-796-1498-8
; Sequence 8, Application US/097961498
; Patent No. 6825033
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796.1498
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-1498-8

Query Match      13.5%; Score 265.5; DB 4; Length 253;
Best Local Similarity 32.2%; Pred. No. 2.3e-21;
Matches 76; Conservative 51; Mismatches 90; Indels 19; Gaps 5;

Qy 45 RDEVIQWLAKYQFNLYPETFALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEE 104
Db 6 RDEVKDLSLTQFFGDTETFSIAVNLDRFLSKMKVQPKHLCVGLSCFYLAVASIEE 65

Qy 105 DERIPVLKVLARDSCGSSSEILRMERIILDKLNWDLHTATPLDPLHIFHAIIVSTRPQ 164
Db 66 ERNVPLATDLIRISQYRFTVSDLRMAKIVLEKVCWKVATTAFQFLQLYYSL----- 118

Qy 165 LLFSLP-KLSPSOHLAVITKQLLHMACNQLQFRGSMALAMVLSLEMEKLIPOWLSLTI 223
Db 119 LQENPLERRNSINFERLEAQLKACHCRIIFSKAKPSVLALSIIALEIOAKCVELTEGI 178
```

```
Qy 224 ELLOK-AQMDSSQLIHCHRELVAAHLSTLOS---SLP-----LNSVVVRPLKHT 268
Db 179 ECLQKSKINGRDLTFWQELVSKCLTEYSSNCKSKPNVQKLKWIIVSGRTARQLKHS 234

RESULT 12
US-09-092-770-3
; Sequence 3, Application US/09092770
; Patent No. 5973119
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 5973119el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/092.770
; CURRENT FILING DATE: 1997-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-092-770-3

Query Match      10.4%; Score 204; DB 2; Length 404;
Best Local Similarity 27.7%; Pred. No. 4.6e-14;
Matches 75; Conservative 54; Mismatches 96; Indels 46; Gaps 12;

Qy 4 PGPLENORLFLLEKAITREAOQWKNVRKMP-----NQNVSPSQRDEVIQWL 52
Db 99 PSLPLD---LSWGCSK-----EVW-LNNLKESRYVHDKHFEVJHSDLEPQMSIILDLWL 149

Qy 53 AKLYQFNLYPETFALASSLLDRFLATVK-AHPKYLSCIAISCFFLAAKTVVEERIPVL 111
Db 150 LEVCEVYTLHRETFYLAQDFDFRMLTQDKINKMQLIGITSFIASKL--EIIYAPKL 207

Qy 112 KVLARDSFCGSSSEILRMERIILDKLNWDLHTATPLDPLHIFHAI-AVSTRPQLLSLP 170
Db 208 QEFAYVTDGACSBEDILRMELIILKALKWELCPVTIISWNLFLQVDALKDAPKVL--LP 265

Qy 171 KLSPSOHLAVITKQLLHMACNQLQFRGSMALAMVLSLEMEKLIPOWLSL---TIELL 226
Db 266 QY---SQETFIQIQLL-----DCLIAIDSLRFQYRILFAALCHFTSIEVV 310

Qy 227 QKAO-MDSSQLIHCHRELVAAHLSTLOS LPL 256
Db 311 KKASGLEWDSISECVDWMPVFNVKSTSPV 341

RESULT 13
US-09-222-851-3
; Sequence 3, Application US/09222851
; Patent No. 6165753
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: No. 6165753el Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/09/222.851
; CURRENT FILING DATE: 1998-12-30
; EARLIER APPLICATION NUMBER: 09/092.770
; EARLIER FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-222-851-3

Query Match      10.4%; Score 204; DB 3; Length 404;
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:24 ; Search time 100.276 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 1962

Sequence: 1 MKFPGLNORLSFLEKAI.....LSROGHASCPPIQPVSV 377

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1962	100.0	377	1 CYCI_HUMAN	Q14094 homo sapien
2	1952	99.5	377	2 Q6FHH0	Q6fhh0 homo sapien
3	1851	94.3	377	2 Q99LF2	Q99lf2 mus musculus
4	1847	94.1	377	1 CYCI_MOUSE	Q922v9 mus musculus
5	1841	93.8	377	2 Q8C7E2	Q8c7e2 mus musculus
6	1325.5	67.6	382	2 Q8P7H3	Q8p7h3 xenopus lae
7	1297.5	66.1	382	2 Q6DQJ8	Q6dqj8 xenopus tro
8	1013	51.6	355	2 Q6NUZ7	Q6nuz7 brachydanio
9	1011	51.5	355	2 Q803P0	Q803p0 brachydanio
10	746.5	38.0	359	2 Q66I20	Q66i20 xenopus lae
11	502.5	25.6	369	2 Q6ZMN8	Q6zmn8 homo sapien
12	327	16.7	344	1 CGS2_MOUSE	Q08918 mus musculus
13	326.5	16.6	344	1 CGG2_HUMAN	Q16589 homo sapien
14	326.5	16.6	344	2 Q8N5D4	Q8n5d4 homo sapien
15	322.5	16.4	356	2 Q6GM00	Q6gm00 xenopus lae
16	320.5	16.3	349	2 Q6NRC3	Q6nrc3 xenopus lae
17	320	16.3	344	2 Q8C9K5	Q8c9k5 mus musculus
18	318.5	16.2	344	2 Q6FGA7	Q6fga7 homo sapien
19	295.5	15.1	299	2 Q6FYI9	Q6fyi9 brachydanio
20	295.5	15.1	299	2 Q6TEN3	Q6ten3 brachydanio
21	295	15.0	295	2 Q802B8	Q802b8 xenopus lae
22	294.5	15.0	295	2 Q6DIY1	Q6diy1 xenopus tro
23	292.5	14.9	299	2 Q72TX1	Q72tx1 brachydanio
24	273.5	13.9	330	2 Q6NZ31	Q6nzz31 brachydanio
25	271.5	13.8	294	1 CGS1_RAT	F39950 rattus norv
26	271.5	13.8	295	1 CGS1_HUMAN	P51959 homo sapien
27	263.5	13.4	294	1 CGG1_MOUSE	P51945 mus musculus
28	229	11.7	171	2 Q6LC40	Q6lc40 mus musculus
29	212	10.8	397	2 Q7ZYC0	Q7zyc0 xenopus lae
30	206.5	10.5	378	2 Q9XG13	Q9xg13 lycopersico
31	204	10.4	300	2 Q9CSV7	Q9csv7 mus musculus

32	204	10.4	374	2	Q8WUE3	Q8wue3 homo sapien
33	204	10.4	404	1	CGE2_HUMAN	Q96020 homo sapien
34	203.5	10.4	410	2	Q9PVT7	Q9pvt7 carassius a
35	202	10.3	404	1	CGE2_MOUSE	Q92238 mus musculus
36	201.5	10.3	410	1	CG1E_BRARE	P47794 brachydanio
37	201	10.2	296	2	Q7Z774	Q7z774 homo sapien
38	197	10.0	407	1	CGE1_CHICK	P49707 gallus gall
39	196	10.0	361	2	Q9SN11	Q9sn11 arabidopsis
40	195	9.9	396	2	Q7PY34	Q7py34 anopheles g
41	192	9.8	311	2	Q95QC1	Q95qc1 caenorhabdi
42	192	9.8	357	2	Q8GVD9	Q8gvd9 helianthus
43	191	9.7	424	1	CG1E_HEMPU	O15995 hemientrot
44	189	9.6	403	2	Q7TWS8	Q7tws8 mus musculus
45	188.5	9.6	373	2	Q9ZRX8	Q9zrx8 nicotiana t

ALIGNMENTS

RESULT 1
CYCI_HUMAN
ID CYCI_HUMAN STANDARD; PRT; 377 AA.
AC Q14094;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Forebrain cortex;
RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
RA Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
RL Exp. Cell Res. 221:534-542(1995).
[2]
RP SEQUENCE FROM N.A.
RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
RA Qiang B.Q.;
RT "Isolating a new cDNA coding for human cyclin protein.";
RN Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[3]
RP SEQUENCE FROM N.A., AND VARIANT ILE-207.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Peel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT "NIH-SNPs, environmental genome project, NIH S515478, Department
of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney, and Muscle;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Griwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalius D.E.,

(J) QJW

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-178 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;
 RA Zhu X., Naz R.K.;
 RT "Expression of a novel isoform of cyclin D in human testis.";
 RL Biochem. Biophys. Res. Commun. 249:56-60(1998);
 CC -!- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
 CC skeletal muscle. Lower levels in adult placenta, lung, kidney and
 CC pancreas. Also high levels in fetal brain and lower levels in
 CC fetal lung, liver and kidney. Also abundant in testis and thyroid.
 CC -!- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
 CC in lung fibroblasts.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D50310; BRA08849.1; -;
 DR EMBL; AY207372; NAO13492.1; -;
 DR EMBL; BC000420; AAH00420.1; -;
 DR EMBL; BC004975; AAH04975.1; -;
 DR EMBL; AF135162; AAF43786.1; -;
 DR PIR; J02624; J02624;
 DR Genew; HGNC:1595; CCNI.
 DR H-invDB; HIX0004313; -;
 DR GO; GO:0007283; P: spermatogenesis; NAS.
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR011028; Cyclin like.
 DR InterPro; IPR006671; Cyclin N.
 DR Pfam; PF00134; Cyclin N; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
 DR Cyclin; Polymorphism.
 FT VARIANT 207 207 V -> I (in dbSNP:4252903).
 FT CONFLICT 9 9 /FTID=VAR_016312.
 FT CONFLICT 58 58 N -> D (in Ref. 5).
 FT CONFLICT 75 75 Q -> R (in Ref. 5).
 FT CONFLICT 75 75 R -> G (in Ref. 5).
 SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA74698F6C CRC64;
 Query Match 100.0%; Score 1962; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 2.1e-152;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQLSFLEKAITREAOQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 DB 1 MKFPGPLENQLSFLEKAITREAOQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 DB 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQWDSQLIHC 240
 DB 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQWDSQLIHC 240
 QY 241 ELVAHHLSTLQSSLPVPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKNSKPEVPV 300
 DB 241 ELVAHHLSTLQSSLPVPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKNSKPEVPV 300
 QY 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 DB 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 QY 361 QEGHASPCLPPLQPVSV 377
 DB 361 QEGHASPCLPPLQPVSV 377

QY 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 DB 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 QY 361 QEGHASPCLPPLQPVSV 377
 DB 361 QEGHASPCLPPLQPVSV 377
 RESULT 2
 Q6FHH0 PRELIMINARY; PRT; 377 AA.
 ID Q6FHH0
 AC Q6FHH0;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE CCNI protein (Fragment).
 GN Name=CCNI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
 RA Neubert P., Kstrang-K., Schatten R., Shen B., Henze S., Mar W.,
 RA Korn B., Zhang Y., LaBaer J.,
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the cyclin family.
 DR EMBL; CR541783; CAG46582.1; -;
 DR InterPro; IPR006670; Cyclin.
 DR InterPro; IPR011028; Cyclin like.
 DR InterPro; IPR006671; Cyclin N.
 DR Pfam; PF00134; Cyclin N; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR KW SMART;
 DR NON TER 377 377
 SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;
 Query Match 99.5%; Score 1952; DB 2; Length 377;
 Best Local Similarity 99.5%; Pred. No. 1.4e-151;
 Matches 375; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQLSFLEKAITREAOQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 DB 1 MKFPGPLENQLSFLEKAITREAOQMKVNVKMPNSQNVSPSORDEVIQWLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 DB 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPLKSPSOHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQWDSQLIHC 240
 DB 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLIIPWLSLTIELLOKQWDSQLIHC 240
 QY 241 ELVAHHLSTLQSSLPVPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKNSKPEVPV 300
 DB 241 ELVAHHLSTLQSSLPVPLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKNSKPEVPV 300
 QY 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 DB 301 RGTAAAFVHHLPAASGCKQTSTKRVEMEVDVDFYDGIKRLYNEDNVSENVSVCCTDLR 360
 QY 361 QEGHASPCLPPLQPVSV 377
 DB 361 QEGHASPCLPPLQPVSV 377

```
RESULT 3
ID Q99LF2 PRELIMINARY; PRT; 377 AA.
AC Q99LF2;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Cyclin I.
DN
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Fellings E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AA03290.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;
Query Match 94.3%; Score 1851; DB 2; Length 377;
Best Local Similarity 94.2%; Pred. No. 2.7e-143;
Matches 355; Conservative 11; Mismatches 11; Indels 0; Gaps 0;
QY 1 MKFPGPLENORLSLEKAITREAQMKVNVKMPNSQNSPSORDEVIOWLAKLYQFN 60
DB 1 MKFPGPLENORLSLEKAITREAQMKVNVKMPNSQNSPSORDEVIOWLAKLYQFN 60
QY 61 LYPETFALLSILDRFLATVAKPKYLSIAISCFFLAAKTVEEDERIPVLKVLARSFC 120
DB 61 LYPETFALLSILDRFLATVAKPKYLSIAISCFFLAAKTVEEDERIPVLKVLARSFC 120
QY 121 GCSSEILRMERILDKLNWDHTATPLDFLHFAIAVSTRPQLLSPLKSPSQHLAV 180
DB 121 GCSSEILRMERILDKLNWDHTATPLDFLHFAIAVSTRPQLLSPLKSPSQHLAV 180
QY 181 LTKQLLHCWACNQLLOFGKSLALAMVSLMEKLIIPDWLSITIELLOKAQWDSOLHCR 240
DB 181 LTKQLLHCWACNQLLOFGKSLALAMVSLMEKLIIPDWLSITIELLOKAQWDSOLHCR 240

RESULT 4
CYCI_MOUSE
ID CYCI_MOUSE STANDARD; PRT; 377 AA.
AC Q922V9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
DN
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99172101; PubMed=10072591;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgeirsson S.S.;
RT "Assignment of the cyclin I gene (Ccni) to mouse chromosome 5E3.3-F1.
RT 3 by in situ hybridization."
RL Cytogenet. Cell Genet. 83:242-243 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgeirsson S.S.;
RT "In vivo expression and genomic organization of the mouse cyclin I
RT gene (Ccni)."
RL Gene 256:59-67 (2000).
CC -1- SIMILARITY: Belongs to the cyclin family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements/
CC or send an email to license@sib.ch).
DR EMBL; AF005896; AA001253.2; -.
DR EMBL; AF228740; AAFA33391.1; -.
DR MGD; MGI:1341077; Ccni.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN; 1.
KW PROSITE; PS00292; CYCLINS; FALSE_NEG.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AE677 CRC64;
Query Match 94.1%; Score 1847; DB 1; Length 377;
Best Local Similarity 93.9%; Pred. No. 5.7e-143;
Matches 354; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
QY 1 MKFPGPLENORLSLEKAITREAQMKVNVKMPNSQNSPSORDEVIOWLAKLYQFN 60
DB 1 MKFPGPLENORLSLEKAITREAQMKVNVKMPNSQNSPSORDEVIOWLAKLYQFN 60
```



```

Q6P7H3 ID Q6P7H3 PRELIMINARY; PRT; 382 AA.
AC Q6P7H3;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 28, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE MGC68660 protein.
GN Name=MGC68660;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC061670; AAH61670.1; -
DR GO; GO:0007049; P:cell cycle; IEA.
DR GO; GO:0000910; P:cytokinesis; IEA.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
KW Cell cycle; Cell division; Cyclin.
SQ SEQUENCE 382 AA; 42913 MW; E19D7C5D8FEC626A CRC64;

Query Match
Best Local Similarity 67.6%; Score 1325.5; DB 2; Length 382;
Matches 260; Conservative 48; Mismatches 68; Indels 7; Gaps 4;

QY 1 MKFPGPLENQRLSFLLEKAITREAQMKVNRKMPNQ--VSPQRDEVIQWLAKLYQ 58
Db 1 MKFSGPLESQRSLFLERAVSREAQMKVYHKTQANDVAVSPQRDEVIQWLAKLYQ 60
QY 59 FNLYPETTALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDS 118

```

RT "Generation and initial analysis of more than 15,000 full-length human

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC044400; AAH44400.1; --
DR HSSP; P30274; 1VIN.
DR ZFIN; ZDB-GENE-040426-2898; cnci.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; UNKNOWN_1.
KW Cyclin.
SQ SEQUENCE 355 AA; 39517 MW; D2999F2E9812C880 CRC64;
Query Match 51.5%; Score 1011; DB 2; Length 355;
Best Local Similarity 55.6%; Pred. No. 1.8e-74;
Matches 212; Conservative 56; Mismatches 77; Indels 36; Gaps 8;
Oy 1 MKFPGPLENORLSFLEKAITREAOQMKVNRKMPNSQ--NVSPSQRDEVIQWLAKLYQ 58
Db 1 MKFTKPLESRKLSLEKAVSREAKLWKVYVPKPTNQDTPDISPKRDEAVRWLRDVHSQ 60
Oy 59 FNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDS 118
Db 61 LKLYPETLCLAIIGLDRLSTIKARPKYLCIAISCFPLAAKTSEEDRIPSLRELASS 120
Oy 119 FCGSSSEILRMERIIIDKLNWDLHTATPLDPLFHFAIAVSTRP-QLLFSLPKLSPSOH 177
Db 121 KCGSPSEILRMERIVLDKLNWDLSATLDFLYIFHANVLUSCKSGRLSUALSGLNPSQH 180
Oy 178 LAVLTQQLLHMACNQLIQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLQKAQMDSSOLI 237
Db 181 VALLTQQLFHCLAHNALLQVRGSLSLGLITLELEKLPDWLALTVDLHLRLQIDSSOLI 240
Oy 238 HCRELVAAHLSTLQSSLPNLYVYRPLKHTLVTCDKGVFRHLPSVPGPDPFSKDNKSKE 297
Db 241 CCRELVARCLSTHTASLPNTVYICRPLPEPR---DEGV--LHVSLAP-----TAPS 287
Oy 298 VPVRGTAFAFHYHLPAAACCKOTSTKRYKEVEVDVFDGIKRLYNEDNVSENVGVCCTD 357
Db 288 DP-----NTHSRSAKRKVEQMEVDYFDGIRKLYNEGNPQB--GALLCTA 331
Oy 358 LSRQEGH-----ASPCPPLQPV 374
Db 332 QTAGGGQPNAGSSPCPPLQPV 352
RESULT 10
ID Q661Z0 PRELIMINARY; PRT; 359 AA.
AC Q661Z0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC83953 protein.
GN Name=MGC83953;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.D., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Oocytes;
RA Klein S., Gerhard D.S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC081135; AAH81135.1; --
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 359 AA; 40577 MW; 230B61BE382A6BC7 CRC64;
Query Match 38.0%; Score 746.5; DB 2; Length 359;
Best Local Similarity 43.4%; Pred. No. 8.9e-53;
Matches 168; Conservative 60; Mismatches 110; Indels 49; Gaps 8;
Oy 1 MKFPGPLENORLSFLEKAITREAOQMKVNRK--MFSNQVSPSQRDEVIQWLAKLYQ 58
Db 1 MKCFGLSDIQRLMISLNSLQLEDTKWVPVCEGTGLKGTDISLTHYEQAVLWMEVTLR 60
Oy 59 FNLYPETPALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDS 118
Db 61 FHYPETFGLAVSILNRLASVRAQVYLCITVACLVLAKTSEEDRIPSVKLAQVS 120
Oy 119 FCGSSSEILRMERIIIDKLNWDLHTATPLDPLFHFAIAVSTRPQLLSPKLSPSOHL 178
Db 121 GCMCSSAEILRMERIVLDKLNWDLYTATPDVDFLNTFHAMLMSNLPFLHLSQMNPSHLL 180
Oy 179 AVLTQQLLHMACNQLIQFRGSMALAMVLSLEMEKLIIPDWLSLTIELLQKAQMDSSQLIH 238

```
Db 181 ALLTRLOQCMACHLVQFRGSTALVITILELEKLTADWPATITELLKAKVDSAKFIL 240
Qy 239 CRELVAVHLSTLOSLPLNSVYVYPLKHTLVTCDKGFRVLRHPSPVGP-----DFSKD 292
Db 241 CKELVDQQLGMLS-----PPNHVYVFSAXR-----DPPAYRREKKSACSAPGCFPOPISMN 292
Qy 293 NSKPEVPVRGTAAFYHPLPAAGCGKQTSTKRKVEEMEDDFYDGTGKLYNEDNYSN--- 349
Db 293 TEVPEVL-----SARKQAEIEMETEFYDGFYLYNEESVSDRRI 334
Qy 350 ----VSGVCGTDLRSQHGASCPPLQ 372
Db 335 KEMVTGKL-----QEA-SCPCPVQL 353

RESULT 11
Q6ZMN8
ID Q6ZMN8 PRELIMINARY; PRT; 369 AA.
AC Q6ZMN8;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein FLJ16793.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Tanigami A., Fujiwara T., Shibahara T., Goto Y., Hirao M., Shimizu F.,
RA Wakebe H., Ono T., Hishigaki H., Watanabe T., Ozaki K., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J.,
RA Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K.,
RA Yanashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
RA Wagatsuma M., Makawa K., Kanehori K., Takahashi-Fujii A., Oshima A.,
RA Sugiyama A., Kawakami B., Suzuki Y., Sugano S., Nagahara K.,
RA Masuho Y., Nagai K., Isogai T.;
RA Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL, AK131553; BAD18687.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR Pfam; PF00134; Cyclin N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 369 AA; 40621 MW; 68B887A9C044708 CRC64;

Query Match 25.6%; Score 502.5; DB 2; Length 369;
Best Local Similarity 44.6%; Pred. No. 9.4e-33;
Matches 111; Conservative 44; Mismatches 89; Indels 5; Gaps 1;

Qy 5 GPLENQLRSLFLEKAITREAOQWKVVKMFSNQVSPSQDEVIOWIAKLYOFNLYPE 64
Db 115 GDLERRLLCHLQAQDREARLRGG-----KPQDEICDAFEVYVLMRLRLQNTFYFSQS 169
Qy 65 TFALASSLLDRFLATVKAHPKYLSCIAISCFPLAATVEEDERIPVLKVLARDSFQCGSS 124
Db 170 TFLNALTIFGRLLSVKYKYLHCATITSLRLAKVNEEEFIPQVDFKHYGSDYSP 229
Qy 125 SEILRMERIIIDKLNWDLHTATPDLFIHFAIAVSTRPQLLPLKPLSQHLAVLTQ 184
Db 230 NELLRMELAILDRHLWDLYIGTFLDTIFHALVVLSPHVLLELPQRNPNSLHVASLTRQ 289
Qy 185 LLHCWACNQLQFGSMALAWVSLMEKLPDMLSLTIELLOKQAWDSSQLIHCRELVA 244
Db 290 LOHCWAGHQLQFGSTLALVITILELERLMPGWCAPISDLILKKAQVDMQYSCCKELVM 349
Qy 245 HHLSTLQSS 253
Db 350 QQLRSLOSS 358
```

```
RESULT 12
CG2_MOUSE
ID CG2_MOUSE STANDARD; PRT; 344 AA.
AC O08918; O35612;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin G2.
GN Name=Cng2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Horne M.C., Donaldson K.L., Goolbey G.L., Tran D., Mulheisen M.,
RA Hell J.W., Wahl A.F.;
RT "Cyclin G2 is up-regulated during growth inhibition and B cell antigen receptor-mediated cell cycle arrest.";
RL J. Biol. Chem. 272:12650-12661(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RA MEDLINE=92234097; PubMed=10216255; DOI=10.1016/S0378-1119(99)00057-8;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgeirsson S.S.;
RT "Gene structure and chromosomal localization of mouse cyclin G2 (Cng2).";
RN [3]
RP SEQUENCE FROM N.A.
RA Kimura S.H., Nojima H.;
RT "Genomic structure, chromosomal mapping and p53-independent induction of mouse cyclin G2 gene.";
CC Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play a role in growth regulation and in negative regulation of cell cycle progression.
CC -!- SUBCELLULAR LOCATION: Primarily cytoplasmic, a minor portion can be detected in some cells in the nucleus.
CC -!- TISSUE SPECIFICITY: Highest levels in intestine. Intermediate levels in spleen, brain and kidney. Low levels in testis, stomach, pancreas, liver, salivary gland and muscle. According to Ref.1 also abundant in thymus.
CC -!- DEVELOPMENTAL STAGE: Expression levels oscillate moderately through the cell cycle.
CC -!- INDUCTION: Activated in B-cells by agents causing growth inhibition or growth arrest.
CC -!- SIMILARITY: Belongs to the cyclin family. Cyclin G subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC
CC EMBL; U95826; AAB58693.1; -.
CC EMBL; AF005885; AAC28496.1; -.
CC EMBL; AF079877; AAC32372.1; -.
CC EMBL; AB015264; BAA87065.1; -.
CC MGD; MGI:1095734; Cng2.
CC InterPro; IPR006670; Cyclin.
CC InterPro; IPR011028; Cyclin like.
CC Pfam; PF00134; Cyclin N; 1.
CC SMART; SM00385; CYCLIN; 1.
CC Cell cycle; Cell division; Cyclin; Mitosis.
SQ SEQUENCE 344 AA; 38847 MW; F6A02698C286D853 CRC64;
```


Query Match 16.7%; Score 327; DB 1; Length 344;
Best Local Similarity 29.4%; Pred. No. 2.1e-18;
Matches 113; Conservative 58; Mismatches 107; Indels 106; Gaps 17;
QY 12 LSFLEKAITREAOQWK-----VNVKQPSNQVPSQ--RDEVIQWLAKLYQFNLYPE 64
DB 21 LNFYLE-----OQRYQPREKGLIMEATPNDNTLCSRLNAKVEDLRSITNFFGSGTE 75
QY 65 TFALASSLLDRFLATVKAHPKYLSCIALSCFFLAAKTVEEDERIPVLKVLARDSFCGSS 124
DB 76 TFVLAVNLDRLALMKVKKHLSGIGVCCFLAARLAEEGDPVPTDVRISQCKCTA 135
QY 125 SEILRMERIIIDKLNWDHTTPDLFIHFAIA---VSTRPQLFSLPKLSPSQHLAVL 181
DB 136 SDIKRMKIIIEKHLHYEATLNFHLHYAIVFCHTSEKIL--SLDKLE----- 186
QY 182 TKQLLHCWACNQLQF---RGSMLALMVSLMEKLIPLDWLSLTIELLQ-----KAQM 231
DB 187 -----AQLKACNCRVVFVKARPSVLALCLNLEIETI-----KSVLELLEILLVKKHLKL 236
QY 232 DSSQLIHCRFLVAHLSTLQSSPLNSVYVVRPLKHTL-----VTCDKGVFLHPSPVPG 286
DB 237 SDTEFFYWRLELVSKLAEYSF-----RCKEDLKLWIVSRRTAQNHLSSYY-- 285
QY 287 PDFSKDNKPEVPVKGTAFAFYHLPAAAGCKQTSTKRVKMEVDDFVYDGIKRLYNEDNV 346
DB 286 -----SVPELPT-----IP-EGGC-----PDGSE---SEDS- 307
QY 347 SENVGSVCGTDLRSRQEGHASPCCP 370
DB 308 -----GEDMSGEESSLSGPP 323

RESULT 13

CGG2_HUMAN STANDARD; PRT; 344 AA.
AC Q16589;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin G2.
GN Name=CCNG2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain, and Fetal spleen;
RX MEDLINE=96400325; PubMed=8806701;
RA Bates S.A., Rowan S., Voudsen K.H.;
RT "Characterisation of human cyclin G1 and G2: DNA damage inducible
RT genes";
RL Oncogene 13:1103-1109 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=96198057; PubMed=8626390; DOI=10.1074/jbc.271.11.6050;
RA Horne M.C., Goolbsy G.L., Donaldson K.L., Tran D., Neubauer M.,
RA Wahl A.P.;
RT "Cyclin G1 and cyclin G2 comprise a new family of cyclins with
RT contrasting tissue-specific and cell cycle-regulated expression";
RL J. Biol. Chem. 271:6050-6061 (1995).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS VAL-4 AND GLY-28.
RA Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA Schackwitz W.S., Sherwood J.K., Wittrak L.A., Nickerson D.A.;
RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department
RT of Genome Sciences, Seattle, WA (URL: <http://esg.gs.washington.edu>)";
RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May play a role in growth regulation and in negative

regulation of cell cycle progression.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- TISSUE SPECIFICITY: High levels in cerebellum, thymus, spleen and prostate. Low levels in skeletal muscle.
-!- DEVELOPMENTAL STAGE: Expression levels increase through the cell cycle to peak in the mid/late-S phase and decrease during G2/M phase.
-!- INDUCTION: Activated by actinomycin-D induced DNA damage.
-!- SIMILARITY: Belongs to the cyclin family. Cyclin G subfamily.

THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.ebi.ac.uk/ebis-sib.ch/announcements> or send an email to license@sib-sib.ch).

EMBL; U47414; AAC50689.1; --
DR EMBL; L49506; AAC41978.1; --
DR EMBL; AF549495; AAN40704.1; --
DR Genew; HGNC:1593; CCNG2.
DR MIM; 603203; --
DR GO; GO:0000075; P:cell cycle checkpoint; TAS.
DR InterPro; IPR011028; Cyclin-like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
KW Cell cycle; Cell division; Cyclin; Mitosis; Polymorphism.
FT VARIANTS 4
FT VARIANTS 28 28 /FTID=VAR_014333.
FT VARIANTS 28 28 /FTID=VAR_014334.
FT SEQUENCE 344 AA; 38865 MW; D434E0CE92760301 CRC64;
Query Match 16.6%; Score 326.5; DB 1; Length 344;
Best Local Similarity 36.4%; Pred. No. 2.3e-18;
Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;
QY 31 VRKMPNQ--VPSQRDEVIQWLAKLYQFNLYPETTALASSLLDRFLATVKAHPKYLSC 89
DB 41 IEATPENDNTLCPGLRNAKVEDLRSANFFGSCCTETFLAVNILDRLALMKVKKHLS 100
QY 90 IASCFPLAATVEEDERIPVLKVLARDSFCGSSSEILRMERIIIDKLNWDHTATPLD 149
DB 101 IGVCFFLAARIVVEDCNIPSTHVDVIRISQCKTASDIKRMKIIIEKHLHYEATL 160
QY 150 FLHIFHAIIV---STRPQLFSLPKLSPSQHLAVLTKQLLHCWACNQLQF---RGSMLA 203
DB 161 FLHUIHILCHTSEKIL--SLDKLE-----AQLKACNCELIFSKAPSVLA 207
QY 204 LAMVSLMEKLIPLDWLSLTIELLQ-----KAQMSQLIHCRFLVAHLSTLQ 252
DB 208 LCLLNLEVEITL-----KSVLELLEILLVKKHKSINDTEFFYWRLELVSKLAEYSS 257
RESULT 14
Q8NSD4
ID Q8NSD4 PRELIMINARY; PRT; 344 AA.
AC Q8NSD4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE CCNG2 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,


```
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC032518; AAH32518.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N.1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 344 AA; 39042 MW; A3C8116DBA4E28DF CRC64;
Query Match 16.6%; Score 326.5; DB 2; Length 344;
Best Local Similarity 36.4%; Pred. No. 2.3e-18;
Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;
QY 31 VRKPSNQN-VSPSORDEVIQWLAKKYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
41 IEATPENDNTLCPLGRNAKVEDLSLANFFGSGTETFTFLAVNILDRLFLAMKVKPHLSC 100
QY 90 IATSCFFLAATVEEDERIPVLKVLARDSPGCGSSSEILRMERIIIDKLNWDLHTATPLD 149
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
101 IGVCFLAARIVEEDCNIPSTHDIRISQCKTASDIKRMKEIKISEKHYELEATTALN 160
QY 150 FLHIFHATAV---STRPOLLESPLKSPSQHLAVLTQKLLHMCACNQLQF---RGSMLA 203
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
151 FLHLYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRILIFS KAKPSVIA 207
QY 204 LAMVSLMEKLIPLWLSLTIELLQ-----KAQMDSSQLIHCRELVAHHLSTLQS 252
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
208 LCLLNLEVTL-----KSVLELTLLVAKKHKINDTEFFYWRVRLVSKCLAEYSS 257
RESULT 15
QEGM00
ID Q6GM00 PRELIMINARY; PRT; 356 AA.
AC Q6GM00;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE MGC84088 protein.
GN Name=MGC84088;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCHI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
```

```
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalilus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC074293; AAH74293.1; -.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N.1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 356 AA; 40563 MW; B53F9C266631C06E CRC64;
Query Match 16.4%; Score 322.5; DB 2; Length 356;
Best Local Similarity 28.9%; Pred. No. 5.1e-18;
Matches 92; Conservative 62; Mismatches 121; Indels 43; Gaps 8;
QY 36 SNQVSPSORDEVIQWLAKKYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 95
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
47 NDSTICPRSNKAKVEDLSLNTNFFGLSMETFLAVNILDRLFLATIMKVKPHLSIGVCCF 106
QY 96 FLAAKTVEEDERIPVLKVLARDSPGCGSSSEILRMERIIIDKLNWDLHTATPLDPLHIF 155
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
107 QLAARVVEEDCNVPSVHDVIRISQCKCTVSDMKRMKEIKISEKHYFEKATALTFLHLYH 166
QY 156 AIAV--STRPQLLSPLKSPSQHLAVLTQKLLHMCACNQLQF---RGSMLAMVSL 210
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 TIVLCHSCERKEVNLNLDKLB-----AQLKACNCRILIFS KAKPSVIALCLLTLE 214
QY 211 MEKLIP-DWLSLTIELLOKQAMDSSQLIHCRELVAHHL----STLQSSILPLNSVTVYPLK 266
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
215 VETLKSLELFEIALRVQKSKVNDLMLYRWELVSKCLADYSSPECCPKDHRKLVTVSR 274
QY 267 HTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPVRGTAAFFVHLPAASGCKOTS----- 320
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
275 RT-----AQLNLSNY-----SVPELFTIPEGGINSESEDSCEMSSGEDSL 318
QY 321 TKRKVEEMEYDDFYDGIK 338
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
319 SSSPPSDEASFFFDNCK 336
Search completed: February 11, 2005, 03:05:15
```

Job time : 104.276 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:09 ; Search time 107.026 Seconds
(without alignments)
1362.372 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 1962
Sequence: 1 MKFPGLNQLRSLLEKAI.....LSRQGHASCPPLQPVSM 377

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1962	100.0	377	2	AAW21965 Human cyc
2	1962	100.0	377	3	AAW21965 Human cyc
3	1962	100.0	377	6	ABR3934 Human pro
4	1962	100.0	377	8	ADP12615 Protein e
5	1960	99.9	377	8	ABM80569 Tumour-as
6	1713.5	87.3	334	7	RAE37938 Human CGD
7	1529.5	78.0	300	3	ADN01131 Human cel
8	667	34.0	131	3	AGN01903 Human sec
9	502.5	25.6	369	4	ABG18403 Novel hum
10	502.5	25.6	369	8	ADR10466 Human pro
11	326.5	16.6	344	5	ABP65178 Hypoxia-r
12	326.5	16.6	344	8	ADP66631 Human cyc
13	326.5	16.6	344	8	ADO19808 Human PRO
14	326.5	16.6	344	8	ADO19317 Human PRO
15	326.5	16.6	344	8	ADP54950 Human PRO
16	326.5	16.6	344	8	ADP23418 PRO poly
17	326.5	16.6	362	8	ADR66294 Human pro
18	326.5	16.6	362	8	ADR68855 Human pro
19	326.5	16.6	380	8	ADP84518 Human bre
20	326.5	16.6	403	8	ADO19315 Human PRO
21	326.5	16.6	403	8	ADP23416 PRO poly
22	271.5	13.8	294	7	ADD46447 Rat Prote
23	271.5	13.8	295	7	ADD46449 Human Pro
24	271.5	13.8	295	8	ABM80697 Tumour-as
25	263.5	13.4	249	5	ABB57103 Mouse isc

26	231	11.8	249	2	AAW24788	AAW24788 Human cyc
27	218	11.1	88	8	ABO56671	ABO56671 Human gen
28	213.5	10.9	277	8	ABM83893	ABM83893 Human dia
29	213.5	10.9	277	8	ABM83894	ABM83894 Human dia
30	204	10.4	404	2	AAW43173	AAW43173 Human cyc
31	204	10.4	404	3	AAW77483	AAW77483 Human cyc
32	204	10.4	404	4	AAW72462	AAW72462 Human cyc
33	204	10.4	404	7	ADB67893	ADB67893 Human lun
34	204	10.4	404	7	ADF48687	ADF48687 Human mod
35	204	10.4	404	8	ADI82506	ADI82506 Human mod
36	204	10.4	404	8	ADN05983	ADN05983 Antipeori
37	204	10.4	404	8	ADO19484	ADO19484 Human PRO
38	202	10.3	403	2	AAW43174	AAW43174 Mouse cyc
39	202	10.3	403	4	AAW72463	AAW72463 Mouse cyc
40	202	10.3	403	7	ADF48688	ADF48688 Murine cy
41	201	10.2	296	7	ADN95215	ADN95215 Human BEC
42	196	10.0	308	3	AGN07076	AGN07076 Arabidops
43	196	10.0	308	3	AGS3865	AGS3865 Arabidops
44	196	10.0	361	3	AGS3864	AGS3864 Arabidops
45	196	10.0	361	3	AGN07075	AGN07075 Arabidops

ALIGNMENTS

RESULT 1
AAW21965
ID AAW21965 standard; protein; 377 AA.

XX AC AAW21965;
XX DT 02-DEC-1997 (first entry)
XX DE Human cyclin I.
XX KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX OS Homo sapiens.
XX PN WO9712973-A1.
XX PD 10-APR-1997.
XX PF 07-OCT-1996; 96WO-JF002905.
XX PR 05-OCT-1995; 95JP-00284663.
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Nakamura T;
XX DR WPI; 1997-226217/20.
XX DR N-PSDB; AAT73937.
XX PT Human cyclin I protein and related (anti-sense) DNA - used for neuron
XX PT labelling method and cancer cell detection.
XX PS Claim 1; Fig 1; 45pp; Japanese.
XX CC This sequence is human cyclin I. Antisense polynucleotides are useful for
XX CC as probes and can be labelled and used for detection of neurones by
XX CC hybridisation with mRNA for cyclin I (contained in the neurones and
XX CC arising by the expression of the cyclin I gene in these cells). The gene
XX CC can be used for detection of cancer cells by detecting the expression of
XX CC the cyclin I gene in these cells. Also antibodies specific for the
XX CC fragments of the protein (especially AAW21966) can be used for detection

SQ Sequence 377 AA;

Query Match 100.0%; Score 1962; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 6.7e-197;
Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
 DB 1 MKFPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
 QY 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 DB 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 QY 181 LTKQLLHCACNQLQFRGSMALAMVLEMEKLIIPDWLSLTIELLOKQMDSSQLIHC 240
 DB 181 LTKQLLHCACNQLQFRGSMALAMVLEMEKLIIPDWLSLTIELLOKQMDSSQLIHC 240
 QY 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLTCTDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 DB 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLTCTDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDYGIKRLYNEDNVSNVSGVCGTDLR 360
 DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDYGIKRLYNEDNVSNVSGVCGTDLR 360
 QY 361 QEGHASPCCPPLQPVSV 377
 DB 361 QEGHASPCCPPLQPVSV 377

RESULT 2

AA52185
 ID AAY52185 standard; protein; 377 AA.
 XX AC AAY52185;

09-FEB-2000 (first entry)

Human cyclin I amino acid sequence.

Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I; ERH; cell cycle; proliferation; cancer; hyperproliferative disorder; atherosclerosis; tumour.

Homo sapiens.

WO925829-A2.

27-MAY-1999.

12-NOV-1998; 98WO-US024095.

13-NOV-1997; 97US-00969106.

(CURA)-CURAGEN CORP.

Yang M, Nandabalan K, Schulz VP;

WPI; 2000-061923/05.

N-PSDB; AAZ37836.

New complexes of the cyclin-dependent kinase 2 protein with its

interacting proteins, used to treat, e.g. atherosclerosis.

Example; Fig 2; 90pp; English.

This is the human Cyclin I amino acid sequence. Cyclin I is expressed at almost constant levels throughout the cell cycle, and is implicated in controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition.

CC Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or atherosclerosis-associated disease by contacting cells or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

XX Sequence 377 AA;

Query Match 100.0%; Score 1962; DB 3; Length 377;

Best Local Similarity 100.0%; Pred. No. 6.7e-197;

Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKFPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
 DB 1 MKFPGPLENORLSFLEKAITREAOQMKVNRKMPNSQNVSPSQRDEVIQWLAKLYQFN 60
 QY 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 DB 61 LYPETFALASLLDRFLATVKAHPKYLSCIAISCFFLAAKTVEEDERIPVLKVLARDSPFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 QY 181 LTKQLLHCACNQLQFRGSMALAMVLEMEKLIIPDWLSLTIELLOKQMDSSQLIHC 240
 DB 181 LTKQLLHCACNQLQFRGSMALAMVLEMEKLIIPDWLSLTIELLOKQMDSSQLIHC 240
 QY 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLTCTDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 DB 241 ELVAHHLSTLQSSPLNSVYVYRPLKHTLTCTDKGVFRLHPSSVPGDFSKDKSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDYGIKRLYNEDNVSNVSGVCGTDLR 360
 DB 301 RGTAAFYHHLPAASGCKQTSTKRKVEEMVEDDFDYGIKRLYNEDNVSNVSGVCGTDLR 360
 QY 361 QEGHASPCCPPLQPVSV 377
 DB 361 QEGHASPCCPPLQPVSV 377

RESULT 3

ABR39934

ID ABR39934 standard; protein; 377 AA.

XX ABR39934;

11-AUG-2003 (first entry)

Human prostate selective polypeptide Pr325.

Prostate; molecular marker; cancer; cytostatic; gene therapy; human.

Homo sapiens.

WO2003014298-A2.

20-FEB-2003.

02-AUG-2002; 2002WO-US024431.

03-AUG-2001; 2001US-0309470P.

30-OCT-2001; 2001US-0330747P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX PI Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
 XX PR WPI; 2003-256562/25.
 XX DR N-PSDB; ACC47339.
 XX XX
 XX PT New polynucleotide, useful for preparing a composition for treating
 XX PT prostate disease, e.g., cancer.
 XX PS Claim 5; Page 147-149; 212pp; English.
 XX XX
 XX CC The invention relates to prostate selective polynucleotides and
 XX CC polypeptides. The polynucleotides are expressed in prostate and are
 XX CC useful as molecular markers, as drug targets, and for detecting,
 XX CC monitoring, preventing or treating diseases and conditions related to
 XX CC prostate, such as prostate cancers. The present sequence represents a
 XX CC prostate specific polypeptide
 XX SQ Sequence 377 AA;
 Query Match 100.0%; Score 1962; DB 6; Length 377;
 Best Local Similarity 100.0%; Pred. No. 6.7e-197;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQRSLFLEKAITREAOQMKVNVKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNVKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
 Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLQKQMDSSQLIHCR 240
 Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLQKQMDSSQLIHCR 240
 QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRKYEMEVDVDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 Db 301 RGTAAFYHHLPAASGCKQTSTKRKYEMEVDVDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 QY 361 QEGHASPCCPPLQPVSV 377
 Db 361 QEGHASPCCPPLQPVSV 377
 RESULT 4
 ADP12615
 ID ADP12615 standard; protein; 377 AA.
 AC ADP12615;
 XX XX
 XX DT 12-AUG-2004 (first entry)
 XX DE
 XX DE Protein encoded by mRNA of the invention #225.
 XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
 XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
 XX OS Homo sapiens.
 XX XX
 XX PN WO2004042346-A2.
 XX XX
 XX PD 21-MAY-2004.

XX PF 24-APR-2003; 2003WO-US012946.
 XX PR 24-APR-2002; 2002US-00131831.
 XX PR 20-DEC-2002; 2002US-00325899.
 XX XX
 XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX XX
 XX PI Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 XX PI Rosenberg S;
 XX WPI; 2004-400724/37.
 XX XX
 XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
 XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 XX PT rejection, in an individual, comprises detecting the expression level of
 XX PT the genes.
 XX PS Claim 65; SEQ ID NO 2624; 1762pp; English.
 XX XX
 XX CC The present invention relates to diagnosing or monitoring transplant
 XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 XX CC comprises detecting the expression level of one or more genes. The
 XX CC methods, system and kits are useful in diagnosing or monitoring
 XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 XX CC islet, lung, bone marrow or stem cell transplant rejection,
 XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
 XX CC individual. The method is also useful in assessing the immune status of
 XX CC an individual. The methods are also useful in diagnosing and monitoring
 XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 XX CC viral, bacterial or fungal infection. The present sequence represents a
 XX CC protein that is encoded by the mRNA of the invention.
 XX SQ Sequence 377 AA;
 Query Match 100.0%; Score 1962; DB 8; Length 377;
 Best Local Similarity 100.0%; Pred. No. 6.7e-197;
 Matches 377; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKFPGPLENQRSLFLEKAITREAOQMKVNVKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 Db 1 MKFPGPLENQRSLFLEKAITREAOQMKVNVKMPNSQNVSPQRDEVIQMLAKLYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
 Db 61 LYPETPALASSLLDRFLATVKAHPKYLSCIAISCFEFLAAKTVEEDERIPVLKVLARDSFC 120
 QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 Db 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIAVSTRPQLLSPKLSQHLAV 180
 QY 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLQKQMDSSQLIHCR 240
 Db 181 LTKQLLHMACNQLQFRGSMALAMVSLMEKLI PDWLSLTIELLQKQMDSSQLIHCR 240
 QY 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 Db 241 ELVAHHLSTLQSSLPNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 QY 301 RGTAAFYHHLPAASGCKQTSTKRKYEMEVDVDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 Db 301 RGTAAFYHHLPAASGCKQTSTKRKYEMEVDVDFYDGIKRLYNEDNVSENVSGVCGTDLR 360
 QY 361 QEGHASPCCPPLQPVSV 377
 Db 361 QEGHASPCCPPLQPVSV 377
 RESULT 5
 ABM80569
 ID ABM80569 standard; protein; 377 AA.
 XX XX

AC ABM80569;
 XX 18-NOV-2004 (first entry)
 XX Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
 DE
 XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 XX Homo sapiens.
 XX WO2004030615-A2.
 XX 15-APR-2004.
 XX 29-SEP-2003; 2003WO-US028547.
 XX 02-OCT-2002; 2002US-0414971P.
 XX (GETH) GENENTECH INC.
 XX Wu TD, Zhang Z, Zhou Y;
 XX WPI: 2004-347921/32.
 XX N-PSDB; ACN38124.
 XX
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 12; SEQ ID NO 1450; 7273pp; English.
 XX
 XX The invention relates to human tumor-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 XX Sequence 377 AA;
 SQ
 Query Match 99.9%; Score 1960; DB 8; Length 377;
 Best Local Similarity 99.7%; Pred. NO. 1.1e-196;
 Matches 376; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKPFGPLENQLRSLFLEKAITREAOQWKNVVRKMPSONVSPQRDEVIOWLAKUKYQFN 60
 DB 1 MKPFGPLENQLRSLFLEKAITREAOQWKNVVRKMPSONVSPQRDEVIOWLAKUKYQFN 60
 QY 61 LYPETPALASSLLDRFLATVKAHPKYLSCIALSCFFLAAKTVEEDRIPLVKLARDSPC 120
 DB 61 LYPETPALASSLLDRFLATVKAHPKYLSCIALSCFFLAAKTVEEDRIPLVKLARDSPC 120

121 GCSSEILRMERIIIDKLNWDLHTATPDLDFLHIFHAIAVSTRPQLLFLSKLSPSOHLAV 180
 121 GCSSEILRMERIIIDKLNWDLHTATPDLDFLHIFHAIAVSTRPQLLFLSKLSPSOHLAV 180
 181 LTKOLLHCMAQNQLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQWSSQLIHC 240
 181 LTKOLLHCMAQNQLQFRGSMIALAMVSLMEKLIIPDWLSLTIELLOKAQWSSQLIHC 240
 241 ELVAHHLSTLQSSLPFLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 241 ELVAHHLSTLQSSLPFLNSVYVYRPLKHTLVTCDKGVFRLHPSSVPGPDFSKDMSKPEVPV 300
 301 RGTAAFYHHLPAASGCKQTSTKRVKVEEMVDDFDGIKRLYNEDNVSENVSGVCGTDL 360
 301 RGTAAFYHHLPAASGCKQTSTKRVKVEEMVDDFDGIKRLYNEDNVSENVSGVCGTDL 360
 361 QEGHASPCLPQPVSV 377
 361 QEGHASPCLPQPVSV 377

RESULT 6
 AAE37938
 ID AAE37938 standard; protein; 334 AA.
 XX
 AC AAE37938;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 DE Human CGDD-27 protein.
 XX
 KW Human; cell growth, differentiation and death protein; CGDD; leukaemia;
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
 KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
 KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
 KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
 KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
 KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
 KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
 KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
 KW protozoacide; nootropic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003050253-A2.
 XX
 PD 19-JUN-2003.
 XX
 PF 04-DEC-2002; 2002WO-US039133.
 XX
 PR 07-DEC-2001; 2001US-0340747P.
 PR 20-DEC-2001; 2001US-0342761P.
 PR 15-JAN-2002; 2002US-0349705P.
 PR 06-FEB-2002; 2002US-0354764P.
 PR 12-FEB-2002; 2002US-0356216P.
 XX
 PA (INCY-) INCYTE GENOMICS INC.
 XX
 XX Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
 PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
 PI Tran UK, Swarnakar A, Lee S, Ison CH, Rafalia AJA, Tran B;
 PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KU, Bhatia U;
 PI Burrill JD, Blake JU, Ho A, Zheng W;
 XX
 DR WPI: 2003-532903/50.
 DR N-PSDB; AAD57247.
 XX
 PT New CGDD polypeptides, useful for diagnosing, preventing, and treating
 PT disorders associated with an abnormal expression or activity of CGDD,
 PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
 PT and/or infections.

PS Claim 1; Page 250; 299pp; English.

XX The present invention relates to novel cell growth, differentiation and
 XX death (CGDD) proteins and polynucleotides encoding them. The sequences of
 CC the invention are useful in diagnosing, preventing and treating disorders
 CC associated with an abnormal expression or activity of CGDD such as
 CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
 CC disease), muscular disorders (e.g. myotonic dystrophy, catatonial),
 CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.
 CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 protein

XX Sequence 334 AA;

SQ

Query Match 87.3%; Score 1713.5; DB 7; Length 334;
 Best Local Similarity 88.6%; Pred. No. 7.3e-171;
 Matches 334; Conservative 0; Mismatches 0; Indels 43; Gaps 1;

QY 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQVSPSQRDEVIOQLAKLYQFN 60
 DB 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQVSPSQRDEVIOQLAKLYQFN 38

QY 61 LYPETAFALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120
 DB 39 -----AHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 77

QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLFLSLPKLSPSOHLAV 180
 DB 78 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLFLSLPKLSPSOHLAV 137

QY 181 LTKQLLHCWACNQLQFRGSMALANVSEMEKLIIPDWLSLTIELLOKQAMDSSQLIHCN 240
 DB 138 LTKQLLHCWACNQLQFRGSMALANVSEMEKLIIPDWLSLTIELLOKQAMDSSQLIHCN 197

QY 241 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 300
 DB 198 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 257

QY 301 RGTAAFYHHLPAASGCKQSTKRVKVEEMEDVDYDGIKELYNEDNVSENVGSCGTDLSR 360
 DB 258 RGTAAFYHHLPAASGCKQSTKRVKVEEMEDVDYDGIKELYNEDNVSENVGSCGTDLSR 317

QY 361 QEGHASPCCPPLPQVSVN 377
 DB 318 QEGHASPCCPPLPQVSVN 334

RESULT 7
 ADN01131
 ID ADN01131 standard; protein; 300 AA.
 XX
 AC ADN01131;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human cell growth, differentiation, and death-associated protein #15.
 XX
 KW human; cell growth; cell differentiation; cell death; CGDD;
 KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
 KW cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
 KW developmental disorder; Cushing's syndrome; hypothyroidism;
 KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
 KW Pick's disease; Huntington's disease; Parkinson's disease;
 KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
 KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
 KW reproductive disorder; infertility; endometriosis; uterine fibroid.

XX Homo sapiens.
 OS
 XX WO2004031364-A2.
 PN
 XX 15-APR-2004.
 PD
 XX 03-OCT-2003; 2003WO-US031441.
 PF
 XX 03-OCT-2002; 2002US-0416205P.
 PR
 XX 25-OCT-2002; 2002US-0421521P.
 PR
 XX 21-NOV-2002; 2002US-0428376P.
 PR
 XX 23-DEC-2002; 2002US-0436258P.
 PR
 XX 10-JAN-2003; 2003US-0439292P.
 PR
 XX 13-FEB-2003; 2003US-0447578P.
 PA (INCY-) INCYTE CORP.
 PA (BURR/) BURRILL J D.
 XX
 XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DM, Khare R;
 PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
 PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
 PI Yang YG, Gietzen KJ, Hafalia AJA;
 DR WPI: 2004-330172/30.
 DR N-PSDB; ADN01156.
 XX
 PT New isolated polypeptides associated with cell growth, differentiation
 PT and death, useful for diagnosing, treating or preventing e.g.
 PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
 PT diabetes mellitus or infertility.
 XX
 XX Claim 1; SEQ ID NO 15; 213pp; English.
 PS
 XX The invention comprises the amino acid and coding sequences of human
 CC proteins that are associated with cell growth, differentiation, and death
 CC (CGDD). The DNA and protein sequences of the invention are useful for
 CC diagnosing, treating or preventing disorders associated with aberrant
 CC expression of CGDD, such as: cell proliferative disorders (e.g.
 CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
 CC polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.
 CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
 CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
 CC disease, Parkinson's disease and multiple sclerosis),
 CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
 CC contact dermatitis and diabetes mellitus), and reproductive disorders
 CC (e.g. infertility, endometriosis and uterine fibroid). The present amino
 CC acid sequence represents a human CGDD-associated protein of the
 CC invention.

XX Sequence 300 AA;

QY Query Match 78.0%; Score 1529.5; DB 8; Length 300;
 Best Local Similarity 79.6%; Pred. No. 1.4e-151;
 Matches 300; Conservative 0; Mismatches 0; Indels 77; Gaps 1;

QY 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQVSPSQRDEVIOQLAKLYQFN 60
 DB 1 MKPPGPLENORLSFLEKAITREAOQWKVNVKRMPSNQVSPSQRDEVIOQLAKLYQFN 60

QY 61 LYPETAFALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120
 DB 61 LYPETAFALASSLLDRFLATVKAHPKYLSCIAISCFPLAAKTVEEDRIPVLKVLARDSPC 120

QY 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLFLSLPKLSPSOHLAV 180
 DB 121 GCSSEILRMERIIIDKLNWDLHTATPLDFLHIFHAIIVSTRPQLFLSLPKLSPSOHLAV 153

QY 181 LTKQLLHCWACNQLQFRGSMALANVSEMEKLIIPDWLSLTIELLOKQAMDSSQLIHCN 240
 DB 154 -----MDSQLIHCN 163

QY 241 ELVAHHLSTLQSSLPNSVYVTRPLKHTLVTCDKGVFRLHPSPVPGDFSKNSKPEVPV 300

Db 164 ELVAHLSLQSSLPNSVYVRPLKHTLVTCDKGVFRLHPSVPGPQDFSKNSRPEV 223
 QY 301 RGTAAFYHLLPAASGCKQTSTRKKEVEVDYDGIKELYNEDNVSENVSGVCGTDLRS 360
 Db 224 RGTAAFYHLLPAASGCKQTSTRKKEVEVDYDGIKELYNEDNVSENVSGVCGTDLRS 283
 QY 361 QEGHASPCCPPLQPVSV 377
 Db 284 QEGHASPCCPPLQPVSV 300

RESULT 8
 AAG01903
 ID AAG01903 standard; protein; 131 AA.
 AC AAG01903;
 XX
 XX 06-OCT-2000 (first entry)
 DE Human secreted protein, SEQ ID NO: 5984.
 XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
 KW gene therapy; chromosome mapping.
 XX Homo sapiens.
 OS
 XX EP1033401-A2.
 XX
 XX 06-SEP-2000.
 XX
 XX 21-FEB-2000; 2000BP-00200610.
 XX
 XX 26-FEB-1999; 99US-0122487P.
 XX
 XX (GEST) GENSET.
 XX
 XX Dumas Milne Edwards J, Duclert A, Giordano J;
 XX
 XX WPI; 2000-500381/45.
 DR N-PSDB; AAC01909.
 XX
 XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
 XX
 XX Claim 13; SEQ ID NO 5984; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
 CC 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
 CC prepared from total human RNAs or polyA+ RNAs derived from 30 different
 CC tissues. EST sequences usually correspond mainly to the 3' untranslated
 CC region (UTR) of the mRNA because they are often obtained from oligo-dT
 CC primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
 CC sequences derived from the 5' ends of mRNAs and even in those cases where
 CC longer cDNA sequences have been obtained, the full 5' UTR is rarely
 CC included. 5' ESTs are derived from mRNAs with intact 5' ends and can
 CC therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
 CC are also used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. They are used to obtain upstream regulatory sequences
 CC and to design expression and secretion vectors

XX Sequence 131 AA;
 Query Match 34.0%; Score 667; DB 3; Length 131;
 Best Local Similarity 100.0%; Pred No. 1.8e-61; Mismatches 0; Indels 0; Gaps 0;
 Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 130 MERIILDKNLWDLHTATPLDFLHIFHAIIVSTRPQLLSPLKPSQHLAVLTQLLHQM 189
 Db 1 MERIILDKNLWDLHTATPLDFLHIFHAIIVSTRPQLLSPLKPSQHLAVLTQLLHQM 60
 QY 190 ACNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCRELVAHLS 249

Db 61 ACNQLQFRGSMALAMVSLMEKLIIPDWLSLTIELLOKAQMDSSQLIHCRELVAHLS 120
 QY 250 LQSSLPNSVY 260
 Db 121 LQSSLPNSVY 131

RESULT 9
 ABG18403
 ID ABG18403 standard; protein; 369 AA.
 AC ABG18403;
 XX
 XX 18-FEB-2002 (first entry)
 XX Novel human diagnostic protein #18394.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS
 XX WO200175067-A2.
 XX
 XX 11-OCT-2001.
 XX
 XX 30-MAR-2001; 2001WO-US008631.
 XX
 XX 31-MAR-2000; 2000US-00540217.
 PR 23-AUG-2000; 2000US-00649167.
 XX
 XX (HYSE-) HYSEQ INC.
 XX
 XX Drmanac RT, Liu C, Tang YT;
 XX
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS82590.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX Claim 20; SEQ ID NO 48762; 103pp; English.
 XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
 CC sequences (I) is useful as hybridisation probes, polymerase chain
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
 CC and in recombinant production of (II). The polynucleotides are also used
 CC in diagnostics as expressed sequence tags for identifying expressed
 CC genes. (I) is useful in gene therapy techniques to restore normal
 CC activity of (II) or to treat disease states involving (II). (II) is
 CC useful for generating antibodies against it, detecting or quantitating a
 CC polypeptide in tissue, as molecular weight markers and as a food
 CC supplement. (II) and its binding partners are useful in medical imaging
 CC of sites expressing (II). (I) and (II) are useful for treating disorders
 CC involving aberrant protein expression or biological activity. The
 CC polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
 CC amino acid sequences of the invention. Note: The sequence data for this
 CC patent did not appear in the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 369 AA;
 Query Match 25.6%; Score 502.5; DB 4; Length 369;
 Best Local Similarity 44.6%; Pred No. 1.7e-43;
 Matches 111; Conservative 44; Mismatches 89; Indels 5; Gaps 1;

PT Identifying a gene involved in disease for treating hypoxia-regulated
 PT conditions, comprises comparing the transcriptome/proteome of two cell
 PT types under different conditions and identifying a differentially
 PT regulated gene.

XX Claim 35; Page 374; 538pp; English.

XX The present invention relates to methods for identifying genes and
 CC proteins that are implicated in a specific disease or physiological
 CC condition. The method comprises comparing the transcriptome/proteome of a
 CC specialised cell type implicated in a disease or condition with that of a
 CC second specialised cell type, under two experimental conditions, and
 CC identifying a gene that is differentially regulated in the two
 CC specialised cell types under experimental conditions. ABV7873-ABV78116
 CC and ABP65061-ABP65257 were identified using the methods of the invention.
 CC The coding sequences and proteins are useful for treating a disease in a
 CC patient, for manufacture of a medicament for treating hypoxia-regulated
 CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
 CC biological response to hypoxia conditions, or hypoxic-associated
 CC pathology in a patient. The coding sequences and proteins are also useful
 CC for monitoring the therapeutic treatment of a disease or physiological
 CC condition, such as cancer, ischaemic conditions, reperfusion injury,
 CC retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory
 CC conditions, wound healing, inflammation, erythropoiesis or hair loss

XX Sequence 344 AA;

Query Match 16.6%; Score 326.5; DB 5; Length 344;
 Best Local Similarity 36.4%; Pred. No. 4.7e-25;
 Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;
 QY 31 VRKMPSON-VSPSORDEVIOWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
 DB 41 IEATPNDNTLCFGLRNAKVEDLSLANFFGSCSTETFLAVNILDRLFLAMKVKPKHLSC 100
 QY 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSCSSSEILRMERIIDKLNWDLHTATPLD 149
 DB 101 IGVCSFLAARIVEEDCNIPSTHDVIRISQCKCTASDIKRMKEIKISEKLHYELEATTALN 160
 QY 150 FLHIFHAIIV---STRPQLLSLPKLSQSHLAVLTQKLLHMACNQLLOF---RGSMLA 203
 DB 161 FLHLYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRLIIFSKAKPSVLA 207
 QY 204 LAMVLSLEMEKLIPOWLSLTIELLO-----KAQDSSQLIHCRELVAHLSTLOS 252
 DB 208 LCLLNLEVETL-----KSVELLEILLVKKHKSINDTEFFYRWELVSKLAEYSS 257

RESULT 12

ADF66631

XX ADF66631 standard; protein; 344 AA.

XX ADF66631;

XX 12-FEB-2004 (first entry)

XX Human cyclin G2 protein.

XX apoptosis inducer; cyclin G2; cyclin box; cytostatic;
 KW antineoplastic drug; cancer; human.

XX Homo sapiens.

XX JP2003238591-A.

XX 27-AUG-2003.

XX 21-FEB-2002; 2002JP-00044335.

XX 21-FEB-2002; 2002JP-00044335.

XX (OOSA-) ZH OOSAKA SANGYO SHINKO KIKO.

XX

DR WPI; 2004-065215/07.

XX Apoptosis inducer comprising polypeptide which consists of amino acid
 PT sequence which is one or all part of cyclin G2, sequence in which 1 or
 PT more amino acid has deletion, substitution or addition in the amino acid
 PT sequence.

XX Disclosure; SEQ ID NO 1; 15pp; Japanese.

XX The invention relates to a novel apoptosis inducer consisting of a
 CC polypeptide comprising an amino acid sequence which is part or all of
 CC cyclin G2 and contains at least a cyclin box and a polypeptide which
 CC consists of an amino acid sequence from which 1 or more amino acid is
 CC deleted, substituted or added in this amino acid sequence and has an
 CC apoptosis induction activity. The polypeptide of the invention
 CC demonstrates cytostatic activity and may be useful for screening
 CC antineoplastic drugs, as well as for treating cancer. The current
 CC sequence is that of the human cyclin G2 protein of the invention.

XX Sequence 344 AA;

Query Match 16.6%; Score 326.5; DB 8; Length 344;
 Best Local Similarity 36.4%; Pred. No. 4.7e-25;
 Matches 86; Conservative 44; Mismatches 73; Indels 33; Gaps 7;

QY 31 VRKMPSON-VSPSORDEVIOWLAKLYQFNLYPETFALASSLLDRFLATVKAHPKYLSC 89
 DB 41 IEATPNDNTLCFGLRNAKVEDLSLANFFGSCSTETFLAVNILDRLFLAMKVKPKHLSC 100
 QY 90 IAISCFFLAAKTVEEDERIPVLKVLARDSFCGSCSSSEILRMERIIDKLNWDLHTATPLD 149
 DB 101 IGVCSFLAARIVEEDCNIPSTHDVIRISQCKCTASDIKRMKEIKISEKLHYELEATTALN 160
 QY 150 FLHIFHAIIV---STRPQLLSLPKLSQSHLAVLTQKLLHMACNQLLOF---RGSMLA 203
 DB 161 FLHLYHTIILCHTSEKIL-SLDKLE-----AQLKACNCRLIIFSKAKPSVLA 207
 QY 204 LAMVLSLEMEKLIPOWLSLTIELLO-----KAQDSSQLIHCRELVAHLSTLOS 252
 DB 208 LCLLNLEVETL-----KSVELLEILLVKKHKSINDTEFFYRWELVSKLAEYSS 257

RESULT 13

AD019808

ID AD019808 standard; protein; 344 AA.

XX AD019808;

XX 12-AUG-2004 (first entry)

XX Human PRO polypeptide #366.

XX Human; PRO; immune related disorder; systemic lupus erythematosus;
 KW rheumatoid arthritis; osteoarthritis; juvenile chronic arthritis;
 KW systemic sclerosis; Sjogren's syndrome; vasculitis; sarcoidosis;
 KW autoimmune haemolytic anaemia; autoimmune thrombocytopenia; thyroiditis;
 KW diabetes mellitus; renal disease; demyelinating disease;
 KW central nervous system; peripheral nervous system;
 KW demyelinating polyneuropathy; Guillain-Barre syndrome;
 KW chronic inflammatory demyelinating polyneuropathy.

XX Homo sapiens.

XX WO2004043361-A2.

XX 27-MAY-2004.

XX 06-NOV-2003; 2003WO-US035268.

XX 08-NOV-2002; 2002US-0425235P.

XX (GETH) GENENTECH INC.

XX

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:36:40 ; Search time 947.803 Seconds
(without alignments)
2354.648 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPCPLENQLSLLEKAI.....LSROEGHASPCLPQPVSVM 377

Scoring table:

OLIGO	Xgapop	60.0	Xgapext	60.0
Ygapop	60.0	Ygapext	60.0	
Fgapop	6.0	Fgapext	7.0	
Delop	6.0	Delext	7.0	

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8776198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2.1/USPTO.spool/US09736250/runat 07022005 154941 20640/app query.fasta_1.718
-DB=N_Geneseq 16Dec04 -QMT=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 586 @runat 07022005 154941 20640 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq 16Dec04:*

1:	Geneseq1980s:*
2:	Geneseq1990s:*
3:	Geneseq2000s:*
4:	Geneseq2001as:*
5:	Geneseq2001bs:*
6:	Geneseq2002as:*
7:	Geneseq2002bs:*
8:	Geneseq2003as:*
9:	Geneseq2003bs:*
10:	Geneseq2003cs:*
11:	Geneseq2003ds:*
12:	Geneseq2004as:*
13:	Geneseq2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377	100.0	1260	3	Aa237836
2	377	100.0	1260	6	ABK83672 Human cDN
3	377	100.0	1260	10	ADK61064
4	377	100.0	1260	11	AD131573 Human cDN
5	377	100.0	1260	13	ADR25465 Breast ca

6	377	100.0	1328	2	AAT73937	Aat73937 DNA encod
7	377	100.0	1384	8	ACC47339	Acc47339 Human pro
8	377	100.0	1889	6	ABL87929	AbL87929 Human ova
9	377	100.0	1890	12	ADP10653	Adp10653 Reference
10	377	100.0	1890	13	ACN38124	Acn38124 Tumour-as
11	296	78.5	1651	9	AAD57247	Aad57247 Human CGD
12	266	70.6	2755	5	ADL63374	AdL63374 Human ova
13	153	40.6	903	12	ADN01156	Adn01156 Human cel
14	144	38.2	444	3	AAC01909	Aac01909 Human sec
15	129	34.2	804	2	AAX40003	Aax40003 Prostate
16	123	32.6	2146	5	ADL63082	AdL63082 Human ova
17	90	23.9	392	2	AAQ61358	AaQ61358 Human bra
18	90	23.9	536	10	ADF82253	Adf82253 Leukaemia
19	88	23.3	1493	2	AZA41284	Aza41284 Human nor
20	84	22.3	409	10	ADF80870	Adf80870 Leukaemia
21	75	19.9	486	5	ADL43407	AdL43407 Human ova
22	66	17.5	329	2	AAT23729	Aat23729 Human gen
23	65	17.2	447	4	AAS25071	Aas25071 Human ova
24	65	17.2	447	5	AAH83716	AaH83716 Human ova
25	62	16.4	889	6	ABL87928	AbL87928 Human ova
26	51	13.5	597	10	ADK61065	AdK61065 Ovarian c
27	49	13.0	426	5	ADL37023	AdL37023 Human ova
28	49	13.0	426	5	ADI71872	AdI71872 Human ova
29	44	11.7	417	2	AAT26236	Aat26236 Human gen
30	41	10.9	389	10	ADK61086	AdK61086 Ovarian c
31	40	10.6	477	5	ADI72632	AdI72632 Human ova
32	40	10.6	477	5	ADL37771	AdL37771 Human ova
33	40	10.6	516	5	ADL44155	AdL44155 Human ova
34	38	10.1	136	2	AAQ76921	AaQ76921 Human gen
35	37	9.8	444	6	ABK45862	AbK45862 cDNA enco
36	34	9.0	304	3	AAC25819	Aac25819 Human sec
37	34	9.0	388	4	AAI91566	AaI91566 Human pol
38	30	8.6	247	6	ABV89029	Abv89029 Human col
39	25	6.6	351	8	AAD51549	AdA51549 Human BCA
40	25	6.6	469	9	ACH26661	Ach26661 Human adu
41	24	6.4	420	8	ABX44645	Abx44645 Bovine ES
42	22	5.8	183	2	AAQ76715	AaQ76715 Human gen
43	21	5.6	298	8	ABZ19815	AbZ19815 Group III
44	21	5.0	60	6	ABN40110	Abn40110 Human spl
45	18	4.8	348	6	ABSG9603	AbSG9603 Novel mur
46	14	3.7	65	6	ABN55748	AbN55748 Mouse spl
47	13	3.4	135	2	AAQ76716	AaQ76716 Human gen
48	10	2.7	50	6	ABZ00749	AbZ00749 Human leu
49	9	2.4	28	12	ADP11644	Adp11644 Tagman pr
50	9	2.4	1643	2	AAX08522	Aax08522 NBP46 (ro
51	9	2.4	1643	6	ABK11098	AbK11098 DNA encod
52	9	2.4	6265	2	AAX08523	Aax08523 NBP46 (ro
53	9	2.4	24389	4	ABL29006	AbL29006 Drosophil
54	9	2.4	16382	13	ABD32659	Abd32659 Human can
55	8	2.1	267	7	ADS65315	AdS65315 Corn seed
56	8	2.1	277	10	ABX81638	Abx81638 Corn ear-
57	8	2.1	279	3	AAC28555	Aac28555 Human sec
58	8	2.1	400	2	AAV75840	Aav75840 Staphyloc
59	8	2.1	435	10	ADF80883	Adf80883 Leukaemia
60	8	2.1	483	8	ABZ53075	Abz53075 Aspergill
61	8	2.1	494	13	ACN56052	Acn56052 Cotton an
62	8	2.1	551	6	ABQ55991	AbQ55991 Human ova
63	8	2.1	554	6	ABT10393	Abt10393 Human bre
64	8	2.1	573	13	ADQ55289	Adq55289 Novel can
65	8	2.1	578	13	ADQ79216	AdQ79216 Novel can
66	8	2.1	738	13	ADR26517	Adr26517 Breast ca
67	8	2.1	744	3	AAA44975	Aaa44975 Human sec
68	8	2.1	791	6	ABQ37048	AbQ37048 Oligonuc1
69	8	2.1	796	6	ABQ37049	AbQ37049 Oligonuc1
70	8	2.1	796	6	ABQ34158	AbQ34158 Oligonuc1
71	8	2.1	796	6	ABQ34159	AbQ34159 Oligonuc1
72	8	2.1	809	10	ADH44941	Adh44941 Murine TC
73	8	2.1	852	4	AAH05379	Aah05379 Human cDN
74	8	2.1	871	13	ADR63643	Adr63643 Cotton cD
75	8	2.1	909	10	ADF41724	Adf41724 Bacillus
76	8	2.1	912	6	AAD28484	Aad28484 Bacillus
77	8	2.1	1053	10	ACC60670	Acc60670 Gene sequ
78	8	2.1	1053	10	ADK62087	AdK62087 Disease t

79	8	2.1	1089	6	ABK24365	Abk24365 DNA encod	152	8	2.1	3486	13	AD899002	Ad899002 Human CDK
80	8	2.1	1099	4	AAH00430	Aah00430 Candida k	153	8	2.1	3568	2	AAH82180	Aah82180 Human p27
c 81	8	2.1	1099	13	ADS96675	Ads96675 Drosophil	154	8	2.1	3568	4	AAH74231	Aah74231 Nucleotid
c 82	8	2.1	1110	8	ACA4674	Aca4674 Prokaryot	155	8	2.1	3578	2	AAH05819	Aax05819 Rat phero
c 83	8	2.1	1119	8	ABZ71977	Abz71977 Human clo	c 156	8	2.1	3706	4	AAH12100	Abl12100 Drosophil
c 84	8	2.1	1119	10	ADD14654	Add14654 Human src	157	8	2.1	3819	4	AAH18644	Aah18644 Human cdn
c 85	8	2.1	1125	10	ADF00364	Adf00364 Bacterial	158	8	2.1	4003	12	ADQ22240	Adq22240 Human sof
c 86	8	2.1	1176	6	ABK24364	Abk24364 DNA encod	159	8	2.1	4230	10	ADRE13178	Adre13178 Human dia
c 87	8	2.1	1233	12	ADL03978	Adl03978 DNA encod	c 160	8	2.1	4284	13	ADR06868	Adr06868 Full leng
c 88	8	2.1	1242	12	ADO30250	Ado30250 Mouse GPC	161	8	2.1	4286	12	ADL12903	Adl12903 Human ste
c 89	8	2.1	1248	10	ADH44926	Adh44926 Human TCH	162	8	2.1	4336	5	AAS64328	Aas64328 DNA encod
c 90	8	2.1	1268	10	ADH44939	Adh44939 Human TCH	163	8	2.1	4388	8	ABX34490	Abx34490 Human mdd
c 91	8	2.1	1294	6	ABL53778	AbL53778 Human com	c 164	8	2.1	4434	8	ACA22280	Aca22280 Prokaryot
c 92	8	2.1	1332	4	ABL23349	AbL23349 Drosophil	c 165	8	2.1	4750	6	ABL68819	AbL68819 Kidney ca
c 93	8	2.1	1355	12	ADN96037	Adn96037 Human NOV	166	8	2.1	4902	4	ABL20352	AbL20352 Drosophil
c 94	8	2.1	1356	9	ACD06214	AcD06214 Human CDN	c 167	8	2.1	5091	4	ABL07051	AbL07051 Drosophil
c 95	8	2.1	1374	6	ABK65337	Abk65337 Arabidops	c 168	8	2.1	5091	13	ADQ89687	Adq89687 Antagonis
c 96	8	2.1	1401	13	ADT45098	Adt45098 Bacterial	c 169	8	2.1	5201	4	ABL14030	AbL14030 Drosophil
c 97	8	2.1	1527	10	ADC92050	Adc92050 E. faeciu	170	8	2.1	6428	4	AAK78562	Aak78562 Human imm
c 98	8	2.1	1550	5	ADL62569	Adl62569 Human ova	171	8	2.1	6539	10	ADE57349	Ade57349 Human gen
c 99	8	2.1	1557	10	AAD57653	Aad57653 Rice enha	172	8	2.1	6669	6	ABL32193	AbL32193 Human imm
c 100	8	2.1	1637	3	AAc48042	Aac48042 Zea may	173	8	2.1	6669	6	ABL92197	AbL92197 Chemical
c 101	8	2.1	1654	4	ABL10415	AbL10415 Drosophil	174	8	2.1	6669	6	ABL49306	AbL49306 Human pol
c 102	8	2.1	1699	4	AAH14082	Aah14082 Human CDN	175	8	2.1	8285	6	AAK98916	Aak98916 Human MAP
c 103	8	2.1	1703	6	ABL90390	AbL90390 Human pol	176	8	2.1	8285	10	ADG90365	Adg90365 Human kin
c 104	8	2.1	1715	2	AAZ24887	Aaz24887 Human sec	177	8	2.1	8522	8	AAD50016	Aad50016 Human kin
c 105	8	2.1	1715	8	ADA39843	Ada39843 Human sec	178	8	2.1	8541	4	ABL07050	AbL07050 Drosophil
c 106	8	2.1	1715	8	ACC50456	Acc50456 Human sec	c 179	8	2.1	9299	6	ABL33724	AbL33724 Human imm
c 107	8	2.1	1715	8	ABZ71255	Abz71255 Human sec	c 180	8	2.1	9352	6	ABL32103	AbL32103 Human imm
c 108	8	2.1	1715	10	ADC73523	Adc73523 Human sec	181	8	2.1	9905	4	ABL28652	AbL28652 Drosophil
c 109	8	2.1	1719	8	ADA70078	Ada70078 Rice gene	182	8	2.1	10274	4	ABL06514	AbL06514 Drosophil
c 110	8	2.1	1771	10	ADF82265	Adf82265 Leukaemia	c 183	8	2.1	10918	5	ABA09581	AbA09581 Human bon
c 111	8	2.1	1790	12	ADQ17542	Adq17542 Human sof	c 184	8	2.1	10920	6	ABN60009	Abn60009 Novel hum
c 112	8	2.1	1831	4	AAF44676	Aaf44676 Novel pro	185	8	2.1	10942	4	ABL29604	AbL29604 Drosophil
c 113	8	2.1	1831	12	ADI29374	Adi29374 Human MAR	186	8	2.1	11827	6	ABK87610	Abk87610 Genomic D
c 114	8	2.1	1907	3	AAc79848	Aac79848 Human sec	187	8	2.1	11827	10	ADH00899	Adh00899 Human kin
c 115	8	2.1	1962	13	ADS56130	Ads56130 Bacterial	188	8	2.1	12099	4	ABL16890	AbL16890 Drosophil
c 116	8	2.1	1986	8	ACA20539	Aca20539 Prokaryot	c 189	8	2.1	12099	6	ABL33718	AbL33718 Human imm
c 117	8	2.1	1989	4	ABL20305	AbL20305 Drosophil	c 190	8	2.1	12099	13	ADG36463	Adg36463 Human aut
c 118	8	2.1	1992	9	ADA31028	Ada31028 DNA encod	c 191	8	2.1	12099	13	ACN37212	Acn37212 Human per
c 119	8	2.1	2000	8	ADA72978	Ada72978 Rice gene	c 192	8	2.1	20512	6	AAK38339	Aak38339 Genomic D
c 120	8	2.1	2000	8	ADA71473	Ada71473 Rice gene	193	8	2.1	21840	11	ACN44054	Acn44054 Human gen
c 121	8	2.1	2007	2	AAx05858	Aax05858 Rat phero	c 194	8	2.1	26071	13	ABD33438	Abd33438 Murine ca
c 122	8	2.1	2007	4	AA51625	Aas1625 Staphyloc	c 195	8	2.1	27310	11	ACN44622	Acn44622 Human gen
c 123	8	2.1	2007	8	ACF74655	AcF74655 Staphyloc	c 196	8	2.1	32220	4	AAAL37568	Aal37568 Human mus
c 124	8	2.1	2010	4	AA54559	Aas4559 Staphyloc	c 197	8	2.1	32220	8	ABX60556	Abx60556 cDNA enco
c 125	8	2.1	2010	8	ACA20319	AcA20319 Prokaryot	c 198	8	2.1	32220	12	ADJ31306	Adj31306 Human mus
c 126	8	2.1	2021	6	ABK73866	Abk73866 Bacillus	c 199	8	2.1	32829	13	ABD33037	Abd33037 Mouse can
c 127	8	2.1	2071	12	ADQ64086	Adq64086 Novel hum	200	8	2.1	35651	4	AAF57595	Aaf57595 ATM compl
c 128	8	2.1	2114	6	ABQ54834	Abq54834 Human ova	c 201	8	2.1	36176	11	ACN45126	Acn45126 Human gen
c 129	8	2.1	2161	2	AAQ58742	Aaq58742 dMEF2. 3/	c 202	8	2.1	39827	12	ADM98979	Adm98979 Diterpene
c 130	8	2.1	2161	9	ADA02835	Ada02835 Human MEF	c 203	8	2.1	43572	12	ADM97861	Adm97861 Mouse can
c 131	8	2.1	2161	10	ADB72573	Adb72573 Human MEF	204	8	2.1	43572	11	ACN45210	Acn45210 Human gen
c 132	8	2.1	2161	10	ADC55314	Adc55314 Human Mef	c 205	8	2.1	50781	11	ACN44360	Acn44360 Mouse gen
c 133	8	2.1	2161	12	ADM74430	Adm74430 Human car	c 206	8	2.1	55996	9	ADA02741	Ada02741 Mouse Tnf
c 134	8	2.1	2165	6	ABK24363	Abk24363 DNA encod	c 207	8	2.1	55996	10	ADB72479	Adb72479 Mouse Tnf
c 135	8	2.1	2165	12	ADL06480	Adl06480 Human tum	c 208	8	2.1	55996	12	ADC85221	Adc85221 Mouse Tnf
c 136	8	2.1	2187	10	ADC91237	Adc91237 E. faeciu	c 209	8	2.1	55996	10	ADM74336	Adm74336 Murine ca
c 137	8	2.1	2287	12	ADQ63099	Adq63099 Novel hum	c 210	8	2.1	70768	6	AAAL41152	Aal41152 Wooden le
c 138	8	2.1	2304	4	ABA08970	AbA08970 Human sem	c 211	8	2.1	72149	10	ADG81173	Adg81173 ML-236B s
c 139	8	2.1	2464	4	ABA08691	AbA08691 Human sec	c 212	8	2.1	72352	12	ADQ97067	Adq97067 Mouse can
c 140	8	2.1	2496	6	ABA05022	AbA05022 Human DNA	c 213	8	2.1	74037	6	ABK94412	AbK94412 DNA encod
c 141	8	2.1	2644	10	ADA30486	Ada30486 Human nov	c 214	8	2.1	85680	3	AAF22299	Aaf22299 BAC conta
c 142	8	2.1	2790	2	AAV28916	Aav28916 Human sem	c 215	8	2.1	88607	12	ADQ97648	Adq97648 Mouse can
c 143	8	2.1	2800	11	ADM01338	Adm01338 Human CDN	c 216	8	2.1	96591	10	ADC85301	Adc85301 Mouse sos
c 144	8	2.1	2986	8	ACF62754	AcF62754 Human p27	c 217	8	2.1	96592	9	ADA02822	Ada02822 Human SOS
c 145	8	2.1	3275	5	ABV23844	Abv23844 Human pro	c 218	8	2.1	96592	10	ADB72560	Adb72560 Human SOS
c 146	8	2.1	3387	12	ADOB4890	AdoB4890 E faecium	c 219	8	2.1	96592	12	ADM74417	Adm74417 Human car
c 147	8	2.1	3394	4	ABL23348	AbL23348 Drosophil	c 220	8	2.1	110000	3	AAF22303	Aaf22303 Continuation (6 of
c 148	8	2.1	3432	2	AAV28915	Aav28915 Human sem	c 221	8	2.1	115780	13	ABD32610	Abd32610 Mouse can
c 149	8	2.1	3486	8	ABZ09880	Abz09880 Human 5'	c 222	8	2.1	119211	4	AAF28553	Aaf28553 Genomic f
c 150	8	2.1	3486	10	ADB53961	AdB53961 CDKN1B ge	c 223	8	2.1	121160	12	ADQ97870	Adq97870 Human can
c 151	8	2.1	3486	10	ADE84022	Ade84022 5' regula	c 224	8	2.1	130207	11	ACN44762	Acn44762 Human gen

225	8	2.1	133632	11	ACN45054	Acn45054 Human gen	C 298	7	1.9	261	4	ABA38513	AbA38513 Probe #16
226	8	2.1	166910	12	ADN01278	Adn01278 Human end	C 299	7	1.9	261	4	AAK47547	AAk47547 Human bon
227	8	2.1	174600	12	ADQ97520	Adq97520 Mouse can	C 300	7	1.9	261	4	AAK21386	AAk21386 Human bra
228	8	2.1	131477	12	ADP69744	Adp69744 Human ROC	C 301	7	1.9	261	4	ABS47282	ABs47282 Human liv
C 229	8	2.1	313234	12	ADQ59437	Adq59437 Human can	C 302	7	1.9	261	6	ABs21644	ABs21644 Human gen
230	8	2.1	349980	6	ABQ81844	Abq81844 Bifidobac	C 303	7	1.9	262	5	ABV56933	ABv56933 Human pro
231	7	1.9	21	12	ADP11892	Adp11892 Set 2 lef	C 304	7	1.9	266	6	ABK93405	ABk93405 Human bre
C 232	7	1.9	22	4	AAF60112	Aaf60112 Human ATM	C 305	7	1.9	268	4	AAK60188	AAk60188 Human imm
233	7	1.9	25	2	AAQ80095	Aaq80095 ADPGPP gl	C 306	7	1.9	268	9	ADA59392	ADa59392 Soybean t
234	7	1.9	25	2	AAQ74550	Aaq74550 Respirato	C 307	7	1.9	268	12	ADP60686	ADp60686 Soybean c
235	7	1.9	25	2	AAQ74552	Aaq74552 Respirato	C 308	7	1.9	273	3	ADF56911	ADf56911 Urogenita
C 236	7	1.9	25	2	AAV03257	Aav03257 Homo eapi	C 309	7	1.9	273	5	ABV60028	ABv60028 Human pro
237	7	1.9	25	9	ACI29910	ACi29910 Human mic	C 310	7	1.9	274	6	ABL69662	ABl69662 Prostate
C 238	7	1.9	25	13	ADR56654	Adr56654 Drug ther	C 311	7	1.9	274	6	ABN93815	ABn93815 Gene #313
239	7	1.9	30	2	AAV03258	Aav03258 Homo sapi	C 312	7	1.9	277	5	ABN14893	ABn14893 Human ner
240	7	1.9	33	2	AAQ73938	Aaq73938 Primer fo	C 313	7	1.9	281	10	ABX87275	ABx87275 Corn ear-
C 241	7	1.9	35	2	AAQ74555	Aaq74555 Respirato	C 314	7	1.9	283	9	ADA59389	ADa59389 Soybean t
242	7	1.9	41	4	AAH44336	Aah44336 Human pro	C 315	7	1.9	283	12	ADP60683	ADp60683 Soybean c
C 243	7	1.9	41	6	ABZ44564	Abz44564 Human ATP	C 316	7	1.9	284	10	ADG37661	ADg37661 Aspergill
C 244	7	1.9	41	6	ABZ447352	Abz447352 Human ATP	C 317	7	1.9	285	10	ABX88348	ABx88348 Corn ear-
C 245	7	1.9	49	2	AAQ80484	Aaq80484 Hepatoma	C 318	7	1.9	287	5	ABV59696	ABv59696 Human pro
246	7	1.9	60	13	ADS52932	Ads52932 Eucalyptu	C 319	7	1.9	291	6	ABL71676	ABl71676 Corn tass
C 247	7	1.9	61	2	AAV38265	Aav38265 Murine li	C 320	7	1.9	291	8	ACA44850	ACa44850 Prokaryot
C 248	7	1.9	65	6	ABN54061	ABn54061 Mouse spl	C 321	7	1.9	292	6	ABZ78070	ABz78070 Human bre
C 249	7	1.9	65	12	ADP97797	Adp97797 C. albica	C 322	7	1.9	293	4	AAZ27973	AAz27973 Novel CDN
250	7	1.9	84	2	AAV50396	Aav50396 Obesity p	C 323	7	1.9	293	6	ABL70921	ABl70921 Corn tass
C 251	7	1.9	105	5	AAQ88481	Aaq88481 Target se	C 324	7	1.9	293	6	ABL72651	ABl72651 Corn tass
C 252	7	1.9	109	3	AAQ25321	Aaq25321 Human sec	C 325	7	1.9	293	10	ADG40687	ADg40687 Human res
253	7	1.9	135	4	AAI26119	AAi26119 Probe #16	C 326	7	1.9	293	11	ADI96651	ADi96651 Human res
254	7	1.9	135	4	ABA73477	ABa73477 Human foe	C 327	7	1.9	293	12	ADQ19591	ADq19591 Human sof
255	7	1.9	135	4	AAI53913	AAi53913 Probe #22	C 328	7	1.9	298	6	ABN16401	ABn16401 Human ORF
256	7	1.9	135	4	ABA38781	ABa38781 Probe #17	C 329	7	1.9	298	10	ADK53642	ADk53642 Plant DNA
257	7	1.9	135	4	AAK48084	AAk48084 Human bon	C 330	7	1.9	299	10	ADL24571	ADl24571 Intestina
258	7	1.9	135	4	AAK21920	AAk21920 Human bra	C 331	7	1.9	299	13	ADS50728	ADs50728 Bacterial
259	7	1.9	135	4	ABZ47798	ABz47798 Human liv	C 332	7	1.9	300	2	AAZ14572	AAz14572 Human gen
260	7	1.9	135	6	ABZ22005	ABz22005 Human gen	C 333	7	1.9	300	2	AAZ13463	AAz13463 Human gen
261	7	1.9	138	6	ABQ94367	ABq94367 Tumour su	C 334	7	1.9	300	5	ABV59677	ABv59677 Human pro
262	7	1.9	154	5	AAI61603	AAi61603 Soybean 3	C 335	7	1.9	300	6	ABL72270	ABl72270 Corn tass
263	7	1.9	156	4	AAI26013	AAi26013 Probe #15	C 336	7	1.9	302	2	ABL72622	ABl72622 Human gen
264	7	1.9	156	4	ABA73082	ABa73082 Human foe	C 337	7	1.9	303	3	AAA82177	AAa82177 N. mening
265	7	1.9	156	4	AAI53511	AAi53511 Probe #22	C 338	7	1.9	303	4	AAZ25149	AAz25149 Human bre
266	7	1.9	156	4	ABA38580	ABa38580 Probe #17	C 339	7	1.9	303	10	ADL24580	ADl24580 Intestina
267	7	1.9	156	4	AAK47677	AAk47677 Human bon	C 340	7	1.9	305	4	AAK58245	AAk58245 Human imm
268	7	1.9	156	4	AAK21515	AAk21515 Human bra	C 341	7	1.9	307	8	ABX54191	ABx54191 Bovine ES
269	7	1.9	156	4	ABZ47412	ABz47412 Human liv	C 342	7	1.9	308	5	ABV02252	ABv02252 Human pro
270	7	1.9	156	6	ABZ21732	ABz21732 Human gen	C 343	7	1.9	312	6	ABN17494	ABn17494 Human ORF
C 271	7	1.9	201	13	ADS41108	Ads41108 Human aut	C 344	7	1.9	313	6	ABN75549	ABn75549 Human ORF
C 272	7	1.9	201	13	ADS41115	Ads41115 Human aut	C 345	7	1.9	313	5	ABV59563	ABv59563 Human pro
C 273	7	1.9	201	13	ADS41111	Ads41111 Human aut	C 346	7	1.9	315	4	ABL22863	ABl22863 Drosophil
C 274	7	1.9	206	5	AAF92541	Aaf92541 Rat T2R14	C 347	7	1.9	315	6	ABQ98980	ABq98980 Human ORF
C 275	7	1.9	206	13	ADR29165	Adr29165 Taste rec	C 348	7	1.9	317	5	ADL171329	ADl171329 Human ova
C 276	7	1.9	212	10	ABX88942	ABx88942 Corn ear-	C 349	7	1.9	317	5	ADL36488	ADl36488 Human ova
C 277	7	1.9	216	10	ABX07022	ABx07022 S. pneumo	C 350	7	1.9	318	5	AAZ34533	AAz34533 Human DNA
C 278	7	1.9	221	3	AAI61671	AAi61671 Human sec	C 351	7	1.9	321	12	ADN98601	ADn98601 Novel hum
279	7	1.9	222	2	AAI12223	AAi12223 Human bia	C 352	7	1.9	321	12	ADO00170	ADo00170 Novel hum
280	7	1.9	222	2	AAI12224	AAi12224 Human bia	C 353	7	1.9	324	4	AAI16306	AAi16306 Human bre
C 281	7	1.9	231	5	ABV59872	ABv59872 Human pro	C 354	7	1.9	324	5	AAZ40074	AAz40074 DNA encod
C 282	7	1.9	234	6	ABL38031	ABl38031 Human col	C 355	7	1.9	324	6	ABN18826	ABn18826 Human ORF
C 283	7	1.9	240	6	ABN75948	ABn75948 Human ORF	C 356	7	1.9	324	11	ADJ09069	ADj09069 Human pro
284	7	1.9	245	5	AAZ78156	AAz78156 DNA encod	C 357	7	1.9	330	5	ADL36584	ADl36584 Human ova
285	7	1.9	245	9	ADA59388	ADa59388 Soybean t	C 358	7	1.9	330	5	ADI71426	ADi71426 Human ova
286	7	1.9	245	12	ADP60682	ADp60682 Soybean c	C 359	7	1.9	330	10	ABT41116	ABt41116 Toxicity
287	7	1.9	246	9	ACH44024	ACH44024 Human foe	C 360	7	1.9	330	12	ADP28773	ADp28773 Human sec
C 288	7	1.9	248	6	ABL82550	ABl82550 Human ova	C 361	7	1.9	331	8	ACC60033	ACC60033 Rice leaf
C 289	7	1.9	251	3	AAI12254	AAi12254 Human sec	C 362	7	1.9	333	5	AAZ33551	AAz33551 Human CDN
C 290	7	1.9	255	5	AAH81835	Aah81835 Rat diffe	C 363	7	1.9	333	10	ADF01017	ADf01017 Bacterial
C 291	7	1.9	256	12	ADQ06443	Adq06443 Soybean t	C 364	7	1.9	333	11	ACH95909	ACH95909 Klebsiell
C 292	7	1.9	257	8	ABZ73190	ABz73190 Rice leaf	C 365	7	1.9	333	12	ADO00101	ADo00101 Novel hum
293	7	1.9	258	10	ADF03777	ADf03777 Bacterial	C 366	7	1.9	333	12	ADN98532	ADn98532 Novel hum
294	7	1.9	260	4	AAK77126	AAk77126 Human imm.	C 367	7	1.9	335	6	ABN19642	ABn19642 Human ORF
C 295	7	1.9	261	4	AAI25973	AAi25973 Probe #15	C 368	7	1.9	338	3	AAZ26641	AAz26641 Human sec
C 296	7	1.9	261	4	ABZ72955	ABz72955 Human foe	C 369	7	1.9	338	5	ABN12454	ABn12454 Human ner
C 297	7	1.9	261	4	AAI53379	AAi53379 Probe #22	C 370	7	1.9	339	3	AAZ56289	AAz56289 Pinus rad

371	7	1.9	341	4	AAI80247	AAI80247 Human pol	C 444	7	1.9	407	4	AAK38822	AAK38822 Human bon
372	7	1.9	342	2	ACT67714	Act67714 H. pylori	C 445	7	1.9	407	4	AAK13094	AAK13094 Human bra
373	7	1.9	342	8	ACD05602	ACD05602 cDNA enco	C 446	7	1.9	407	4	ABS38407	ABS38407 Human liv
374	7	1.9	342	9	ADB12224	ADB12224 Alliococ	C 447	7	1.9	407	5	RAI05349	RAI05349 Probe #53
375	7	1.9	345	2	AAQ04582	AAQ04582 Translate	C 448	7	1.9	407	5	ABA13888	ABA13888 Human ner
376	7	1.9	347	3	AAI19786	AAI19786 Human sec	C 449	7	1.9	407	6	ABS12903	ABS12903 Human gen
377	7	1.9	347	6	ABN95719	Abn95719 Gene #221	450	7	1.9	408	2	RAAX22311	RAAX22311 Human Tan
378	7	1.9	348	8	ABX40729	Abx40729 Bovine ES	451	7	1.9	411	3	AAA77900	AAA77900 cDNA enco
379	7	1.9	350	9	ADA01647	Ada01647 Mouse Cct	452	7	1.9	411	4	AAI28638	AAI28638 Colon tum
380	7	1.9	350	10	ADB71386	Adb71386 Mouse car	453	7	1.9	411	8	ABZ32824	ABZ32824 Human col
381	7	1.9	351	5	ADI67925	Adi67925 Human ova	C 454	7	1.9	411	11	ABDI5173	ABDI5173 Pseudomon
382	7	1.9	351	6	ADI74301	Adi74301 Human ova	C 455	7	1.9	412	6	ABN23489	ABN23489 Human ORF
383	7	1.9	351	6	ABN75387	Abn75387 Human ORF	456	7	1.9	412	9	ACH15795	ACH15795 Human adu
384	7	1.9	352	6	ABV77970	Abv77970 Hypoxia-r	C 457	7	1.9	413	8	ABX50478	ABX50478 Bovine ES
385	7	1.9	355	8	ABX40295	Abx40295 Bovine ES	458	7	1.9	413	11	ACN86250	ACN86250 Breast ca
386	7	1.9	357	2	AAQ90416	AAQ90416 Anti-idio	459	7	1.9	415	8	ABZ55892	ABZ55892 Aspergill
387	7	1.9	357	6	ABN21278	Abn21278 Human ORF	C 460	7	1.9	416	9	ACH46178	ACH46178 Human inf
388	7	1.9	358	10	ACD95887	ACD95887 Human col	C 461	7	1.9	417	8	ACA25770	ACA25770 Prokaryot
389	7	1.9	363	2	AAI67949	AAI67949 H. pylori	462	7	1.9	421	4	ABA08282	ABA08282 Human phe
390	7	1.9	364	5	ABV06784	Abv06784 Human pro	463	7	1.9	421	8	ACD05890	ACD05890 Novel hum
391	7	1.9	366	12	ADJ40403	Adj40403 Plant cDN	C 464	7	1.9	423	5	ABV00616	ABV00616 Human pro
392	7	1.9	367	5	ABV03385	Abv03385 Human pro	C 465	7	1.9	423	8	ABX52708	ABX52708 Bovine ES
393	7	1.9	369	2	AAQ59659	AAQ59659 Human bra	C 466	7	1.9	425	5	ABV09785	ABV09785 Human pro
394	7	1.9	369	13	ADS45423	Ads45423 Bacterial	467	7	1.9	426	6	ABN63474	ABN63474 Human can
395	7	1.9	371	4	AAI84375	AAI84375 Human pol	468	7	1.9	426	4	RAK55615	RAK55615 Human imm
396	7	1.9	371	9	ACL15554	ACL15554 DNA clone	C 469	7	1.9	426	12	ADQ76027	ADQ76027 Murine GM
397	7	1.9	372	8	ABX38062	Abx38062 Bovine ES	470	7	1.9	427	4	AAI13726	AAI13726 Probe #36
398	7	1.9	373	6	ABL67565	ABL67565 Oesophagu	471	7	1.9	427	4	ABA55438	ABA55438 Human foe
399	7	1.9	373	6	ABL64867	ABL64867 Lung canc	472	7	1.9	427	4	AAI35084	AAI35084 Probe #37
400	7	1.9	375	4	AAI47669	AAI47669 Human ins	473	7	1.9	427	4	ABA44962	ABA44962 Human bre
401	7	1.9	375	4	AAI14767	AAI14767 Human IGF	474	7	1.9	427	4	ABA25160	ABA25160 Probe #36
402	7	1.9	375	5	AAI65869	AAI65869 DNA enco	475	7	1.9	427	4	AAK29135	AAK29135 Human bon
403	7	1.9	375	10	ADI60316	Adi60316 Secreted	476	7	1.9	427	5	AAK03677	AAK03677 Human bra
404	7	1.9	375	10	ADK41560	Adk41560 Anti-cell	477	7	1.9	427	5	AAI03604	AAI03604 Probe #35
405	7	1.9	375	10	ADK41562	Adk41562 Anti-cell	478	7	1.9	427	6	ABS03688	ABS03688 Human gen
406	7	1.9	377	2	AAQ60973	AAQ60973 Human bra	479	7	1.9	429	4	AAAL06799	AAAL06799 Human rep
407	7	1.9	377	5	AAI89106	AAI89106 Human pol	480	7	1.9	429	4	RAAL06797	RAAL06797 Human rep
408	7	1.9	380	4	AAI89106	AAI89106 Bovine ES	481	7	1.9	429	4	AAAL06798	AAAL06798 Human ova
409	7	1.9	381	8	ABX47046	Abx47046 Bovine ES	482	7	1.9	429	4	ABA08071	ABA08071 Human ova
410	7	1.9	383	9	ACH31119	ACH31119 Human bon	483	7	1.9	429	4	ABA08072	ABA08072 Human ova
411	7	1.9	384	4	AAF72002	AAF72002 Corynebac	484	7	1.9	429	4	ABA08073	ABA08073 Human ova
412	7	1.9	384	4	AAF72194	AAF72194 Corynebac	485	7	1.9	429	6	ABT03068	ABT03068 Human bre
413	7	1.9	384	4	AAF71325	AAF71325 Corynebac	C 486	7	1.9	429	8	ABX54173	ABX54173 Bovine ES
414	7	1.9	384	5	ABV15276	ABV15276 Human pro	C 487	7	1.9	430	13	ADQ54156	ADQ54156 Novel can
415	7	1.9	386	6	ABQ85205	ABQ85205 Arabidops	C 488	7	1.9	432	9	ACH47302	ACH47302 Human inf
416	7	1.9	386	11	ADI31366	Adi31366 Human cDN	C 489	7	1.9	432	5	ABV41491	ABV41491 Human pro
417	7	1.9	387	5	AAI85155	AAI85155 DNA enco	490	7	1.9	433	5	ABV32566	ABV32566 Human pro
418	7	1.9	388	5	AAF64808	AAF64808 Novel hum	491	7	1.9	436	9	ACL13362	ACL13362 DNA clone
419	7	1.9	390	4	AAI81259	AAI81259 Human pol	492	7	1.9	437	4	RAAL02250	RAAL02250 Human rep
420	7	1.9	390	9	ADA49159	Ada49159 Maize gen	493	7	1.9	437	4	ABA07622	ABA07622 Human ova
421	7	1.9	390	10	ADB51050	Adb51050 Primary r	C 494	7	1.9	437	13	ADRI4935	ADRI4935 Rosa sp K
422	7	1.9	390	11	ADT95801	Adt95801 Colon can	C 495	7	1.9	438	5	AAI80906	AAI80906 DNA enco
423	7	1.9	390	12	ADJ44295	Adj44295 Plant cDN	C 496	7	1.9	439	10	ADDI6090	ADDI6090 cDNA (Seq
424	7	1.9	392	4	AAK84890	AAK84890 Human imm	497	7	1.9	439	10	ABX61036	ABX61036 Arabidops
425	7	1.9	399	2	AAQ90425	AAQ90425 DNA enco	C 498	7	1.9	441	9	ACH49658	ACH49658 Human leu
426	7	1.9	399	5	ADL42968	ADL42968 Human ova	499	7	1.9	443	9	ACH49855	ACH49855 Human leu
427	7	1.9	399	8	ABX41703	Abx41703 Bovine ES	500	7	1.9	445	5	ABV11421	ABV11421 Human pro
428	7	1.9	400	2	AAV75163	AAV75163 Staphyloc	501	7	1.9	449	4	RAI12248	RAI12248 Probe #21
429	7	1.9	400	5	ADL42872	ADL42872 Human ova	502	7	1.9	449	4	ABA53951	ABA53951 Human foe
430	7	1.9	402	2	AAQ90426	AAQ90426 DNA enco	503	7	1.9	449	4	AAI33603	AAI33603 Probe #22
431	7	1.9	402	2	AAV75593	AAV75593 Staphyloc	504	7	1.9	449	4	ABA43502	ABA43502 Human bre
432	7	1.9	402	12	ADP93228	ADP93228 Cotton ex	505	7	1.9	449	4	ABA23702	ABA23702 Probe #21
433	7	1.9	403	6	ABN23600	Abn23600 Human ORF	506	7	1.9	449	4	AAK27668	AAK27668 Human bon
434	7	1.9	403	10	ADD45829	Add45829 Rat gene	507	7	1.9	449	4	AAK02221	AAK02221 Human bra
435	7	1.9	403	10	ADE60275	Ade60275 Rat gene	508	7	1.9	449	4	ABS27240	ABS27240 Human liv
436	7	1.9	404	6	ABL81522	ABL81522 Human ova	509	7	1.9	449	5	AAI02162	AAI02162 Probe #21
437	7	1.9	404	9	ACH31539	ACH31539 Human bon	510	7	1.9	449	6	ABS02129	ABS02129 Human gen
438	7	1.9	406	5	AAH42811	AAH42811 Nucleotid	511	7	1.9	450	6	ABZ08415	ABZ08415 Human leu
439	7	1.9	407	4	AAI19630	AAI19630 Probe #95	C 512	7	1.9	451	9	ACH28063	ACH28063 Human adu
440	7	1.9	407	4	ABA64656	ABA64656 Human foe	C 513	7	1.9	452	3	AAI55932	AAI55932 Eucalyptu
441	7	1.9	407	4	AAI44826	AAI44826 Probe #13	C 514	7	1.9	452	4	ABA58691	ABA58691 Human foe
442	7	1.9	407	4	AAI46776	AAI46776 Human bre	515	7	1.9	452	4	AAI38370	AAI38370 Probe #70
443	7	1.9	407	4	ABA31781	ABA31781 Probe #10	516	7	1.9	452	4	AAK32544	AAK32544 Human bon

517	7	1.9	452	4	AAK06826	Aak06826 Human bra	c 590	7	1.9	501	6	ABL80020	Ab180020 Human ova
518	7	1.9	452	4	ABSS32255	Abss32255 Human liv	c 591	7	1.9	503	10	ADE81605	Ade81605 Arabidops
519	7	1.9	452	6	ABe07334	ABe07334 Human gen	c 592	7	1.9	505	4	ABL28019	Ab128019 Drosophil
520	7	1.9	453	6	ABQ58127	ABq58127 Human col	c 593	7	1.9	505	6	ABV87781	ABv87781 Human col
521	7	1.9	454	4	AAK66418	AAk66418 Human imm	c 594	7	1.9	505	10	ADd48316	Ad48316 Human gen
c 522	7	1.9	455	9	ACH34588	Ach34588 Human end	595	7	1.9	505	10	ADd48680	Ad48680 Human gen
c 523	7	1.9	456	4	AAAL12180	AAal12180 Human bre	c 596	7	1.9	506	8	AAAS1602	Aaas1602 Human li-
c 524	7	1.9	456	5	ABAI13783	ABai13783 Human ner	c 597	7	1.9	506	8	ABZ73143	Abz73143 Rice leaf
c 525	7	1.9	456	9	ACH39713	Ach39713 Human foe	c 598	7	1.9	507	5	AAAS92128	Aaas92128 DNA encod
c 526	7	1.9	456	10	ADCI19743	Adci19743 H. influe	c 599	7	1.9	507	6	ABL37469	Ab137469 Human col
c 527	7	1.9	457	10	ADF80960	Adf80960 Leukemia	c 600	7	1.9	512	11	ACN88132	Acn88132 Breast ca
c 528	7	1.9	458	9	ACH41606	Ach41606 Human foe	c 601	7	1.9	513	10	ADSE1651	Ade61651 Rat gene
c 529	7	1.9	459	9	ACH39977	Ach39977 Human foe	c 602	7	1.9	513	13	ADQS2500	Adqs2500 Novel can
c 530	7	1.9	460	5	ABV09637	ABv09637 Human pro	c 603	7	1.9	514	8	ABT23525	Abt23525 Cellobioh
c 531	7	1.9	460	5	ABV36071	ABv36071 Human pro	c 604	7	1.9	514	12	ADJ10792	Adj10792 Recombina
c 532	7	1.9	460	6	ABL93667	ABl93667 Arabidops	c 605	7	1.9	515	12	ACH75341	Ach75341 Human gen
c 533	7	1.9	460	10	ADRE85381	Adre85381 Farnesyl	c 606	7	1.9	515	8	ABX73133	Abx73133 Metabolic
c 534	7	1.9	461	5	ABV39780	ABv39780 Human pro	c 607	7	1.9	519	10	ADRE81284	Ade81284 Arabidops
c 535	7	1.9	461	5	ABV30812	ABv30812 Human pro	c 608	7	1.9	519	13	ADRI4918	Adri4918 Rosa sp f
c 536	7	1.9	461	6	ABL93657	ABl93657 Arabidops	c 609	7	1.9	519	13	ACN55312	Acn55312 Cotton an
c 537	7	1.9	464	3	AAAC41326	AAc41326 Zea mays	c 610	7	1.9	520	9	ACH41144	Ach41144 Human foe
c 538	7	1.9	464	4	AAI15538	AAi15538 Probe #54	c 611	7	1.9	520	12	ACH77657	Ach77657 Human gen
c 539	7	1.9	464	4	ABA57441	ABa57441 Human foe	c 612	7	1.9	522	6	ABK79326	Abk79326 Bacillus
c 540	7	1.9	464	4	ABA36989	ABa36989 Probe #56	c 613	7	1.9	523	4	ABAL01862	Abal01862 Human rep
c 541	7	1.9	464	4	ABA26946	ABa26946 Probe #54	c 614	7	1.9	523	4	ADP91511	Adp91511 Cotton ex
c 542	7	1.9	464	4	AAK31080	AAk31080 Human bon	c 615	7	1.9	523	12	ADRG2200	Adrg2200 Cotton cd
c 543	7	1.9	464	4	AAK05479	AAk05479 Human bra	c 616	7	1.9	523	13	AAAX30891	Aax30891 Streptoco
c 544	7	1.9	464	4	ABSS30759	ABs30759 Human liv	c 617	7	1.9	524	2	ACN59855	Acn59855 Cotton gy
c 545	7	1.9	464	6	ABSS05831	ABs05831 Human gen	c 618	7	1.9	524	13	ACN59855	Acn59855 Cotton gy
c 546	7	1.9	467	5	ABV30959	ABv30959 Human pro	c 619	7	1.9	525	11	ACN90721	Acn90721 Breast ca
c 547	7	1.9	468	4	AAI16073	AAi16073 Probe #60	c 620	7	1.9	525	13	ACN55620	Acn55620 Cotton an
c 548	7	1.9	468	4	AAAS8604	AAa8604 Human foe	c 621	7	1.9	528	4	AAK60038	Aak60038 Human imm
c 549	7	1.9	468	4	ABA73901	ABa73901 Human foe	c 622	7	1.9	529	4	AAI16929	Aai16929 Probe #68
c 550	7	1.9	468	4	AAI54349	AAi54349 Probe #23	c 623	7	1.9	529	4	ABA60951	Abas60951 Human foe
c 551	7	1.9	468	4	AAI38273	AAi38273 Probe #69	c 624	7	1.9	529	4	AAI40848	Aai40848 Probe #95
c 552	7	1.9	468	4	ABA27615	ABa27615 Probe #60	c 625	7	1.9	529	4	ABA28912	Abas28912 Probe #73
c 553	7	1.9	468	4	AAK48520	AAk48520 Human bon	c 626	7	1.9	529	4	AAK35131	Aak35131 Human bon
c 554	7	1.9	468	4	AAK32436	AAk32436 Human bon	c 627	7	1.9	529	4	AAK09241	Aak09241 Human bra
c 555	7	1.9	468	4	AAK22352	AAk22352 Human bra	c 628	7	1.9	529	4	ABSS4883	ABs4883 Human liv
c 556	7	1.9	468	4	AAK06731	AAk06731 Human bra	c 629	7	1.9	529	6	ABSS0582	ABs0582 Human gen
c 557	7	1.9	468	4	ABSS32142	ABs32142 Human liv	c 630	7	1.9	529	13	ACN59618	Acn59618 Cotton gy
c 558	7	1.9	468	6	ABSS07220	ABs07220 Human gen	c 631	7	1.9	530	13	ACN59899	Acn59899 Cotton gy
c 559	7	1.9	469	12	ADOS5031	Ados5031 Gene #128	c 632	7	1.9	531	5	ADL39151	Adl39151 Human ova
c 560	7	1.9	470	12	ADP94395	Adp94395 Cotton ex	c 633	7	1.9	531	5	ADL45379	Adl45379 Human ova
c 561	7	1.9	471	5	AAAS72725	AAa72725 DNA encod	c 634	7	1.9	534	2	AAAX22309	Aax22309 Human Tan
c 562	7	1.9	474	3	AAAS27922	AAa27922 Human int	c 635	7	1.9	535	13	ACN46743	Acn46743 Cotton pr
c 563	7	1.9	474	9	ACH34675	Ach34675 Human end	c 636	7	1.9	536	12	ADQ35883	Adq35883 Novel mou
c 564	7	1.9	474	9	ACH13231	Ach13231 Human adu	c 637	7	1.9	538	13	ADR64047	Adr64047 Cotton cd
c 565	7	1.9	474	9	ACH37923	Ach37923 Human end	c 638	7	1.9	539	10	ADK71789	Adk71789 Rice endo
c 566	7	1.9	475	10	ADD33286	Add33286 Mouse mit	c 639	7	1.9	539	12	ACH77687	Ach77687 Human gen
c 567	7	1.9	477	3	AAAG2522	Aag2522 Human sec	c 640	7	1.9	542	6	ABK77577	Abk77577 Bacillus
c 568	7	1.9	477	4	AAH22696	Aah22696 Human sec	c 641	7	1.9	542	9	ACL15549	ACL15549 DNA clone
c 569	7	1.9	477	9	ACH39326	Ach39326 Human foe	c 642	7	1.9	542	13	ADQ51087	Adq51087 Novel can
c 570	7	1.9	477	10	ADB50879	Adb50879 Primary r	c 643	7	1.9	542	4	AAH07228	Aah07228 Human cdn
c 571	7	1.9	480	5	ABV59672	ABv59672 Human pro	c 644	7	1.9	545	4	AAAF5084	Aaf5084 Human col
c 572	7	1.9	481	9	ACH45615	Ach45615 Human foe	c 645	7	1.9	547	5	ABV27247	ABv27247 Human pro
c 573	7	1.9	481	10	ACD97344	ACd97344 Human col	c 646	7	1.9	547	5	ABV21429	ABv21429 Human pro
c 574	7	1.9	482	6	ABL87814	ABl87814 Human col	c 647	7	1.9	549	5	AAAS86439	Aaas86439 DNA encod
c 575	7	1.9	487	6	ABN64706	ABn64706 Human can	c 648	7	1.9	549	6	ABN68972	ABn68972 Streptoco
c 576	7	1.9	487	12	ADP91540	Adp91540 Cotton ex	c 649	7	1.9	549	12	ADJ44635	Adj44635 Plant CDN
c 577	7	1.9	488	9	ACH39832	Ach39832 Human foe	c 650	7	1.9	549	12	ACH75752	Ach75752 Human gen
c 578	7	1.9	492	6	ABL82980	ABl82980 Human ova	c 651	7	1.9	549	12	ACH75813	Ach75813 Human gen
c 579	7	1.9	494	9	ACH50815	Ach50815 Human mam	c 652	7	1.9	550	12	ADN13574	Adn13574 Human pro
c 580	7	1.9	495	5	ADL39538	Adl39538 Human ova	c 653	7	1.9	551	4	AAH35458	Aah35458 Human col
c 581	7	1.9	495	6	AAAS62278	Aaas62278 CDNA sequ	c 654	7	1.9	551	4	AAAS28307	Aas28307 Genomic s
c 582	7	1.9	496	5	ABV36730	ABv36730 Human pro	c 655	7	1.9	551	4	AAAS28308	Aas28308 Genomic s
c 583	7	1.9	497	5	ABV59612	ABv59612 Human pro	c 656	7	1.9	551	10	ADGA1504	Adga1504 Human res
c 584	7	1.9	498	9	ACH15614	ACH15614 Human'adu	c 657	7	1.9	551	10	ADGA1503	Adga1503 Human res
c 585	7	1.9	498	13	ADQ54525	Adq54525 Novel can	c 658	7	1.9	551	11	ADI97277	Adi97277 Human res
c 586	7	1.9	500	3	AAAC94167	AAc94167 Cat fleva	c 659	7	1.9	551	11	ADI97278	Adi97278 Human res
c 587	7	1.9	500	9	ACL15565	ACL15565 DNA clone	c 660	7	1.9	552	12	ADJ43263	Adj43263 Plant CDN
c 588	7	1.9	501	2	AAAX22310	Aax22310 Human Tan	c 661	7	1.9	553	8	ABZ76797	Abz76797 Nicotiana
c 589	7	1.9	501	5	ADL40459	Adl40459 Human ova	662	7	1.9	554	4	AAAL21110	Aal21110 Human bre

c 663	7	1.9	554	4	AAH11992	Aah11992 Human cDN	c 736	7	1.9	584	3	AAA46489	Aaa46489 cDNA enco
c 664	7	1.9	556	2	AXX33953	Aax33953 Human HCM	c 737	7	1.9	585	13	ACN45563	Acn45563 Cotton pr
c 665	7	1.9	556	8	ABZ54243	Abz54243 Aspergill	c 738	7	1.9	585	9	ACL13285	ACL13285 DNA clone
c 666	7	1.9	556	10	ADB55637	Adb55637 Toxicity-	c 739	7	1.9	586	12	ACH78948	Ach78948 Human gen
c 667	7	1.9	556	10	ADB50202	Adb50202 Primary r	c 740	7	1.9	589	4	AKA65258	Aka65258 Human imm
c 668	7	1.9	557	5	ADI73914	Adi73914 Human ova	c 741	7	1.9	589	13	ACN60788	Acn60788 Cotton gy
c 669	7	1.9	557	5	ADI67525	Adi67525 Human ova	c 742	7	1.9	590	4	AAH04344	Aah04344 Human cDN
c 670	7	1.9	557	9	ACH39700	Ach39700 Human foe	c 743	7	1.9	590	5	ABV58632	Abv58632 Human pro
c 671	7	1.9	557	13	ADQ54826	Adq54826 Novel can	c 744	7	1.9	590	12	ACH87126	Ach87126 Human gen
c 672	7	1.9	559	4	RAI44261	Rai44261 Probe #12	c 745	7	1.9	591	3	RAF08818	Raf08818 Fusarium
c 673	7	1.9	559	12	ADN12578	Adn12578 Human pro	c 746	7	1.9	591	6	ABN67375	Abn67375 Streptoco
c 674	7	1.9	559	13	ADQ54088	Adq54088 Novel can	c 747	7	1.9	592	13	ACN56853	Acn56853 Cotton gy
c 675	7	1.9	561	3	AAA51603	Aaa51603 Human IL-	c 748	7	1.9	593	5	ABV56007	Abv56007 Human pro
c 676	7	1.9	561	13	ACN62192	Acn62192 Cotton gy	c 749	7	1.9	593	10	ADG37982	Adg37982 Aspergill
c 677	7	1.9	563	13	ADS54336	Ads54336 Bacterial	c 750	7	1.9	594	3	AAA51361	Aaa51361 Streptoco
c 678	7	1.9	563	13	ACN61910	Acn61910 Cotton gy	c 751	7	1.9	594	3	AAA27921	Aaa27921 Human int
c 679	7	1.9	564	5	ABV60508	Abv60508 Human pro	c 752	7	1.9	594	4	AAH22755	Aah22755 Human sec
c 680	7	1.9	564	10	ADK56162	Adk56162 Plant DNA	c 753	7	1.9	598	2	AAV69356	Aav69356 Wheat gly
c 681	7	1.9	565	4	AAI19210	Aai19210 Probe #91	c 754	7	1.9	598	4	AAD09256	Aad09256 Wheat wat
c 682	7	1.9	565	4	ABL19203	Ab119203 Drosophil	c 755	7	1.9	598	6	ABK15097	Abk15097 cDNA enco
c 683	7	1.9	565	4	ABA64219	Aba64219 Human foe	c 756	7	1.9	598	10	AAU58846	Aad58846 Wheat gly
c 684	7	1.9	565	4	ABA31364	Aba31364 Probe #98	c 757	7	1.9	599	3	AAC01514	Aac01514 Human sec
c 685	7	1.9	565	6	ABS12473	Ab12473 Human gen	c 758	7	1.9	600	4	RAA54035	Raa54035 Klebsiell
c 686	7	1.9	566	5	ABV50387	Abv50387 Human pro	c 759	7	1.9	600	12	ADQ84110	Adq84110 Human tum
c 687	7	1.9	567	4	AAH02883	Aah02883 Human she	c 760	7	1.9	601	9	ACL15555	ACL15555 DNA clone
c 688	7	1.9	567	13	ADS50706	Ads50706 Bacterial	c 761	7	1.9	604	5	RAA572939	Raa572939 DNA enco
c 689	7	1.9	569	4	AAH22954	Aah22954 Human tes	c 762	7	1.9	606	3	ACA3625	Aac3625 Arabidops
c 690	7	1.9	569	4	ABA61403	Aba61403 Human foe	c 763	7	1.9	606	5	RAA66222	Raa66222 DNA enco
c 691	7	1.9	569	4	RAI41311	Rai41311 Probe #99	c 764	7	1.9	606	13	ADQ57641	Adq57641 Novel can
c 692	7	1.9	569	4	AKA35595	Aak35595 Human bon	c 765	7	1.9	606	13	ACN53150	Acn53150 Cotton an
c 693	7	1.9	569	4	AAK09701	Aak09701 Human bra	c 766	7	1.9	607	9	ACL15560	ACL15560 DNA clone
c 694	7	1.9	569	6	AAK037357	Aak037357 R7 adeny1	c 767	7	1.9	607	12	ADQ36603	Ado36603 Isoquinol
c 695	7	1.9	569	6	AAK037356	Aak037356 R8 adeny1	c 768	7	1.9	609	13	ACN62482	Acn62482 Cotton de
c 696	7	1.9	570	6	ABN69480	Abn69480 Streptoco	c 769	7	1.9	610	9	ACL15547	ACL15547 DNA clone
c 697	7	1.9	570	6	ABN69479	Abn69479 Streptoco	c 770	7	1.9	610	13	ADQ52192	Adq52192 Novel can
c 698	7	1.9	570	9	ACL15548	ACL15548 DNA clone	c 771	7	1.9	611	4	ABL17811	Ab117811 Drosophil
c 699	7	1.9	571	3	AAFI1446	Aaf11446 Aspergill	c 772	7	1.9	613	6	ABQ35544	Abq35544 Oligonuc1
c 700	7	1.9	572	10	ADC72409	Adc72409 DNA Seq I	c 773	7	1.9	613	6	ABQ35545	Abq35545 Oligonuc1
c 701	7	1.9	572	10	ADC75507	Adc75507 DNA homol	c 774	7	1.9	614	13	ADR59299	Adr59299 Cotton cD
c 702	7	1.9	573	6	ABT07883	Abt07883 Human lun	c 775	7	1.9	616	3	ACA39314	Aac39314 Arabidops
c 703	7	1.9	573	11	ACH98095	Ach98095 Klebsiell	c 776	7	1.9	624	8	ACF74964	Acf74964 Staphyloc
c 704	7	1.9	574	4	AAI16778	Aai16778 Probe #67	c 777	7	1.9	625	10	ADFI13344	Adf13344 Human 3-h
c 705	7	1.9	574	4	ABA60416	Aba60416 Human foe	c 778	7	1.9	625	12	ADJ84429	Adj84429 Human phe
c 706	7	1.9	574	4	AAI40300	Aai40300 Probe #89	c 779	7	1.9	626	3	AAA51601	Aaa51601 Human IL-
c 707	7	1.9	574	4	ABA28636	Aba28636 Probe #71	c 780	7	1.9	627	5	ABV53042	Abv53042 Human pro
c 708	7	1.9	574	4	AKA34581	Aak34581 Human bon	c 781	7	1.9	627	10	ADQ33423	Adq33423 Mouse mit
c 709	7	1.9	574	4	RAK08694	Rak08694 Human bra	c 782	7	1.9	629	3	AAA51594	Aaa51594 Human IL-
c 710	7	1.9	574	4	ABS34354	Ab34354 Human liv	c 783	7	1.9	629	13	ACN54253	Acn54253 Cotton an
c 711	7	1.9	574	6	ABS09212	Ab09212 Human gen	c 784	7	1.9	630	5	AAH43117	Aah43117 Human EXC
c 712	7	1.9	574	12	ACH73401	Ach73401 Human gen	c 785	7	1.9	630	12	ADL66931	Adl66931 Human ext
c 713	7	1.9	576	4	AAI16818	Aai16818 Probe #67	c 786	7	1.9	632	5	AAH42815	Aah42815 Nucleotid
c 714	7	1.9	576	4	ABA60543	Aba60543 Human foe	c 787	7	1.9	633	10	ADFI13345	Adf13345 Human 3-h
c 715	7	1.9	576	4	RAI40432	Rai40432 Probe #91	c 788	7	1.9	633	10	ABX95401	Abx95401 cDNA enco
c 716	7	1.9	576	4	ABA28703	Aba28703 Probe #71	c 789	7	1.9	633	12	ADFS3256	Adfs3256 Human pro
c 717	7	1.9	576	4	AAK34711	Aak34711 Human bon	c 790	7	1.9	634	6	ABL63301	Ab163301 Breast ca
c 718	7	1.9	576	4	AAH55621	Aah55621 Human bre	c 791	7	1.9	634	6	ABL63092	Ab163092 Breast ca
c 719	7	1.9	576	4	AAK08823	Aak08823 Human bra	c 792	7	1.9	634	6	ABK35563	Abk35563 Gene ISG1
c 720	7	1.9	576	4	ABS34484	Ab34484 Human liv	c 793	7	1.9	634	6	ABT10900	Abt10900 Human bre
c 721	7	1.9	576	6	ABS09300	Ab09300 Human gen	c 794	7	1.9	634	6	ABZ35078	Abz35078 Human gen
c 722	7	1.9	576	10	ABX56863	Abx56863 Arabidops	c 795	7	1.9	634	6	ABK83926	Abk83926 Human cDN
c 723	7	1.9	576	12	ADN40391	Adn40391 Human bre	c 796	7	1.9	634	6	ACC51007	Acc51007 Human bla
c 724	7	1.9	578	12	ACH79716	Ach79716 Human gen	c 797	7	1.9	634	8	ACC50195	Acc50195 Breast ca
c 725	7	1.9	579	3	AAA27918	Aaa27918 Human int	c 798	7	1.9	634	8	ACC50195	Acc50195 Breast ca
c 726	7	1.9	579	8	ACA49968	Aca49968 Prokaryot	c 799	7	1.9	634	8	ACC51210	Acc51210 Human plk
c 727	7	1.9	579	10	ADC76945	Adc76945 DNA homol	c 800	7	1.9	634	10	ADD19019	Add19019 Human dis
c 728	7	1.9	579	12	ADN05879	Adn05879 Antipori	c 801	7	1.9	634	10	ADF76521	Adf76521 Novel hum
c 729	7	1.9	581	9	ACL15550	ACL15550 DNA clone	c 802	7	1.9	634	10	ACC72677	Acc72677 Human can
c 730	7	1.9	581	10	ACD94462	Acd94462 Human col	c 803	7	1.9	634	11	ADN95888	Adn95888 Human BEC
c 731	7	1.9	582	5	ABV39927	Abv39927 Human pro	c 804	7	1.9	634	11	ADN95816	Adn95816 Human BEC
c 732	7	1.9	582	12	ACH72109	Ach72109 Human gen	c 805	7	1.9	634	12	ADJ74815	Adj74815 Marker ge
c 733	7	1.9	582	13	ACN45993	Acn45993 Cotton pr	c 806	7	1.9	634	12	ADL83099	Adl83099 Human PRO
c 734	7	1.9	582	13	ACN55807	Acn55807 Cotton an	c 807	7	1.9	634	12	ADN04149	Adn04149 Antipori
c 735	7	1.9	583	4	AAK70689	Aak70689 Human imm	c 808	7	1.9	634	12	ADO24416	Ado24416 Human PRO

809	7	1.9	634	13	ADRL14230	Adrl14230 Human NF-	c 882	7	1.9	706	12	ADJ42232	Adj42232 Plant cdn
810	7	1.9	634	13	ADP56303	Adp56303 Human PRO	883	7	1.9	708	2	AAT68277	Aat68277 H. pylori
811	7	1.9	634	13	ADRS2863	Adrs2863 Drug ther	884	7	1.9	710	4	AAH06458	Aah06458 Human cdn
812	7	1.9	634	13	ADP23872	Adp23872 PRO poly	c 885	7	1.9	710	4	AAH08141	Aah08141 Human cdn
813	7	1.9	634	13	ADS64440	Ads64440 Human int	c 886	7	1.9	711	12	ACH91585	Ach91585 Human gen
814	7	1.9	635	5	ABV271143	Abv271143 Human pro	c 887	7	1.9	716	11	ACN91844	Acn91844 Breast ca
815	7	1.9	635	5	ABV21124	Abv21124 Human pro	c 888	7	1.9	717	6	ABK74060	Abk74060 Bacillus
816	7	1.9	635	5	ADL62343	Adl62343 Human ova	889	7	1.9	719	3	AAF12941	Aaf12941 Aspergill
817	7	1.9	636	11	ACN90695	Acn90695 Breast ca	890	7	1.9	719	3	AAH99862	Aah99862 Human pro
818	7	1.9	636	3	ADAO0211	Ada00211 Human zil	891	7	1.9	720	6	ABQ51364	Abq51364 Oligonuc1
819	7	1.9	636	10	ADH89069	Adh89069 DNA encod	c 892	7	1.9	720	6	ABQ51365	Abq51365 Oligonuc1
820	7	1.9	636	10	ADH83044	Adh83044 Enterococ	c 893	7	1.9	722	12	ADO24382	Ado24382 Human PRO
c 821	7	1.9	638	6	ABN62368	Abn62368 Human can	c 894	7	1.9	729	6	ABN68013	Abn68013 Streptoco
c 822	7	1.9	639	4	AAI21063	Aai21063 Human bre	895	7	1.9	729	8	ABZ36826	Abz36826 Human GEN
c 823	7	1.9	640	3	AAF14923	Aaf14923 Trichoder	896	7	1.9	729	12	ADQ37046	Adq37046 Cell prol
824	7	1.9	641	13	ACN46548	Acn46548 Cotton pr	897	7	1.9	730	2	AAQ05940	Aaq05940 Complete
825	7	1.9	642	8	ABX63536	Abx63536 Human cdn	c 898	7	1.9	730	13	ADQ55259	Adq55259 Novel can
c 826	7	1.9	643	4	AAH05305	Aah05305 Human cdn	c 899	7	1.9	731	3	AAK36471	Aac36471 Arabidops
c 827	7	1.9	650	2	AAH19258	Aah19258 Alfalfa d	c 900	7	1.9	731	3	AAK36471	Aac36471 Arabidops
828	7	1.9	650	3	AAAS1592	Aas1592 Human il-	c 901	7	1.9	733	4	AAI23532	Aai23532 Human bre
c 829	7	1.9	651	13	ADT46877	Adt46877 Bacterial	c 902	7	1.9	737	4	AAH04385	Aah04385 Human cdn
830	7	1.9	652	9	ACL15546	Act15546 DNA clone	c 903	7	1.9	739	4	AAH08552	Aah08552 Human cdn
831	7	1.9	652	9	ACL15558	Act15558 DNA clone	c 904	7	1.9	740	12	ADO15236	Ado15236 Influenza
832	7	1.9	655	5	ABV24354	Abv24354 Human pro	c 905	7	1.9	741	12	ADI42544	Adi42544 Plant tra
833	7	1.9	657	3	ADAO0212	Ada00212 Human zil	c 906	7	1.9	741	12	ADO02873	Ado02873 Corn orth
834	7	1.9	657	3	AAAO8513	Aaa08513 Primate i	c 907	7	1.9	744	4	AAH04493	Aah04493 Human cdn
835	7	1.9	657	3	AAAT27920	Aaa27920 Human int	c 908	7	1.9	744	10	ADD33422	Add33422 Mouse mit
836	7	1.9	657	6	ABK93116	Abk93116 Human pro	909	7	1.9	745	2	AAZ16327	Aaz16327 Human gen
837	7	1.9	657	10	ADH89074	Adh89074 DNA encod	910	7	1.9	747	4	AAK67494	Aak67494 Human imm
838	7	1.9	657	12	ADJ88305	Adj88305 Human int	911	7	1.9	747	4	AAK67492	Aak67492 Human imm
839	7	1.9	657	12	ADL15867	Adl15867 Human int	c 912	7	1.9	747	12	ADI57648	Adi57648 Human bre
840	7	1.9	657	12	ADAO04678	Ado04678 Human int	913	7	1.9	750	2	AAI15255	Aai15255 DNA encod
841	7	1.9	659	4	AAH99340	Aah99340 Human pro	914	7	1.9	750	4	AAI15255	Aai15255 DNA encod
842	7	1.9	660	2	AAV90532	Aav90532 EST clone	c 915	7	1.9	750	4	AAI15255	Aai15255 DNA encod
c 843	7	1.9	663	3	ACA46399	Aca46399 Arabidops	c 916	7	1.9	753	10	ACF67085	Acf67085 Phototrab
c 844	7	1.9	663	9	ADA30546	Ada30546 DNA encod	917	7	1.9	754	3	AAAS1593	Aas1593 Processed
845	7	1.9	663	10	ADD33693	Add33693 Mouse mit	918	7	1.9	754	4	AAI15255	Aai15255 DNA encod
846	7	1.9	663	10	ADL13944	Adl13944 Osteoarth	919	7	1.9	754	6	ABZ74448	Abz74448 Human cdn
847	7	1.9	664	10	ADL18461	Adl18461 Human pro	920	7	1.9	754	8	ACA91234	Ac91234 Novel hum
848	7	1.9	668	2	AAZ77534	Aaz77534 Human ova	921	7	1.9	754	8	ACD81611	Acd81611 Human cdn
849	7	1.9	669	2	AAK30436	Aak30436 H. pylori	922	7	1.9	754	8	ACA60433	ACA60433 Novel hum
850	7	1.9	669	10	ABZ83065	Abz83065 Toxicolog	923	7	1.9	754	8	ACA58880	ACA58880 CDNA enco
851	7	1.9	670	2	AAZ33612	Aaz33612 Human bre	924	7	1.9	754	8	ACA64056	ACA64056 CDNA enco
852	7	1.9	671	2	AAI64341	Aai64341 Human sma	925	7	1.9	754	8	ACA91320	ACA91320 CDNA enco
c 853	7	1.9	671	3	AAAC44260	Aac44260 Arabidops	926	7	1.9	754	8	ACD45219	Acd45219 Human sec
854	7	1.9	675	6	AAAS21054	Aas21054 Isolated	927	7	1.9	754	8	ACA93767	ACA93767 Human cdn
c 855	7	1.9	676	3	AAFI1973	Aafi1973 Aspergill	928	7	1.9	754	8	ACA67341	ACA67341 cDNA enco
856	7	1.9	678	12	ADQ17878	Adq17878 Human sof	929	7	1.9	754	8	ACH66314	Ach66314 Novel hum
857	7	1.9	681	10	ADG84255	Adg84255 Human TMD	930	7	1.9	754	8	ACH66314	Ach66314 Novel hum
858	7	1.9	681	12	ADJ43202	Adj43202 Plant cdn	931	7	1.9	754	8	ACH66314	Ach66314 Novel hum
c 859	7	1.9	681	13	ADRS9475	Adrs9475 Cotton cd	932	7	1.9	754	8	ACH66314	Ach66314 Novel hum
860	7	1.9	682	13	ADQ49828	Adq49828 Novel can	933	7	1.9	754	8	ACH66314	Ach66314 Novel hum
c 861	7	1.9	685	3	AAFI18131	Aafi18131 Lung canc	934	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 862	7	1.9	685	10	ACF66159	Acf66159 Phototrab	935	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 863	7	1.9	686	6	ABZ77078	Abz77078 Frog embr	936	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 864	7	1.9	687	5	ABA18465	Abal8465 Human ner	937	7	1.9	754	9	ACH66314	Ach66314 Novel hum
865	7	1.9	687	5	AAAS76180	Aas76180 DNA encod	938	7	1.9	754	9	ACH66314	Ach66314 Novel hum
866	7	1.9	687	5	AAAS77047	Aas77047 DNA encod	939	7	1.9	754	9	ACH66314	Ach66314 Novel hum
867	7	1.9	687	5	AAAS76262	Aas76262 DNA encod	940	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 868	7	1.9	687	5	AAAS91886	Aas91886 DNA encod	941	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 869	7	1.9	687	12	ADL181821	Adl181821 P. aerugi	942	7	1.9	754	9	ACH66314	Ach66314 Novel hum
c 870	7	1.9	689	4	AAK55189	Aak55189 Human imm	943	7	1.9	754	10	ADB68393	Adb68393 Human PRO
c 871	7	1.9	689	5	ABA12883	Abal2883 Human ner	944	7	1.9	754	10	ADB68200	Adb68200 Human PRO
c 872	7	1.9	692	4	AAH06066	Aah06066 Human cDN	945	7	1.9	754	10	ADB91017	Adb91017 Novel hum
c 873	7	1.9	700	4	AAH92694	Aah92694 Human inf	946	7	1.9	754	10	ADB91017	Adb91017 Novel hum
874	7	1.9	700	4	AAH93213	Aah93213 Human inf	947	7	1.9	754	10	ADC07097	Adc07097 Human PRO
875	7	1.9	700	4	AAH93212	Aah93212 Human inf	948	7	1.9	754	10	ADC17276	Adc17276 cDNA sequ
c 876	7	1.9	700	13	ACN56525	Acn56525 Cotton gy	949	7	1.9	754	10	ADC14974	Adc14974 Novel hum
877	7	1.9	701	3	AAAC34778	Aac34778 Arabidops	950	7	1.9	754	10	ADC52469	Adc52469 Novel hum
878	7	1.9	702	6	ABK78598	Abk78598 Bacillus	951	7	1.9	754	10	ADG01146	Adg01146 Novel hum
c 879	7	1.9	703	12	ADQ20103	Adq20103 Human sof	952	7	1.9	754	10	ADG08699	Adg08699 Novel hum
c 880	7	1.9	703	13	ADZ5925	Adz5925 Breast ca	953	7	1.9	754	10	ADP95320	Adp95320 Novel hum
881	7	1.9	705	8	ACA33296	Aca33296 Prokaryot	954	7	1.9	754	10	ADH24173	Adh24173 Novel hum

955 7 1.9 754 10 ADH34199 Novel hum
 956 7 1.9 754 10 ADH30032 Novel hum
 957 7 1.9 754 10 ADH24003 Novel hum
 958 7 1.9 754 10 ADG85407 Novel hum
 959 7 1.9 754 10 ADH24683 Novel hum
 960 7 1.9 754 10 ADH37539 Human sec
 961 7 1.9 754 10 ADH02128 Human PRO
 962 7 1.9 754 10 ADH37709 Human sec
 963 7 1.9 754 10 ADG85747 Novel hum
 964 7 1.9 754 10 ADH24343 Novel hum
 965 7 1.9 754 10 ADH38637 Novel hum
 966 7 1.9 754 10 ADG383758 Human PRO
 967 7 1.9 754 10 ADH29566 Novel hum
 968 7 1.9 754 10 ADH27682 Novel hum
 969 7 1.9 754 10 ADH37879 Human sec
 970 7 1.9 754 10 ADH38056 Human sec
 971 7 1.9 754 10 ADH57476 Novel hum
 972 7 1.9 754 10 ADH53618 Novel hum
 973 7 1.9 754 10 ADH53788 Novel hum
 974 7 1.9 754 10 ADH52124 Novel hum
 975 7 1.9 754 10 ADH49979 Novel hum
 976 7 1.9 754 10 ADI25489 Novel hum
 977 7 1.9 754 10 ADH90282 Novel hum
 978 7 1.9 754 10 ADI25659 Novel hum
 979 7 1.9 754 10 ADH97833 Novel hum
 980 7 1.9 754 10 ADI03681 Novel hum
 981 7 1.9 754 10 ADI12038 Human PRO
 982 7 1.9 754 10 ADH90112 Novel hum
 983 7 1.9 754 10 ADH98513 Novel hum
 984 7 1.9 754 10 ADI11188 Human PRO
 985 7 1.9 754 10 ADI11698 Human PRO
 986 7 1.9 754 10 ADH98343 Novel hum
 987 7 1.9 754 10 ADH98683 Novel hum
 988 7 1.9 754 10 ADH98173 Novel hum
 989 7 1.9 754 10 ADI05161 Novel hum
 990 7 1.9 754 10 ADI03511 Novel hum
 991 7 1.9 754 10 ADI04906 Novel hum
 992 7 1.9 754 10 ADH78360 Human PRO
 993 7 1.9 754 10 ADI19704 Novel hum
 994 7 1.9 754 10 ADH90452 Novel hum
 995 7 1.9 754 10 ADI03171 Novel hum
 996 7 1.9 754 10 ADH78020 Human PRO
 997 7 1.9 754 10 ADH98003 Novel hum
 998 7 1.9 754 10 ADI01388 Novel hum
 999 7 1.9 754 10 ADI02083 Novel hum
 1000 7 1.9 754 10 ADI03341 Novel hum

ALIGNMENTS

RESULT 1
 AAZ37836
 ID AAZ37836 standard; DNA; 1260 BP.

XX AC AAZ37836;

XX DT 09-FEB-2000 (first entry)

XX DE Human cyclin I nucleotide sequence.

XX KW Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
 ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
 KW atherosclerosis; tumour; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX CDS 1..1134
 XX FT /*tag= a
 XX FT /product= "Cyclin_I"

XX PN W09925829-A2.

XX

Adh34199 Novel hum
 Adh30032 Novel hum
 Adh24003 Novel hum
 Adg85407 Novel hum
 Adh24683 Novel hum
 Adh37539 Human sec
 Adh02128 Human PRO
 Adh37709 Human sec
 Adg85747 Novel hum
 Adh24343 Novel hum
 Adh38637 Novel hum
 Adg83758 Human PRO
 Adh29566 Novel hum
 Adh27682 Novel hum
 Adh37879 Human sec
 Adh38056 Human sec
 Adh57476 Novel hum
 Adh53618 Novel hum
 Adh53788 Novel hum
 Adh52124 Novel hum
 Adh49979 Novel hum
 Adi25489 Novel hum
 Adh90282 Novel hum
 Adi25659 Novel hum
 Adh97833 Novel hum
 Adi03681 Novel hum
 Adi12038 Human PRO
 Adh90112 Novel hum
 Adh98513 Novel hum
 Adi1188 Human PRO
 Adi11698 Human PRO
 Adh98343 Novel hum
 Adh98683 Novel hum
 Adh98173 Novel hum
 Adi05161 Novel hum
 Adi03511 Novel hum
 Adi04906 Novel hum
 Adh78360 Human PRO
 Adi19704 Novel hum
 Adh90452 Novel hum
 Adi03171 Novel hum
 Adh78020 Human PRO
 Adh98003 Novel hum
 Adi01388 Novel hum
 Adi02083 Novel hum
 Adi03341 Novel hum

PD 27-MAY-1999.
 XX 12-NOV-1998; 98WO-US024095.
 PF 13-NOV-1997; 97US-00969106.
 XX (CURA-) CURAGEN CORP.
 FA Yang M, Nandabalan K, Schulz VP;
 PI WPI; 2000-061923/05.
 XX P-PSDB; AAY52185.

New complexes of the cyclin-dependent kinase 2 protein with its interacting proteins, used to treat, e.g. atherosclerosis.

Example; Fig 2; 90pp; English.

This sequence is the human Cyclin I nucleotide sequence. Cyclin I is expressed at almost constant levels throughout the cell cycle, and is implicated in controlling cell cycle progression and transcriptional control. Cyclins form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent kinase 2, is used in the invention which relates to complexes of the CDK2 protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S transition. Compositions containing a CDK2 complex, an antibody targeting the complex, and nucleotide sequences encoding CDK2 or its derivatives can be used therapeutically. The complexes and their nucleotide sequences can be used to treat diseases or disorders associated with increased or decreased levels of the complex. Screening the complex, or a derivative or a modulator of the complex for neoplastic activity by measuring the survival or proliferation of cells from a malignant cell line when in contact with the complex can be used to indicate if the the complex has anti-neoplastic activity. Screening for molecules that modulate the formation of the complexes can be used for treating or preventing atherosclerosis or other atherosclerosis-associated disease by contacting cells or using a test animal, in which tumour growth or regression is measured to test whether anti-neoplastic activity is displayed. Diseases which can be treated or prevented by molecule/s which modulate the function of the complex include cancer, hyperproliferative disorders and atherosclerosis

XX Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 1260
 Score: 377.00 Matches: 377
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x AAZ37836 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 1 ATCAAGTTTCAGGGCCCTTGGAAAACACAGAGATTGCTTCTCTGTGGAAAGCGCAATC 60
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnVal 40
 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTCGGAAATGCCTTCAATCAGAAATGTT 120
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
 121 TCTCCATCCACAGAGATGAAGTAATTCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTACGATACCGTA 240
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaTleSerCysPhePheLeuAlaAlaLys 100
 241 AAGGCTCATCCAAATACTGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300


```
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCATCCAGAGAGATGAATTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGATTTTGTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGATGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgGluProValLeuLysValLeuAlaAAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATCCAGTACTAAGGATATTGCAAGAGACAGATTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCTCATCTGAAATTTTGAAGATGAGAGATTTATTCGATAAGTTCGAATTGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGACACACACCATGATTTCTTCATATTTTCCATGTCATTCGAGTGTCAC 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCTAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCAACTTCTGCAATTCAGAGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAACTCAATCTCGATTGGCTTCT 660

Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLysHisCysArg 240
Db 661 CTTCAATGTAACTGCTTCAGAAAGCAGAGATGATAGTCCCAAGTTCATTCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGACATCACTTTTACTCTGAGTCTTCCCTGCTGCTGAATTCGGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCCCAGCCAGACTTCTCCAAAGGACACACAGCAAGCCAGAGTCCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTCAGACAGCTTTTACATCATCTCCAGCTGCGAGTGGGTGGCAAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGCAATGGAAGTATGATGATCTTATGTAATCAACAGCGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAAGATATATGTTCTAGAAATATGGGTTCTGTGTGGCAGCTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCCTTGTCCAGCTGTTTCTGTGATG 1131

RESULT 4
ADI31573
ID ADI31573 standard; cDNA; 1260 BP.
XX
AC ADI31573;
```

```
XX 17-JUN-2004 (first entry)
XX DE Human cDNA #899.
XX KW Human; Gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
KW acute monocytic leukaemia; antiinflammatory; antirheumatic; antitumor;
KW osteopathic; antiarthritic; antirheumatic; cytostatic.
XX OS Homo sapiens.
XX XX US6607879-B1.
XX PN 19-AUG-2003.
XX PD 09-FEB-1998; 98US-00023655.
XX PF 09-FEB-1998; 98US-00023655.
XX PR (ENCY-) INCYTE CORP.
XX PA Cocks BG, Stuart SG, Seifamer JJ;
XX PI WPI; 2003-895307/82.
XX DR A composition comprising a plurality of cDNAs, useful for detecting
XX PT altered expression of genes in an immunological response or for
XX FT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX PT or osteoarthritis.
XX PS Claim 1; SEQ ID NO 899; 50pp; English.
XX CC The invention relates to a composition comprising a plurality of cDNAs
XX CC for detecting the altered expression of genes in an immunological
XX CC response. The invention also relates to a method of diagnosing or
XX CC monitoring the treatment of an immunopathological condition in a sample,
XX CC comprising obtaining nucleic acids from a sample, contacting the nucleic
XX CC acids of the sample with an array comprising the plurality of cDNAs under
XX CC conditions to form one or more hybridisation complexes, detecting the
XX CC hybridisation complexes and comparing the levels of the detected
XX CC hybridisation complexes with the level of hybridisation complexes
XX CC detected in a non-diseased sample, where an altered level of the detected
XX CC hybridisation complexes correlates with the presence of an
XX CC immunopathological condition. Also disclosed are an expression profile
XX CC comprising a microarray and a plurality of detectable probes. The cDNAs
XX CC method for identifying a plurality of polynucleotide probes. The cDNAs
XX CC are useful as hybridisable array elements in a microarray for monitoring
XX CC the expression of target polynucleotides. The microarray can be used in
XX CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
XX CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
XX CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
XX CC identifying agents for the treatment of the diseases. The microarray may
XX CC also be used in drug discovery and development, toxicological and
XX CC carcinogenicity studies, forensics or pharmacogenomics. The composition
XX CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
XX CC genomic fragments. This sequence represents a human cDNA of the
XX CC invention. Note: The sequence data for this patent did not form part of
XX CC the printed specification but was obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html.
XX SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-1 (1-377) x ADI31573 (1-1260)
```


Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAAAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180

Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTGGATAGTATTAGTACCGTA 240

Qy 81 LysAlaHisProLysTrpLysSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAAATCTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGATTCAGTACTAAGGTATTGGCAAGACAGATTCTGT 360

Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGATGGAGAGATTAATCTGGATAAGTGAATGG 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATGATTTCTTCATATTTTCCATGTCATTCAGTGTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCTAGTTACTTTTCAGTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGGCTGTGCAACCAACTCTGCAATTCAGAGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCAATCTGATGGCTTCT 660

Qy 221 LeuThrIleGluLeuGluLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTCAATTTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTGATCCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGGTTAT 780

Qy 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGCACAAAGGAGTGTTCAGATTACAT 840

Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTTCTCTGTCACAGGCCCGAGCTTCTCAAGGACACAGCAAGCCAGAAAGTGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTrpHisLeuProAlaHisLeuProAlaHisLeuGlnThrSer 320
Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCGCAGTGGGTGCAAGCAGACTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGAAATGGAAGTGAATGATCTTCTATGATGGAATCAAAAGGCTC 1020

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValGlySerGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGCTTCAGAAATATGTTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTGTTTCTGTCTATG 1131

RESULT 5

ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX
AC ADR25465;
XX
DT 21-OCT-2004 (first entry)
XX
DE Breast cancer prognosis marker #1326.
XX
KW ds; breast cancer; prognosis; gene expression; diagnosis.
XX
OS Homo sapiens.
XX
FN WO2004065545-A2.
XX
PD 05-AUG-2004.
XX
PF 15-JAN-2004; 2004WO-US001100.
XX
PR 15-JAN-2003; 2003US-00342887.
XX
PA (ROSE-) ROSETTA INPHARMATICS LLC.
PA (NECA-) NETHERLANDS CANCER INST.
XX
PI Van't Veer LJ, He Y;
XX
DR WPI; 2004-593473/57.

XX
XX
PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
PS Disclosure; SEQ ID NO 1326; 226pp; English.
XX
CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-1 (1-377) x ADR25465 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTCGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAAAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180

```

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTCTTTTACGTCACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGTGTATTCGAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGAGATGAGAGATTCAGTACTTAAGGTATTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGATGAGAGATTAATCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGTCCTGCAACCAACTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTGCGCATGTTAGTCTGGAATGAGAACTCAATTCCTGATGCTTCT 660
Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACAATTAAGTCTTCAGAAAGCAGATGATGATCTCCAGTTGATCATTTGCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCCTTCTTACTCTGCGTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCCCTGCTGACCTGTGCAAAAGGAGTGTTCAGATTTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCCTCTGCTCCAGGCCAGACTTCTCCAGGACACAGCAAGCCCAAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCCCTTTTACCATCATCTCCAGCTGCGAGTGGTGGCAAGCAGCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATAATGCTTCAGAAATGTGGTCTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGCATGCTTCCCTTGTCCACCTTTCAGCCTGTTCTGTGTCATG 1131

```

RESULT 6

AAT73937

ID AAT73937 standard; DNA; 1328 BP.

XX AC

XX AAT73937;

XX DT

02-DEC-1997 (first entry)

XX

```

DE DNA encoding human cyclin I.
XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 69..1202
XX /*tag= a
XX
XX W09712973-A1.
XX PN 10-APR-1997.
XX PD
XX PF 07-OCT-1996; 96WO-JP002905.
XX PR 05-OCT-1995; 95JP-00284663.
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX Nakamura T;
XX WPI; 1997-226217/20.
XX P-PSDB; AAW21965.
XX
XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
XX labelling method and cancer cell detection.
XX
XX Example 1; Fig 1; 45pp; Japanese.
XX
XX This sequence encodes human cyclin I. Antisense polynucleotides are
XX useful for as probes and can be labelled and used for detection of
XX neurones by hybridisation with mRNA for cyclin I (contained in the
XX cells). The gene can be used for detection of cancer cells by detecting
XX the expression of the cyclin I gene in these cells. Also antibodies
XX specific for the fragments of the protein (especially AAW21966) can be
XX used for detection
XX
XX Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

```

Alignment Scores:

```

Pred. NO.: 0 Length: 1328
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

```

US-09-736-250-1 (1-377) x AAT73937 (1-1328)

```

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 69 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATGCTTCTTCTGTTGGAAAGGCAATC 128
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 129 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGCGGAAATGCCTTCAATCAGAAATGTT 188
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 189 TCTCCATCCACAGAGATGAAGTAATTCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 248
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 249 CTTTACCAGAAACATTTGCTGCTGAGTACAGTCTTTTGGATAGTCTTTAGTACCGTA 308
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 309 AAGGCTCATCCAAATACTTGGTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 368
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120

```

Db 369 ACTGTTAGGAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 428
 Qy 121 GlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
 Db 429 GGATGTTCTCATCTGAATTTTGAGATGAGAGAAATATTCTGGATAAGTTGATGG 488
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 489 GATCTTCACACAGCCACCATGATTTCTTCATATTTTCCATGTCATTCAGTGTCA 548
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 Db 549 ACTAGGCTCAGTTACTTTTTCAGTTTGCCAAATGAGCCCATCTCAACATTTGGCAGTC 608
 Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
 Db 609 CTTACCAAGCAACTACTTCACTGTATGCTGACCACTTCTGCAATTCAGAGGATCC 668
 Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
 Db 669 ATGCTTGCTCTGGCCATGCTTAGTCTGGAATGGAGAACTCATCTCTGATTTGGCTTCT 728
 Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
 Db 729 CTTCAATGAACTGCTTCAGAAAGCACAGATGATAGCTCCAGTTGATCCATTTGTCGG 788
 Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 Db 789 GAGCTTGCGGCATCATCTTCTACTCTGCACTTCTCCCTGCTCTGAATTCGGTTAT 848
 Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 Db 849 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAGATTACAT 908
 Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 Db 909 CCCCTCTGTCGAGGCCAGACTTCTCCAAAGACAAACAGCAAGCCAGAGTGCAGTC 968
 Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 Db 969 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAGCAGCTCT 1028
 Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
 Db 1029 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAATCAAAACGGCTC 1088
 Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1089 TATATGAGATATATGCTCAGAAATGTGGTCTCTGTGTGGCAGTATTTATCAAGA 1148
 Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1149 CAAGAGGACATGCTTCCCTTGTCACCTTTGCAGCTGTTCTGTGTCATG 1199

RESULT 7

ACC47339
 ID ACC47339 standard; cDNA; 1384 BP.

XX AC

XX AC

XX AC

DT 11-AUG-2003 (first entry)

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

XX DE

FN WO2003014298-A2.
 XX 20-FEB-2003.
 XX 02-AUG-2002; 2002WO-US024431.
 XX 03-AUG-2001; 2001US-0309470P.
 PR 30-OCT-2001; 2001US-0330747P.
 XX (ORIG-) ORIGENE TECHNOLOGIES INC.
 XX Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
 FI WPI; 2003-256562/25.
 DR P-PSDB; ABR39934.
 XX New polynucleotide, useful for preparing a composition for treating
 PT prostate disease, e.g., cancer.
 XX Claim 1; Page 147-149; 212pp; English.
 XX The invention relates to prostate selective polynucleotides and
 CC polypeptides. The polynucleotides are expressed in prostate and are
 CC useful as molecular markers, as drug targets, and for detecting,
 CC monitoring, preventing or treating diseases and conditions related to
 CC prostate, such as prostate cancers. Sequences ACC47325-356 represent
 CC specific examples of prostate specific polynucleotides
 XX
 SQ Sequence 1384 BP; 364 A; 329 C; 324 G; 367 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0 Length: 1384
 Score: 377.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-736-250-1 (1-377) x ACC47339 (1-1384)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 Db 200 ATGAAGTTTCAGGCGCTTTGGAAACACAGAGATGTCTTCCTGTGGAAAGCGCAATC 259
 Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 Db 260 ACTAGGAGACACAGATGTGGAAGTCAATGCGGAAATGCCTTCAATCAGATGTT 319
 Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 Db 320 TCTCCATCCCAGACAGATGAAGTAATTAATGGCTGGCCAAACTCAAGTACCAATTCAAC 379
 Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 Db 380 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTAGCTACCGTA 439
 Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 Db 440 AAGGCTCATCCAAATACTTGGATTGTATTCGAATCAGCTGTTTTTCTTAGTGGCCAAAG 499
 Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 Db 500 ACTGTTGAGGAAGATGAGAGAAATTCAGATCTAAAGGTATTGGCAAGACAGATTTCTGT 559
 Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 Db 560 GGATGTTCTCATCTGAATTTTGAGATGAGAGAAATATTCTGGATAAGTTGATGG 619
 Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 Db 620 GATCTTCACACAGCCACCATGATTTCTTCATATTTTCCATGTCATTCAGTGTCA 679
 Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180

Human prostate selective polynucleotide Pr325.

Prostate; molecular marker; cancer; cytostatic; gene therapy; human;

gene; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS 200..1333

XX /*tag= a

```
Db 680 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATAGCCCATCTCAACATTTGGCAGTC 739
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 740 CTTACCAAGCAACTACTTCTCAGTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 799
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuPheAspTrpLeuSer 220
Db 800 ATGCTTGCTCTGGCCATGGTATGCTGGAAATGGAGAAACTCATTCCTGATTTGGCTTTCT 859
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 860 CTTACAAATGAACTCTTCAGAAACACAGATGATAGTCCAGTTGATCAATTCGTCGG 919
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 920 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAATTCGGTTAT 979
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 980 GTCTACCGTCCCTCAAGCACACCCCTGTGTACCTGTGACAAAGGAGTGTTCAGATTACAT 1039
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1040 CCCTCTCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAAAGTGCAGTC 1099
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1100 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGCCTCT 1159
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 1160 ACTAAACGCAAAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAAATCAAAACGGCTC 1219
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1220 TATAATGAAGATAATGTCTCGAAATATGGGTCTGTGTGGCAGCTGTTCTGTCTATG 1279
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1280 CNAAGAGGACATGCTTCCCTTGTCCACTTTGACGCTGTTCTGTCTATG 1330
```

RESULT 8

```
ABL87929
ID ABL87929 standard; DNA; 1889 BP.
XX ABL87929;
AC ABL87929;
XX 17-MAY-2002 (first entry)
XX Human ovarian cancer related DNA clone SEQ ID NO:10907.
XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ds.
XX Homo sapiens.
XX WO200192581-A2.
XX 06-DEC-2001.
XX 29-MAY-2001; 2001WO-US017756.
XX 26-MAY-2000; 2000US-0207484P.
XX (CORI-) CORIXA CORP.
XX Algate PA, Harlocker SL, Jones R;
XX WPI; 2002-122075/16.
XX Composition for therapy and diagnosis of ovarian cancer comprising
PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
```

polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.

Claim 1; SEQ ID NO 10907; 489pp; English.

The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), or antigen presenting cells that express (II). (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to (S1) can be used for detecting ovarian cancer in a patient's biological sample preferably serum or ovarian tissue. The method comprises contacting a biological sample from a patient with (IV), detecting the amount of polynucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynucleotide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour cDNA library using well known techniques

Sequence 1889 BP; 473 A; 501 C; 436 G; 479 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	0	Length:	1889
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-736-250-1 (1-377) x ABL87929 (1-1889)

Qy	1	MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle	20
Db	544	ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGTTCTTCTGTTGGAAAGGCAATC	603
Qy	21	ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal	40
Db	604	ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGSCCTTCAATCAGAATGTT	663
Qy	41	SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn	60
Db	664	TCTCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC	723
Qy	61	LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal	80
Db	724	CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTTTAGTACCGTA	783
Qy	81	LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys	100
Db	784	AAGGCTCATCCAAATACTTGAATGTATTGCAATCAGCTGTTTTTCTAGTGCCTAAG	843
Qy	101	ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys	120
Db	844	ACTGTGTGAGGAAGATGAGAGAAATTCAGATCTAAAGGTATTGGCAAGAGACAGTTTCT	903
Qy	121	GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp	140
Db	904	GGATGTTCTCATCTGAAATTTTGGAATGAGAGAAATATTCTGGATAAGTTGATTTGG	963
Qy	141	AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer	160
Db	964	GATCTTCACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTCAGTGCA	1023
Qy	161	ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal	180
Db	1024	ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC	1083

QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAenGlnLeuLeuGlnPheArgLysSer 200
 DB 1084 CTTACCAAGCACTACTTCACTGATGATGCGTCCACCAACTCTGCAATTCAGAGATCC 1143
 QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
 DB 1144 ATGCTTGCTGCGCATGTTAGTCTGGAATGGAGAACTCATTCCTGATGGCTTCT 1203
 QY 221 LeuThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArg 240
 DB 1204 CTTCAATGTGAACCTCTCAGAAAGCAGATGGATAGTCCAGTTCATTCATTCGCG 1263
 QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
 DB 1264 GAGCTTGCGGCATCATCTTCTACTCTGAGTCTTCCTGCTCGCTCGAATTCGTTTAT 1323
 QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
 DB 1324 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
 QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
 DB 1384 CCCTCTCTGTCGCCAGGCCAGACTTCTCCAAGGACAAACAGCAAGTGGCAGTCC 1443
 QY 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
 DB 1444 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGACACTCT 1503
 QY 321 ThrLysArgLysValGluMetGluValAspPheTyrAspGlyLleLysArgLeu 340
 DB 1504 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAAACGGCTC 1563
 QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
 DB 1564 TATATGAAGATAATGTCTCAGAAATATGGGTCTCTGTGTGGCAGCTGTTCGTGTCATG 1623
 QY 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 DB 1624 CAAGAGGACATGCTTCCCTGTGCCACTTTCAGACCTGTTCGTGTCATG 1674

RESULT 9
 ADP10653
 ID ADP10653 standard; DNA; 1890 BP.
 AC ADP10653;
 XX
 XX
 DT 12-AUG-2004 (first entry)
 DE
 DE Reference mRNA sequences for marker probe #330.
 XX
 XX transplant rejection; immune system; rheumatoid arthritis; lupus;
 KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO2004042346-A2.
 PN
 XX
 PD 21-MAY-2004.
 XX
 PF 24-APR-2003; 2003WO-US012946.
 XX
 PR 24-APR-2002; 2002US-00131831.
 PR 20-DEC-2002; 2002US-00325899.
 XX
 PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
 XX
 XX Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
 PI Rosenberg S;
 PI
 DR WPI; 2004-400724/37.
 XX
 PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,

PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
 PT rejection, in an individual, comprises detecting the expression level of
 PT the genes.
 XX Claim 80; SEQ ID NO 662; 1762pp; English.
 PS
 XX The present invention relates to diagnosing or monitoring transplant
 CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
 CC comprises detecting the expression level of one or more genes. The
 CC methods, system and kits are useful in diagnosing or monitoring
 CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
 CC islet, lung, bone marrow or stem cell transplant rejection,
 CC xenotransplant rejection or mechanical organ replacement rejection, in an
 CC individual. The method is also useful in assessing the immune status of
 CC diseases that involve the immune system, e.g. rheumatoid arthritis,
 CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
 CC viral, bacterial or fungal infection. The present sequence represents a
 CC mRNA reference sequence for a 50 mer oligonucleotide marker for diagnosis
 CC and monitoring of allograft rejection and other disorders.
 XX

Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;

Alignment Scores:
 Pred. NO.: 0 Length: 1890
 Score: 377.00 Matches: 377
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x ADP10653 (1-1890)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
 DB 545 ATGAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTTCCTGTGGAAAGGCAATC 604
 QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
 DB 605 ACTAGGAGNAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGT 664
 QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
 DB 665 TCTCCATCCCAGAGAGATGAAGTAATTCATATGGTGGCCAACTCAAGTACCAATTCAC 724
 QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
 DB 725 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTGTAGCTACC 784
 QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
 DB 785 AAGGCTCATCCAAATACTTGGATTGTATTGCAATCAGCTGTTCCTAGCTGCCAAG 844
 QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
 DB 845 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 904
 QY 121 GlyCysSerSerSerGluLleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
 DB 905 GGATGTTCTCATCTGAAATTTTGGAGATGGAGAAATTTCTGGATAAGTTGAATTTGG 964
 QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
 DB 965 GATCTTCACAGCCACACCATTCGATTTCTTCATATTTCCATTCATTCAGTGTGCA 1024
 QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
 DB 1025 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATGGAGCCCATCTCAACATTTGCGAGTC 1084
 QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
 DB 1085 CTTACCAAGCACTACTTCTACTGTATGGCTTGCACCAACTTCTGCATTCAGAGATCC 1144

```
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db 1145 ATGCTTGCTGCGCCATGTTAGTCTGGAATGGAGAACTCATCTCGATGGCTTTCT 1204
Qy 221 LeuThrIleGluLeuGluLeuAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1205 CTTACAATTGAACGCTTCAGAAAGCAGAGATGATAGTCCAGTTGATCCATTGTCGG 1264
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1265 GAGCTTGCGCACATCAGCTTTACTCTGAGTCTCCCTGCTCTGAAATTCGGTTAT 1324
Qy 261 ValTyrArgProLeuLeuHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1325 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGACAAAGGAGTGTTCAGATTAT 1384
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1385 CCTCTCTGTCGCCAGGCCAGACTTCTCCAAAGGACACAGCAGCAGAGTGCAGTC 1444
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1445 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCGCAGTGGGTGCAAGCAGACCTCT 1504
Qy 321 ThrLysArgLysValGluGluMetGluValAlaAspPheTyrAspGlyLysArgLeu 340
Db 1505 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAAATCAAACGGGCTC 1564
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1565 TATAATGAAGATAATGCTTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAAGA 1624
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1625 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCACCTTGTTCATG 1675

RESULT 10
ACN38124
ID ACN38124 standard; cDNA; 1890 BP.
AC ACN38124;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target ('TAT') cDNA DNA324488, SEQ ID NO:1449.
DE
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic; gene; ss.
XX
OS Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX
XX 02-OCT-2002; 2002US-0414971P.
XX
XX (GETH ) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
XX
XX WPI; 2004-347921/32.
XX
XX P-PSDB; ABM80569.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
XX useful in preparing a medicament for treating or detecting a
```

```
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 1; SEQ ID NO 1449; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
XX polypeptides, and their related nucleic acids. The TAT polypeptides are
XX overexpressed in cancer tissues compared to normal tissues, and may thus
XX serve as effective targets for the diagnosis and treatment of cancer in
XX mammals. The invention also relates to nucleic acid and polypeptide
XX sequences at least 80% identical to the TAT nucleic acids and
XX polypeptides; expression vectors and host cells comprising a TAT nucleic
XX acid; an antibody specific for a TAT polypeptide; a peptide or organic
XX molecule which binds to a TAT polypeptide; fusion proteins comprising a
XX TAT polypeptide; and methods and compositions for the treatment or
XX diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
XX antibodies, antagonists, binding molecules and compositions are useful
XX for diagnosing or treating a cell proliferative disorder associated with
XX increased TAT expression, particularly cancers such as breast cancer,
XX colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
XX cancer, pancreatic cancer, cervical cancer, cancers of the central
XX nervous system, melanoma and leukaemia. TAT nucleic acids may further be
XX used as hybridisation probes, in chromosome and gene mapping, in
XX chromosome identification and in gene therapy. The present sequence
XX represents a TAT nucleic acid of the invention
XX
XX Sequence 1890 BP; 473 A; 501 C; 436 G; 480 T; 0 U; 0 Other;
SQ

Alignment Scores:
Pred No.: 0 Length: 1890
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-1 (1-377) x ACN38124 (1-1890)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 545 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTTCTGTGGAAAGGCAATC 604
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db 605 ACTAGGAAGACACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT 664
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 665 TCTCATCCACAGAGATGAAGTAAATTCATGGTGGCCAACTCAAGTACCAATTCAC 724
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 725 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTGGATAGTGTTCAGTACCGTA 784
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 785 AAGGCTCATCCAAATATCTTGAGTTGATTGCAATCAGCTGTTTTCTAGCTGCCAAG 844
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 845 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGTATTGGCAGAGACAGATTTCTGT 904
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 905 GGATGTTCTCATCTGAAATTTTGGAGATGAGAGAAATATTCTGGATAAGTGAATTGG 964
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 965 GATCTTCACAGCAGCACCATTCGATTTTCTTCATATTTTCCATGTCATTCAGTGTCA 1024
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1025 ACTAGGCTCAGTTACTTTTCAGTTGCTCCCAATTTGAGCCCATCTCAACATTTGGCAGTC 1084
```


Db 538 AGGCTCAGTTTACCTTTTCCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTCTT 597
Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMet 201
Db 598 ACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCATTCAGAGGATCCATG 657
Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTTrpLeuSerLeu 221
Db 658 CTTGCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATCTCGATTGGCTTCTCTT 717
Qy 222 ThrLeuLeuLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGlu 241
Db 718 ACAATTGAATGCTTTCAGAAAGCAGATGATGATGATGATGATGATGATGATGATGATG 777
Qy 242 LeuValAlaHisLeuSerThrLeuGlnSerLeuSerLeuProLeuAsnSerValTrpVal 261
Db 778 CTTGTGGCAGCATCACCCTTCTACTCTGAGTCTTCCCTGCTCTGATTCGGTTATGTC 837
Qy 262 TyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisPro 281
Db 838 TACCGTCCCTCAAGCACACCTGTCACCTGTGACAAAGGAGTGTTCAGATTACATCCC 897
Qy 282 SerSerValProGlyProAspPheSerLysAspSerLysProGluValProValArg 301
Db 898 TCCTCTGTGCCAGCCAGACTTCTCCAAAGGACACACAGCAGAGTCCAGTCCAGT 957
Qy 302 GlyThrAlaAlaPheTyrHisLeuProAlaSerGlyCysLysGlnThrSerThr 321
Db 958 GGTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACT 1017
Qy 322 LysArgLysValGluGluMetGluValAspPheTyrAspGlyLysLeuArgLeuTyr 341
Db 1018 AAAGCAAGATAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTCTAT 1077
Qy 342 AsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGln 361
Db 1078 AATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGTGCACTGATTTATCAAGCAA 1137
Qy 362 GluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1138 GAGGACATGTTTCCCTTGTCCACCTTGGAGCTGTCTTCTGTCATG 1185

RESULT 12

ADL63374
ID ADL63374 standard; DNA; 2755 BP.

AC ADL63374;

XX 20-MAY-2004 (first entry)

XX Human ovarian cancer DNA marker #21586.

XX Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.

XX Homo sapiens.

XX WO200170979-A2.

XX 27-SEP-2001.

XX 21-MAR-2001; 2001WO-US009126.

XX 21-MAR-2000; 2000US-0191031P.

XX 25-MAY-2000; 2000US-0207124P.

XX 15-JUN-2000; 2000US-0211940P.

XX 07-JUL-2000; 2000US-0216820P.

XX 25-JUL-2000; 2000US-0220661P.

XX 21-DEC-2000; 2000US-0257672P.

XX (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX Lee J, Lillie J;

XX WPI; 2001-611502/70.

XX Novel isolated nucleic acid molecules (markers) overexpressed in ovarian cancer cells as compared to their normal non-cancerous ovarian cells are used to characterize stage, grade, histological type of ovarian cancer.

XX Disclosure; SEQ ID NO 21586; 106pp; English.

XX The invention relates to nucleic acid markers which are overexpressed in ovarian cancer cells as compared to their expression in normal (i.e. non-cancerous) ovarian cells. The invention also relates to polypeptides encoded by the markers, antibodies that selectively bind to the polypeptides, a method of inhibiting ovarian cancer in a patient at risk of developing ovarian cancer involving inhibiting expression of a gene corresponding to a marker of the invention and a method of treating a patient afflicted with ovarian cancer comprising providing to cells of the patient an antisense oligonucleotide complementary to a marker of the invention. The markers are useful for assessing if a patient is afflicted with ovarian cancer, which involves comparing the level of expression of a marker in a patient sample and a normal level of expression of the marker in a control non-ovarian cancer sample. A difference between the expression levels indicates ovarian cancer. The level of expression of a marker corresponds to a secreted protein or to a transcribed polynucleotide or its portion. The level of expression of the marker is assessed by detecting the presence in the sample, a protein or protein fragment corresponding to the marker. The presence of protein or protein fragment is detected using an antibody that specifically binds with the protein or protein fragment. Alternatively, the level of expression of the marker is assessed by detecting the presence of a transcribed polynucleotide which anneals with the marker or anneals with a portion of the polynucleotide comprising the marker, under stringent conditions. The marker is also used for monitoring the progression of ovarian cancer in a patient which involves detecting expression of the marker in a patient sample at a first point in time, repeating the method at a subsequent time and comparing the level of expression. The method is carried out using an ovarian tissue sample. A composition comprising a marker, polypeptide or antibody of the invention is used to treat ovarian cancer. This sequence represents a human ovarian cancer DNA marker of the invention.

XX Sequence 2755 BP; 749 A; 673 C; 606 G; 727 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.55e-250 Length: 2755
Score: 266.00 Matches: 266
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.56% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x ADL63374 (1-2755)

Qy 103 GluLysAspGluArgLysProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
Db 1099 GAGGAAGATGAGAGAAATTCAGTACTAAAGTATTTGGCAGAGACAGTTTCTGTGGATGT 1158
Qy 123 SerSerSerGluLysLeuArgMetGluArgLysLeuAspLysLeuAsnTrpAspLeu 142
Db 1159 TCCTCATCTGAATTTTGGAGATGGAGAGAAATTTCTGGATAAGTTGAATGGATCTT 1218
Qy 143 HisThrAlaThrProLeuAspPheLeuHisLysPheHisAlaLysLysSerThrArg 162
Db 1219 CACACAGCCACCATTTGGATTTTCTCATATTTTCCATTTCCCATTTGCAAGTCACTAGG 1278
Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValThr 182
Db 1279 CCTCAGTTACTTTTTCAGTTTGGCCCAATTTGAGCCATCTCAACATTTGGCAGTCTTACC 1338
Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeu 202
Db 1339 AAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTT 1398

QY 203 AlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuLeuProAspTrpLeuSerLeuThr 222
Db 1399 GCTCTGGCCATGGTTAGTCTGGAATGAGAACTCATCTCGATTGGCTTCTTACA 1458
QY 223 IleGluLeuLeuGlnLysAlaGlnMetAspSerGlnLeuLeuLeuHisCysArgGluLeu 242
Db 1459 ATTGAACCTGCTTCAGAAAGCAGATGATAGCTCCCAAGGAGTTCATTCATCGGAGCTT 1518
QY 243 ValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 1519 GTGGCACATCACCTTTACTCTGAGTCTTCCCTGCTGAAATTCGGTTATGTCTAC 1578
QY 263 ArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSer 282
Db 1579 CGTCCCTCAGCACACCTCTGTGACCTGTGACAAAGGAGTTCAGATTACATCCCTCC 1638
QY 283 SerValProGlyProAspPheSerLysAspAsnSerLysProGluValProValArgGly 302
Db 1639 TCTGTCCAGGCCAGACTTCTCAAGGACACACAGCAGCAAGTCCAGTCCAGAGGT 1698
QY 303 ThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLys 322
Db 1699 ACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGTGGCAGCAGACCTCTACAAA 1758
QY 323 ArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsn 342
Db 1759 CGCAAGTAGAGGAATGGAAGTGGATGACTTCTATGATGAATCAACGGCTCTATAAT 1818
QY 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
Db 1819 GAAGATATATGCTCAGAAAATGTGGTTCTGTGTGGCACTGATTTATCAAGACAAGAG 1878
QY 363 GlyHisAlaSerProCys 368
Db 1879 GGACATGCTTCCCTTGT 1896
RESULT 13
ID ADN01156 standard; DNA; 903 BP.
XX AC ADN01156;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human cell growth, differentiation, and death-associated coding seq #15.
XX
KW human; cell growth; cell differentiation; cell death; CGDD;
KW cell proliferative disorder; arteriosclerosis; bursitis;
KW cirrhosis; hepatitis; polycythemia vera; psoriasis; cancer;
KW developmental disorder; Cushing's syndrome; hypothyroidism;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease;
KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
KW reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
KW ds.
XX
OS Homo sapiens.
XX
PN WO2004031364-A2.
XX
PD 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
PR 03-OCT-2002; 2002US-0416205P.
PR 25-OCT-2002; 2002US-0421521P.
PR 21-NOV-2002; 2002US-0428376P.
PR 23-DEC-2002; 2002US-0436258P.
PR 10-JAN-2003; 2003US-0439292P.
PR 13-FEB-2003; 2003US-0447578P.
XX
PA (INCY-) INCYTE CORP.

PA (BURR/) BURRILL J D.
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
PI Yang YG, Gietzen KJ, Hafalia AJA;
XX
DR WPI; 2004-330172/30.
DR P-PSDB; ADN01131.
XX
PT New isolated polypeptides associated with cell growth, differentiation
PT and death, useful for diagnosing, treating or preventing e.g.
PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
PT diabetes mellitus or infertility.
XX
PS Claim 5; SEQ ID NO 40; 213pp; English.
XX
CC The invention comprises the amino acid and coding sequences of human
CC proteins that are associated with cell growth, differentiation, and death
CC (CGDD). The DNA and protein sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of CGDD, such as: cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
CC polycythemia vera, psoriasis and cancers), developmental disorders (e.g.
CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
CC disease, Parkinson's disease and multiple sclerosis),
CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
CC contact dermatitis and diabetes mellitus), and reproductive disorders
CC (e.g. infertility, endometriosis and uterine fibroid). The present DNA
CC sequence encodes a human CGDD-associated protein of the invention.
XX
SQ Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 4.19e-140 Length: 903
Score: 153.00 Matches: 153
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 40.58% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x ADN01156 (1-903)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 2 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGGCAATC 61
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 62 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCCTTCAAATCAGAATGTT 121
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 122 TCTCATTCACAGAGATGAAGTAATTAATTCAGTGGCTGCCAACTCAAGTACCAATTCAC 181
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 182 CTTTACCCAGAAACATTTGCTGCTGGTAGCAGCTTTTGGATAGTGTTCAGTACCGTA 241
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 242 AAGGCTCATCCAAATACTTGGAGTTGATTGCAATCAGCTGTGTTTTTCTAGCTGCCAAG 301
QY 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 302 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAAGGATATTGGCAGAGACAGTTTCTGT 361
QY 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 362 GGATGTTCTCTCACTGAATTTTGGAGATGGAGAGATTTATCTGGATAGTCAATTGG 421
QY 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153

```
Db 422 GATCTTCACAGCAGCACCACATTGGATTCTTCTCATATT 460
|||||
RESULT 14
AAC01909
ID AAC01909 standard; cDNA; 444 BP.
XX
AC AAC01909;
XX
XX 06-OCT-2000 (first entry)
XX
XX Human secreted protein 5' EST, SEQ ID NO: 1907.
XX
XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping; ss.
XX
XX Homo sapiens.
XX
XX EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GSEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX
XX WPI; 2000-500381/45.
XX
XX P-PSDB; AAG01903.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
PT diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 1907; 71pp + Sequence Listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
CC mRNAs encoding secreted proteins. An ORF has been identified within the
CC sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
CC derived from 30 different tissues. EST sequences usually correspond
CC mainly to the 3' untranslated region (UTR) of the mRNA because they are
CC often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
CC well suited for isolating cDNA sequences derived from the 5' ends of
CC mRNAs and even in those cases where longer cDNA sequences have been
CC obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
CC mRNAs with intact 5' ends and can therefore be used to obtain full length
CC cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
CC gene therapy and chromosome mapping procedures. They are used to obtain
CC upstream regulatory sequences and to design expression and secretion
CC vectors
XX
XX Sequence 444 BP; 106 A; 106 C; 87 G; 143 T; 0 U; 2 Other;
SQ
Alignment Scores:
Pred. No.: 1.44e-131 Length: 444
Score: 144.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.20% Indels: 0
DB: 3 Gaps: 0
US-09-736-250-1 (1-377) x AAC01909 (1-444)
Qy 117 AspSerPheCysGlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuAsp 136
|||||
Db 13 GACAGTTCTCTGGATGTTCTCTCATCTGAAATTTTGAAGATGGAGAAATTATTCTGGAT 72
|||||
Qy 137 LysLeuAanTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAla 156
|||||
Db 73 AAGTTGAATTGGGATCTTCACACAGCCACACCAATTGGATTTTCTTCATATTTTCATGCC 132
|||||
```

157 IleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGln 176
133 ATTGCAGTGTCAACTAGGCCTCAGTTACTTTTCAGTTTGGCCAAATTGAGCCCATCTCAA 192
177 HisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGln 196
193 CATTTGGCAGTCTTACCAAGCAACTACTTACATGTATGGCTCGCAACCAACTTCTGCA 252
197 PheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIlePro 216
253 TTCAGAGGATCCATGCTTGTCTGGCCATGTTAGTCTGGAATGGAGAAACTCATTCCT 312
217 AspTrpLeuSerLeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeu 236
313 GATTGGCTTTCTCTTACAAATTGAACCTCTTCAAGAACACAGATGGATAGTCCAGTTG 372
237 IleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeu 256
373 ATCCATTGTCGGAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTG 432
257 AsnSerValTyr 260
433 AATTCCGTTTAT 444
RESULT 15
AAAX40003/C
ID AAAX40003 standard; DNA; 804 BP.
XX
AC AAAX40003;
XX
DT 02-JUL-1999 (first entry)
XX
DE Prostate cancer associated gene.
XX
XX Cancer associated antigen; diagnosis; research; treatment; human;
KW breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
KW prostate cancer; ss.
XX
OS Homo sapiens.
XX
XX WO9904265-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US014679.
XX
PR 17-JUL-1997; 97US-00896164.
PR 10-OCT-1997; 97US-0061599P.
PR 10-OCT-1997; 97US-0061765P.
PR 10-OCT-1997; 97US-00948705.
PR 11-OCT-1997; 97GB-00021697.
PR 22-JUN-1998; 98US-00102322.
XX
XX (LUDW-) LUDWIG INST CANCER RES.
XX
XX Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
PI O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX
XX WPI; 1999-132448/11.
XX
XX New isolated cancer associated nucleic acids and polypeptides - isolated
PT using sera from cancer patients, used to develop products for the
PT diagnosis, monitoring or treatment of cancers.
XX
XX Claim 67; Page 630; 787pp; English.
XX
XX The invention relates to a method for diagnosing a disorder characterised
CC by expression of a human cancer associated antigen precursor coded for by
CC a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC biological sample isolated from a subject with an agent that specifically
CC binds to the NAM, an expression product or a fragment of an expression
CC product complexed with an HLA molecule; and (b) determining the

CC interaction between the agent and the NAM or the expression product as a
 CC determination of the disorder. The products and methods can be used in
 CC the diagnosis, monitoring, research, or treatment of conditions
 CC characterised by the expression of various cancer associated antigens.
 CC The invention provides nucleic acid sequences and encoded polypeptides
 CC which are cancer associated antigen precursors expressed in human breast
 CC cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
 CC lung cancer
 XX

SQ Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;

Alignment Scores:

Pred. No.: 1.34e-116 Length: 804
 Score: 129.00 Matches: 129
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 34.22% Indels: 0
 DB: 2 Gaps: 0

US-09-736-250-1 (1-377) x AAX40003 (1-804)

Qy	249	ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThr	268
Db	583	ACTGTGAGTCTTCCCTGCCCTGAATTCGGTTTATGTCTACCGTCCCTCAAGCACACC	524
Qy	269	LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp	288
Db	523	CTGGTGACCTGTGACAAAGAGTGTTCAGATTACATCCCTCTCTGTCCTCCAGGCCAGAC	464
Qy	289	PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis	308
Db	463	TTCTCCAAGGACAAACAGACAGCCAGAGTGCAGGTACAGCAGCCCTTTTACCAT	404
Qy	309	HisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMet	328
Db	403	CATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGGAATG	344
Qy	329	GluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGlu	348
Db	343	GAAGTGGATGACTTCTATGATGGATCAACGGCTCTATATATGAAGATATGTCTCAGAA	284
Qy	349	AsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys	368
Db	283	AATGTGGGTCTGTGTGTGGCACTGATTTATCAAGACAAGAGGACATGCTTCCCTTGT	224
Qy	369	ProProLeuGlnProValSerValMet	377
Db	223	CCACCTTTCAGCCCTGTTCTGTGTCATG	197

Search completed: February 11, 2005, 10:38:39
 Job time : 1046.8 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame plus p2n model

Run on: February 11, 2005, 09:52:50 ; Search time 299.864 Seconds
(without alignments)
2057.184 Million cell updates/sec

Title: US-09-736-250-1

Perfect score:

Sequence: 1 MKFPGPLENQRLSFLEKAI.....LSRQEGHASPCPPLQPVSM 377

Scoring table:

Learning curve.	CHRO
Xgapop 60.0 , Xgapext 60.0	60.0
Ygapop 60.0 , Ygapext 60.0	60.0
Fgapop 6.0 , Fgapext 7.0	7.0
Delop 6.0 , Delext 7.0	7.0

Searched: 1202784 reqs. 818138359 residues

Word size:

Total number of bits satisfying chosen parameters: 2400006

Minimum DB set length: 0

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Listing first 1000 summaries

Command line parameters:

```
-MODEL=frame+ p2n.model -DEV=xlh
-COMMAND-line parameters:
-runat_07022005_154942_20670/app_query.fasta_1.718
-Q/cgcn2_l/UPTO spool/U909736250
-D$-issued Patents NA -QWMT=fastap -SUFFIX=oligo.rni -MINMATCH=0.1 -LOOPCL=0
-BB=human40.cdi -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LOOPTXT=0 -UNITS=bits -THATR SCORE=quality -THR_MIN=1 -ALIGN=LOCAL
-LIST=1000 -DOCALIGN=200 -THATR SCORE=quality -THR_MIN=1 -ALIGN=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USBR=U909736250 @CGN_1_1_93 @runat_07022005_154942_20670 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORE=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEVTIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOB=6 -DELEXT=7
```

```
Database : Issued_Patents_NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUT COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	%		SUMMARIES					Description
	Score	Query Match	Length	DB	ID			
1	377	100.0	1133	3	US-09-054-492B-2	Sequence 2, Appli		
2	377	100.0	1260	2	US-08-969-106-5	Sequence 5, Appli		
3	377	100.0	1260	4	US-09-338-125-5	Sequence 5, Appli		
4	377	100.0	1260	4	US-09-023-6555-899	Sequence 899, App		
5	144	38.2	446	4	US-09-513-999C-1907	Sequence 1907, App		
6	34	9.0	304	4	US-09-513-999C-29894	Sequence 29894, A		
7	9	2.4	1643	3	US-09-129-112-1	Sequence 1, Appli		
8	9	2.4	6265	3	US-09-129-112-3	Sequence 3, Appli		
9	8	2.1	277	4	US-09-313-294A-98	Sequence 98, Appli		
c 10	8	2.1	279	4	US-09-513-999C-32630	Sequence 32630, A		
11	8	2.1	382	4	US-09-270-767-26393	Sequence 26393, A		
12	8	2.1	400	4	US-08-956-171E-1529	Sequence 1529, App		

86	7	1.9	33	3	US-09-054-492B-3	Sequence 3, Appli	c 159	7	1.9	601	4	US-09-949-016-23104	Sequence 23104, A
c 87	7	1.9	35	3	US-08-691-045-38	Sequence 38, Appli	c 160	7	1.9	601	4	US-09-949-016-24168	Sequence 24168, A
c 88	7	1.9	73	4	US-09-270-767-29784	Sequence 29784, A	c 161	7	1.9	601	4	US-09-949-016-24407	Sequence 24407, A
c 89	7	1.9	84	2	US-08-788-943A-14	Sequence 14, Appli	c 162	7	1.9	601	4	US-09-949-016-24408	Sequence 24408, A
c 90	7	1.9	84	5	PCT-US96-00952-15	Sequence 15, Appli	c 163	7	1.9	601	4	US-09-949-016-24409	Sequence 24409, A
c 91	7	1.9	87	2	US-08-788-943A-15	Sequence 15, Appli	c 164	7	1.9	601	4	US-09-949-016-24410	Sequence 24410, A
c 92	7	1.9	87	5	PCT-US96-00952-16	Sequence 16, Appli	c 165	7	1.9	601	4	US-09-949-016-24411	Sequence 24411, A
c 93	7	1.9	93	3	US-09-565-156A-17	Sequence 17, Appli	c 166	7	1.9	601	4	US-09-949-016-24412	Sequence 24412, A
c 94	7	1.9	97	4	US-09-270-767-27272	Sequence 27272, A	c 167	7	1.9	601	4	US-09-949-016-24746	Sequence 24746, A
c 95	7	1.9	109	4	US-09-513-999C-29336	Sequence 29336, A	c 168	7	1.9	601	4	US-09-949-016-27369	Sequence 27369, A
c 96	7	1.9	166	3	US-09-465-355-34	Sequence 34, Appli	c 169	7	1.9	601	4	US-09-949-016-27815	Sequence 27815, A
c 97	7	1.9	196	4	US-09-270-767-29745	Sequence 29745, A	c 170	7	1.9	601	4	US-09-949-016-28245	Sequence 28245, A
c 98	7	1.9	211	4	US-09-270-767-29750	Sequence 29750, Ap	c 171	7	1.9	601	4	US-09-949-016-29230	Sequence 29230, A
c 99	7	1.9	211	4	US-09-270-767-18257	Sequence 18257, A	c 172	7	1.9	601	4	US-09-949-016-29231	Sequence 29231, A
c 100	7	1.9	212	4	US-09-313-294A-7402	Sequence 7402, Ap	c 173	7	1.9	601	4	US-09-949-016-29232	Sequence 29232, A
c 101	7	1.9	219	4	US-09-583-110-1832	Sequence 1832, Ap	c 174	7	1.9	601	4	US-09-949-016-29233	Sequence 29233, A
c 102	7	1.9	221	4	US-09-513-999C-20246	Sequence 20246, A	c 175	7	1.9	601	4	US-09-949-016-29234	Sequence 29234, A
c 103	7	1.9	237	4	US-09-248-796A-11710	Sequence 11710, A	c 176	7	1.9	601	4	US-09-949-016-29235	Sequence 29235, A
c 104	7	1.9	251	4	US-09-513-999C-16329	Sequence 16329, A	c 177	7	1.9	601	4	US-09-949-016-29236	Sequence 29236, A
c 105	7	1.9	258	4	US-09-543-681A-4062	Sequence 4062, Ap	c 178	7	1.9	601	4	US-09-949-016-29237	Sequence 29237, A
c 106	7	1.9	281	4	US-09-313-294A-5735	Sequence 5735, Ap	c 179	7	1.9	601	4	US-09-949-016-29738	Sequence 29738, A
c 107	7	1.9	285	4	US-09-313-294A-6808	Sequence 6808, Ap	c 180	7	1.9	601	4	US-09-949-016-30563	Sequence 30563, A
c 108	7	1.9	333	4	US-09-543-681A-1302	Sequence 1302, Ap	c 181	7	1.9	601	4	US-09-949-016-30564	Sequence 30564, A
c 109	7	1.9	333	4	US-09-489-039A-1704	Sequence 1704, Ap	c 182	7	1.9	601	4	US-09-949-016-30565	Sequence 30565, A
c 110	7	1.9	334	4	US-09-270-767-28790	Sequence 28790, A	c 183	7	1.9	601	4	US-09-949-016-30567	Sequence 30567, A
c 111	7	1.9	338	4	US-09-513-999C-30716	Sequence 30716, A	c 184	7	1.9	601	4	US-09-949-016-30568	Sequence 30568, A
c 112	7	1.9	339	4	US-09-640-211A-420	Sequence 420, App	c 185	7	1.9	601	4	US-09-949-016-34213	Sequence 34213, A
c 113	7	1.9	347	1	US-09-513-999C-23861	Sequence 23861, A	c 186	7	1.9	601	4	US-09-949-016-34214	Sequence 34214, A
c 114	7	1.9	357	1	US-08-318-970B-31	Sequence 31, Appli	c 187	7	1.9	601	4	US-09-949-016-34737	Sequence 34737, A
c 115	7	1.9	367	4	US-09-621-976-10003	Sequence 10003, A	c 188	7	1.9	601	4	US-09-949-016-34738	Sequence 34738, A
c 116	7	1.9	384	4	US-09-603-777A-375	Sequence 375, App	c 189	7	1.9	601	4	US-09-949-016-35470	Sequence 35470, A
c 117	7	1.9	386	4	US-09-023-655-692	Sequence 692, App	c 190	7	1.9	601	4	US-09-949-016-37042	Sequence 37042, A
c 118	7	1.9	395	4	US-09-621-976-10223	Sequence 10223, A	c 191	7	1.9	601	4	US-09-949-016-37929	Sequence 37929, A
c 119	7	1.9	399	1	US-08-318-970B-40	Sequence 40, Appli	c 192	7	1.9	601	4	US-09-949-016-37930	Sequence 37930, A
c 120	7	1.9	400	4	US-08-958-171E-852	Sequence 852, App	c 193	7	1.9	601	4	US-09-949-016-39132	Sequence 39132, A
c 121	7	1.9	400	4	US-08-781-986A-852	Sequence 852, App	c 194	7	1.9	601	4	US-09-949-016-39454	Sequence 39454, A
c 122	7	1.9	402	1	US-08-318-970B-41	Sequence 41, Appli	c 195	7	1.9	601	4	US-09-949-016-39455	Sequence 39455, A
c 123	7	1.9	402	4	US-08-956-171E-1282	Sequence 1282, Ap	c 196	7	1.9	601	4	US-09-949-016-39913	Sequence 39913, A
c 124	7	1.9	402	4	US-08-781-986A-1282	Sequence 1282, Ap	c 197	7	1.9	601	4	US-09-949-016-39916	Sequence 39916, A
c 125	7	1.9	408	3	US-09-128-155-10	Sequence 10, Appli	c 198	7	1.9	601	4	US-09-949-016-39917	Sequence 39917, A
c 126	7	1.9	411	4	US-09-252-931A-13777	Sequence 13777, A	c 199	7	1.9	601	4	US-09-949-016-40395	Sequence 40395, A
c 127	7	1.9	411	4	US-09-401-084-180	Sequence 180, App	c 200	7	1.9	601	4	US-09-949-016-40396	Sequence 40396, A
c 128	7	1.9	452	4	US-09-621-976-493	Sequence 493, App	c 201	7	1.9	601	4	US-09-949-016-40397	Sequence 40397, A
c 129	7	1.9	452	4	US-09-640-211A-63	Sequence 63, Appli	c 202	7	1.9	601	4	US-09-949-016-40398	Sequence 40398, A
c 130	7	1.9	465	4	US-09-270-767-11456	Sequence 11456, A	c 203	7	1.9	601	4	US-09-949-016-40399	Sequence 40399, A
c 131	7	1.9	477	4	US-09-248-796A-2135	Sequence 2135, Ap	c 204	7	1.9	601	4	US-09-949-016-40400	Sequence 40400, A
c 132	7	1.9	482	4	US-09-270-767-1337	Sequence 1337, Ap	c 205	7	1.9	601	4	US-09-949-016-40401	Sequence 40401, A
c 133	7	1.9	482	4	US-09-270-767-16619	Sequence 16619, A	c 206	7	1.9	601	4	US-09-949-016-46815	Sequence 46815, A
c 134	7	1.9	490	2	US-08-967-101-76	Sequence 76, Appli	c 207	7	1.9	601	4	US-09-949-016-46816	Sequence 46816, A
c 135	7	1.9	490	2	US-08-592-541-76	Sequence 76, Appli	c 208	7	1.9	601	4	US-09-949-016-46817	Sequence 46817, A
c 136	7	1.9	490	3	US-09-124-698-76	Sequence 76, Appli	c 209	7	1.9	601	4	US-09-949-016-46818	Sequence 46818, A
c 137	7	1.9	490	3	US-09-127-480-76	Sequence 76, Appli	c 210	7	1.9	601	4	US-09-949-016-46819	Sequence 46819, A
c 138	7	1.9	490	3	US-08-496-841C-76	Sequence 76, Appli	c 211	7	1.9	601	4	US-09-949-016-46820	Sequence 46820, A
c 139	7	1.9	490	3	US-09-124-523-76	Sequence 76, Appli	c 212	7	1.9	601	4	US-09-949-016-46821	Sequence 46821, A
c 140	7	1.9	490	4	US-09-636-796A-76	Sequence 76, Appli	c 213	7	1.9	601	4	US-09-949-016-46822	Sequence 46822, A
c 141	7	1.9	490	4	US-08-431-048F-76	Sequence 76, Appli	c 214	7	1.9	601	4	US-09-949-016-46828	Sequence 46828, A
c 142	7	1.9	496	4	US-09-949-016-170229	Sequence 170229, A	c 215	7	1.9	601	4	US-09-949-016-46829	Sequence 46829, A
c 143	7	1.9	501	3	US-09-128-155-6	Sequence 6, Appli	c 216	7	1.9	601	4	US-09-949-016-46830	Sequence 46830, A
c 144	7	1.9	534	3	US-09-128-155-3	Sequence 3, Appli	c 217	7	1.9	601	4	US-09-949-016-46831	Sequence 46831, A
c 145	7	1.9	543	4	US-09-248-796A-9429	Sequence 9429, Ap	c 218	7	1.9	601	4	US-09-949-016-46832	Sequence 46832, A
c 146	7	1.9	563	4	US-09-949-016-170230	Sequence 170230, A	c 219	7	1.9	601	4	US-09-949-016-46833	Sequence 46833, A
c 147	7	1.9	564	4	US-09-327-138C-33	Sequence 33, Appli	c 220	7	1.9	601	4	US-09-949-016-46834	Sequence 46834, A
c 148	7	1.9	573	4	US-09-489-039A-3890	Sequence 3890, Ap	c 221	7	1.9	601	4	US-09-949-016-50242	Sequence 50242, A
c 149	7	1.9	584	4	US-09-187-999-26	Sequence 26, Appli	c 222	7	1.9	601	4	US-09-949-016-50861	Sequence 50861, A
c 150	7	1.9	594	4	US-09-868-352-7	Sequence 7, Appli	c 223	7	1.9	601	4	US-09-949-016-51256	Sequence 51256, A
c 151	7	1.9	598	3	US-09-073-237-25	Sequence 25, Appli	c 224	7	1.9	601	4	US-09-949-016-51477	Sequence 51477, A
c 152	7	1.9	599	4	US-09-513-999C-1512	Sequence 1512, Ap	c 225	7	1.9	601	4	US-09-949-016-51478	Sequence 51478, A
c 153	7	1.9	601	4	US-09-949-016-22064	Sequence 22064, A	c 226	7	1.9	601	4	US-09-949-016-51479	Sequence 51479, A
c 154	7	1.9	601	4	US-09-949-016-22696	Sequence 22696, A	c 227	7	1.9	601	4	US-09-949-016-53438	Sequence 53438, A
c 155	7	1.9	601	4	US-09-949-016-22697	Sequence 22697, A	c 228	7	1.9	601	4	US-09-949-016-53439	Sequence 53439, A
c 156	7	1.9	601	4	US-09-949-016-22698	Sequence 22698, A	c 229	7	1.9	601	4	US-09-949-016-53848	Sequence 53848, A
c 157	7	1.9	601	4	US-09-949-016-22699	Sequence 22699, A	c 230	7	1.9	601	4	US-09-949-016-53849	Sequence 53849, A
c 158	7	1.9	601	4	US-09-949-016-22777	Sequence 22777, A	c 231	7	1.9	601	4	US-09-949-016-57448	Sequence 57448, A

C 232	7	1.9	601	4	US-09-949-016-57743	Sequence 57743, A	C 305	7	1.9	601	4	US-09-949-016-102547	Sequence 102547,
C 233	7	1.9	601	4	US-09-949-016-57744	Sequence 57744, A	306	7	1.9	601	4	US-09-949-016-105061	Sequence 105061,
C 234	7	1.9	601	4	US-09-949-016-57745	Sequence 57745, A	307	7	1.9	601	4	US-09-949-016-105062	Sequence 105062,
C 235	7	1.9	601	4	US-09-949-016-58593	Sequence 58593, A	308	7	1.9	601	4	US-09-949-016-105063	Sequence 105063,
C 236	7	1.9	601	4	US-09-949-016-60285	Sequence 60285, A	309	7	1.9	601	4	US-09-949-016-105064	Sequence 105064,
C 237	7	1.9	601	4	US-09-949-016-60686	Sequence 60686, A	310	7	1.9	601	4	US-09-949-016-105065	Sequence 105065,
C 238	7	1.9	601	4	US-09-949-016-61280	Sequence 61280, A	311	7	1.9	601	4	US-09-949-016-105066	Sequence 105066,
C 239	7	1.9	601	4	US-09-949-016-63167	Sequence 63167, A	C 312	7	1.9	601	4	US-09-949-016-105227	Sequence 105227,
C 240	7	1.9	601	4	US-09-949-016-64844	Sequence 64844, A	313	7	1.9	601	4	US-09-949-016-105597	Sequence 105597,
C 241	7	1.9	601	4	US-09-949-016-64845	Sequence 64845, A	314	7	1.9	601	4	US-09-949-016-107759	Sequence 107759,
C 242	7	1.9	601	4	US-09-949-016-65234	Sequence 65234, A	315	7	1.9	601	4	US-09-949-016-107760	Sequence 107760,
C 243	7	1.9	601	4	US-09-949-016-66126	Sequence 66126, A	C 316	7	1.9	601	4	US-09-949-016-107761	Sequence 107761,
C 244	7	1.9	601	4	US-09-949-016-66127	Sequence 66127, A	C 317	7	1.9	601	4	US-09-949-016-108617	Sequence 108617,
C 245	7	1.9	601	4	US-09-949-016-66128	Sequence 66128, A	C 318	7	1.9	601	4	US-09-949-016-108618	Sequence 108618,
C 246	7	1.9	601	4	US-09-949-016-66698	Sequence 66698, A	319	7	1.9	601	4	US-09-949-016-109288	Sequence 109288,
C 247	7	1.9	601	4	US-09-949-016-70615	Sequence 70615, A	320	7	1.9	601	4	US-09-949-016-109289	Sequence 109289,
C 248	7	1.9	601	4	US-09-949-016-70616	Sequence 70616, A	321	7	1.9	601	4	US-09-949-016-109290	Sequence 109290,
C 249	7	1.9	601	4	US-09-949-016-70796	Sequence 70796, A	322	7	1.9	601	4	US-09-949-016-109291	Sequence 109291,
C 250	7	1.9	601	4	US-09-949-016-72369	Sequence 72369, A	323	7	1.9	601	4	US-09-949-016-109292	Sequence 109292,
C 251	7	1.9	601	4	US-09-949-016-72370	Sequence 72370, A	324	7	1.9	601	4	US-09-949-016-111466	Sequence 111466,
C 252	7	1.9	601	4	US-09-949-016-72371	Sequence 72371, A	325	7	1.9	601	4	US-09-949-016-111467	Sequence 111467,
C 253	7	1.9	601	4	US-09-949-016-72665	Sequence 72665, A	326	7	1.9	601	4	US-09-949-016-111468	Sequence 111468,
C 254	7	1.9	601	4	US-09-949-016-76511	Sequence 76511, A	327	7	1.9	601	4	US-09-949-016-111469	Sequence 111469,
C 255	7	1.9	601	4	US-09-949-016-76512	Sequence 76512, A	328	7	1.9	601	4	US-09-949-016-111470	Sequence 111470,
C 256	7	1.9	601	4	US-09-949-016-77659	Sequence 77659, A	329	7	1.9	601	4	US-09-949-016-111471	Sequence 111471,
C 257	7	1.9	601	4	US-09-949-016-79423	Sequence 79423, A	330	7	1.9	601	4	US-09-949-016-111472	Sequence 111472,
C 258	7	1.9	601	4	US-09-949-016-81228	Sequence 81228, A	331	7	1.9	601	4	US-09-949-016-111473	Sequence 111473,
C 259	7	1.9	601	4	US-09-949-016-83050	Sequence 83050, A	332	7	1.9	601	4	US-09-949-016-111480	Sequence 111480,
C 260	7	1.9	601	4	US-09-949-016-85110	Sequence 85110, A	333	7	1.9	601	4	US-09-949-016-111481	Sequence 111481,
C 261	7	1.9	601	4	US-09-949-016-85111	Sequence 85111, A	334	7	1.9	601	4	US-09-949-016-111482	Sequence 111482,
C 262	7	1.9	601	4	US-09-949-016-85112	Sequence 85112, A	335	7	1.9	601	4	US-09-949-016-111483	Sequence 111483,
C 263	7	1.9	601	4	US-09-949-016-85261	Sequence 85261, A	336	7	1.9	601	4	US-09-949-016-111484	Sequence 111484,
C 264	7	1.9	601	4	US-09-949-016-85262	Sequence 85262, A	C 337	7	1.9	601	4	US-09-949-016-111485	Sequence 111485,
C 265	7	1.9	601	4	US-09-949-016-85263	Sequence 85263, A	338	7	1.9	601	4	US-09-949-016-112183	Sequence 112183,
C 266	7	1.9	601	4	US-09-949-016-85762	Sequence 85762, A	C 339	7	1.9	601	4	US-09-949-016-112224	Sequence 112224,
C 267	7	1.9	601	4	US-09-949-016-85763	Sequence 85763, A	340	7	1.9	601	4	US-09-949-016-115329	Sequence 115329,
C 268	7	1.9	601	4	US-09-949-016-86783	Sequence 86783, A	341	7	1.9	601	4	US-09-949-016-115632	Sequence 115632,
C 269	7	1.9	601	4	US-09-949-016-86784	Sequence 86784, A	342	7	1.9	601	4	US-09-949-016-115725	Sequence 115725,
C 270	7	1.9	601	4	US-09-949-016-86785	Sequence 86785, A	343	7	1.9	601	4	US-09-949-016-115818	Sequence 115818,
C 271	7	1.9	601	4	US-09-949-016-87167	Sequence 87167, A	344	7	1.9	601	4	US-09-949-016-115911	Sequence 115911,
C 272	7	1.9	601	4	US-09-949-016-87400	Sequence 87400, A	345	7	1.9	601	4	US-09-949-016-116004	Sequence 116004,
C 273	7	1.9	601	4	US-09-949-016-87838	Sequence 87838, A	346	7	1.9	601	4	US-09-949-016-116097	Sequence 116097,
C 274	7	1.9	601	4	US-09-949-016-95218	Sequence 95218, A	347	7	1.9	601	4	US-09-949-016-116190	Sequence 116190,
C 275	7	1.9	601	4	US-09-949-016-95219	Sequence 95219, A	348	7	1.9	601	4	US-09-949-016-116283	Sequence 116283,
C 276	7	1.9	601	4	US-09-949-016-95574	Sequence 95574, A	C 350	7	1.9	601	4	US-09-949-016-116376	Sequence 116376,
C 277	7	1.9	601	4	US-09-949-016-95752	Sequence 95752, A	349	7	1.9	601	4	US-09-949-016-117633	Sequence 117633,
C 278	7	1.9	601	4	US-09-949-016-96629	Sequence 96629, A	C 351	7	1.9	601	4	US-09-949-016-117659	Sequence 117659,
C 279	7	1.9	601	4	US-09-949-016-96895	Sequence 96895, A	C 352	7	1.9	601	4	US-09-949-016-118193	Sequence 118193,
C 280	7	1.9	601	4	US-09-949-016-97161	Sequence 97161, A	C 353	7	1.9	601	4	US-09-949-016-120679	Sequence 120679,
C 281	7	1.9	601	4	US-09-949-016-97427	Sequence 97427, A	354	7	1.9	601	4	US-09-949-016-125698	Sequence 125698,
C 282	7	1.9	601	4	US-09-949-016-97693	Sequence 97693, A	C 355	7	1.9	601	4	US-09-949-016-126044	Sequence 126044,
C 283	7	1.9	601	4	US-09-949-016-97959	Sequence 97959, A	C 356	7	1.9	601	4	US-09-949-016-128329	Sequence 128329,
C 284	7	1.9	601	4	US-09-949-016-98225	Sequence 98225, A	C 357	7	1.9	601	4	US-09-949-016-128330	Sequence 128330,
C 285	7	1.9	601	4	US-09-949-016-98491	Sequence 98491, A	C 358	7	1.9	601	4	US-09-949-016-129016	Sequence 129016,
C 286	7	1.9	601	4	US-09-949-016-98575	Sequence 98575, A	C 359	7	1.9	601	4	US-09-949-016-134208	Sequence 134208,
C 287	7	1.9	601	4	US-09-949-016-99023	Sequence 99023, A	C 360	7	1.9	601	4	US-09-949-016-134209	Sequence 134209,
C 288	7	1.9	601	4	US-09-949-016-99289	Sequence 99289, A	C 361	7	1.9	601	4	US-09-949-016-134210	Sequence 134210,
C 289	7	1.9	601	4	US-09-949-016-99555	Sequence 99555, A	362	7	1.9	601	4	US-09-949-016-134945	Sequence 134945,
C 290	7	1.9	601	4	US-09-949-016-99821	Sequence 99821, A	363	7	1.9	601	4	US-09-949-016-135021	Sequence 135021,
C 291	7	1.9	601	4	US-09-949-016-100087	Sequence 100087, A	364	7	1.9	601	4	US-09-949-016-135022	Sequence 135022,
C 292	7	1.9	601	4	US-09-949-016-100353	Sequence 100353, A	365	7	1.9	601	4	US-09-949-016-136283	Sequence 136283,
C 293	7	1.9	601	4	US-09-949-016-100619	Sequence 100619, A	366	7	1.9	601	4	US-09-949-016-137806	Sequence 137806,
C 294	7	1.9	601	4	US-09-949-016-100885	Sequence 100885, A	C 367	7	1.9	601	4	US-09-949-016-139726	Sequence 139726,
C 295	7	1.9	601	4	US-09-949-016-101189	Sequence 101189, A	C 368	7	1.9	601	4	US-09-949-016-139786	Sequence 139786,
C 296	7	1.9	601	4	US-09-949-016-101455	Sequence 101455, A	C 369	7	1.9	601	4	US-09-949-016-140403	Sequence 140403,
C 297	7	1.9	601	4	US-09-949-016-101721	Sequence 101721, A	C 370	7	1.9	601	4	US-09-949-016-142722	Sequence 142722,
C 298	7	1.9	601	4	US-09-949-016-101987	Sequence 101987, A	371	7	1.9	601	4	US-09-949-016-142723	Sequence 142723,
C 299	7	1.9	601	4	US-09-949-016-102043	Sequence 102043, A	372	7	1.9	601	4	US-09-949-016-149820	Sequence 149820,
C 300	7	1.9	601	4	US-09-949-016-102099	Sequence 102099, A	C 373	7	1.9	601	4	US-09-949-016-153218	Sequence 153218,
C 301	7	1.9	601	4	US-09-949-016-102155	Sequence 102155, A	C 374	7	1.9	601	4	US-09-949-016-153219	Sequence 153219,
C 302	7	1.9	601	4	US-09-949-016-102211	Sequence 102211, A	C 375	7	1.9	601	4	US-09-949-016-153220	Sequence 153220,
C 303	7	1.9	601	4	US-09-949-016-102267	Sequence 102267, A	C 376	7	1.9	601	4	US-09-949-016-153222	Sequence 153222,
C 304	7	1.9	601	4	US-09-949-016-102407	Sequence 102407, A	C 377	7	1.9	601	4	US-09-949-016-157645	Sequence 157645,

C 378	7	1.9	601	4	US-09-949-016-157646	Sequence 157646,	451	7	1.9	621	3	US-09-221-017B-608	Sequence 608, App
C 379	7	1.9	601	4	US-09-949-016-161716	Sequence 161716,	452	7	1.9	634	4	US-09-917-254-33	Sequence 33, Appl
C 380	7	1.9	601	4	US-09-949-016-164878	Sequence 164878,	453	7	1.9	636	4	US-09-134-000C-929	Sequence 929, App
C 381	7	1.9	601	4	US-09-949-016-165765	Sequence 165765,	454	7	1.9	648	4	US-09-949-016-5717	Sequence 5717, Ap
C 382	7	1.9	601	4	US-09-949-016-165766	Sequence 165766,	455	7	1.9	657	4	US-09-398-412B-3	Sequence 3, Appl
C 383	7	1.9	601	4	US-09-949-016-166744	Sequence 166744,	C 456	7	1.9	663	4	US-09-328-352-1833	Sequence 1833, Ap
C 384	7	1.9	601	4	US-09-949-016-166846	Sequence 168466,	457	7	1.9	690	4	US-09-270-767-11657	Sequence 11657, A
C 385	7	1.9	601	4	US-09-949-016-166847	Sequence 168467,	458	7	1.9	696	4	US-09-248-796A-969	Sequence 969, App
C 386	7	1.9	601	4	US-09-949-016-166869	Sequence 168689,	459	7	1.9	696	4	US-09-902-540-8542	Sequence 8542, Ap
C 387	7	1.9	601	4	US-09-949-016-166866	Sequence 168686,	460	7	1.9	708	4	US-09-248-796A-1181	Sequence 1181, Ap
C 388	7	1.9	601	4	US-09-949-016-170085	Sequence 170085,	461	7	1.9	750	3	US-09-446-504-2	Sequence 2, Appl
C 389	7	1.9	601	4	US-09-949-016-170086	Sequence 170086,	462	7	1.9	750	3	US-09-712-266-2	Sequence 2, Appl
C 390	7	1.9	601	4	US-09-949-016-170231	Sequence 170231,	C 463	7	1.9	756	4	US-09-506-286B-3	Sequence 3, Appl
C 391	7	1.9	601	4	US-09-949-016-170231	Sequence 170231,	C 464	7	1.9	756	4	US-09-506-286B-6	Sequence 6, Appl
C 392	7	1.9	601	4	US-09-949-016-172693	Sequence 172693,	C 465	7	1.9	756	4	US-09-762-861B-3	Sequence 3, Appl
C 393	7	1.9	601	4	US-09-949-016-172694	Sequence 172694,	C 466	7	1.9	756	4	US-09-762-861B-6	Sequence 6, Appl
C 394	7	1.9	601	4	US-09-949-016-172695	Sequence 172695,	C 467	7	1.9	756	4	US-10-065-133A-3	Sequence 3, Appl
C 395	7	1.9	601	4	US-09-949-016-172696	Sequence 172696,	C 468	7	1.9	756	4	US-10-065-133A-6	Sequence 6, Appl
C 396	7	1.9	601	4	US-09-949-016-172755	Sequence 172755,	C 469	7	1.9	756	4	US-10-434-811A-3	Sequence 3, Appl
C 397	7	1.9	601	4	US-09-949-016-175310	Sequence 175310,	C 470	7	1.9	756	4	US-10-434-811A-6	Sequence 6, Appl
C 398	7	1.9	601	4	US-09-949-016-175311	Sequence 175311,	C 471	7	1.9	759	4	US-09-107-532A-2865	Sequence 2865, Ap
C 399	7	1.9	601	4	US-09-949-016-175868	Sequence 175868,	C 472	7	1.9	762	4	US-09-270-767-11453	Sequence 11453, A
C 400	7	1.9	601	4	US-09-949-016-176849	Sequence 176849,	C 473	7	1.9	765	4	US-09-248-796A-3490	Sequence 3490, Ap
C 401	7	1.9	601	4	US-09-949-016-179379	Sequence 179379,	C 474	7	1.9	768	4	US-09-583-110-906	Sequence 906, App
C 402	7	1.9	601	4	US-09-949-016-179380	Sequence 179380,	C 475	7	1.9	800	4	US-09-252-991A-13462	Sequence 13462, A
C 403	7	1.9	601	4	US-09-949-016-181018	Sequence 181018,	C 476	7	1.9	771	4	US-09-107-433-1732	Sequence 1732, Ap
C 404	7	1.9	601	4	US-09-949-016-181071	Sequence 181071,	C 477	7	1.9	774	4	US-09-148-545-13	Sequence 13, Appl
C 405	7	1.9	601	4	US-09-949-016-181137	Sequence 181137,	C 478	7	1.9	776	4	US-09-148-545-13	Sequence 13, Appl
C 406	7	1.9	601	4	US-09-949-016-182519	Sequence 182519,	C 479	7	1.9	792	4	US-09-248-796A-933	Sequence 933, App
C 407	7	1.9	601	4	US-09-949-016-182520	Sequence 182520,	C 480	7	1.9	800	4	US-09-270-767-6262	Sequence 6262, Ap
C 408	7	1.9	601	4	US-09-949-016-182639	Sequence 182639,	C 481	7	1.9	802	3	US-09-270-767-22154	Sequence 21544, A
C 409	7	1.9	601	4	US-09-949-016-182640	Sequence 182640,	C 482	7	1.9	803	3	US-09-293-625-1	Sequence 1, Appl
C 410	7	1.9	601	4	US-09-949-016-185239	Sequence 185239,	C 483	7	1.9	816	4	US-09-311-784A-13	Sequence 13, Appl
C 411	7	1.9	601	4	US-09-949-016-185240	Sequence 185240,	C 484	7	1.9	816	4	US-09-328-352-133	Sequence 133, App
C 412	7	1.9	601	4	US-09-949-016-185242	Sequence 185242,	C 485	7	1.9	825	4	US-09-902-540-7095	Sequence 7095, Ap
C 413	7	1.9	601	4	US-09-949-016-185372	Sequence 185372,	C 486	7	1.9	826	4	US-09-328-352-1318	Sequence 1318, Ap
C 414	7	1.9	601	4	US-09-949-016-186441	Sequence 186441,	C 487	7	1.9	826	4	US-09-270-767-2213	Sequence 2213, Ap
C 415	7	1.9	601	4	US-09-949-016-186442	Sequence 186442,	C 488	7	1.9	831	4	US-09-107-532A-1114	Sequence 1114, Ap
C 416	7	1.9	601	4	US-09-949-016-186443	Sequence 186443,	C 489	7	1.9	831	4	US-09-107-532A-1114	Sequence 1114, Ap
C 417	7	1.9	601	4	US-09-949-016-186854	Sequence 186854,	C 490	7	1.9	842	3	US-09-902-540-4228	Sequence 4228, Ap
C 418	7	1.9	601	4	US-09-949-016-187337	Sequence 187337,	C 491	7	1.9	857	4	US-09-154-750A-72	Sequence 72, Appl
C 419	7	1.9	601	4	US-09-949-016-187338	Sequence 187338,	C 492	7	1.9	864	4	US-09-500-035A-9	Sequence 9, Appl
C 420	7	1.9	601	4	US-09-949-016-187339	Sequence 187339,	C 493	7	1.9	864	4	US-09-489-039A-3716	Sequence 3716, Ap
C 421	7	1.9	601	4	US-09-949-016-187340	Sequence 187340,	C 494	7	1.9	885	4	US-09-270-767-12924	Sequence 12924, A
C 422	7	1.9	601	4	US-09-949-016-187729	Sequence 187729,	C 495	7	1.9	908	3	US-09-714-948-2	Sequence 2, Appl
C 423	7	1.9	601	4	US-09-949-016-187770	Sequence 187770,	C 496	7	1.9	908	3	US-09-457-046B-7	Sequence 7, Appl
C 424	7	1.9	601	4	US-09-949-016-189658	Sequence 189658,	C 497	7	1.9	908	3	US-09-457-046B-23	Sequence 23, Appl
C 425	7	1.9	601	4	US-09-949-016-190362	Sequence 190362,	C 498	7	1.9	908	4	US-09-866-570B-7	Sequence 7, Appl
C 426	7	1.9	601	4	US-09-949-016-191511	Sequence 191511,	C 499	7	1.9	915	4	US-09-866-570B-23	Sequence 23, Appl
C 427	7	1.9	601	4	US-09-949-016-191689	Sequence 191689,	C 500	7	1.9	920	3	US-09-107-532A-354	Sequence 354, App
C 428	7	1.9	601	4	US-09-949-016-191867	Sequence 191867,	C 501	7	1.9	920	4	US-09-457-046B-1	Sequence 1, Appl
C 429	7	1.9	601	4	US-09-949-016-192045	Sequence 192045,	C 502	7	1.9	920	4	US-09-866-570B-1	Sequence 1, Appl
C 430	7	1.9	601	4	US-09-949-016-192297	Sequence 192297,	C 503	7	1.9	960	2	US-08-683-908-2	Sequence 2, Appl
C 431	7	1.9	601	4	US-09-949-016-192549	Sequence 192549,	C 504	7	1.9	960	4	US-10-000-489-45	Sequence 45, Appl
C 432	7	1.9	601	4	US-09-949-016-194183	Sequence 194183,	C 505	7	1.9	969	4	US-09-328-352-1363	Sequence 1363, Ap
C 433	7	1.9	601	4	US-09-949-016-195681	Sequence 195681,	C 506	7	1.9	969	4	US-09-543-681A-2774	Sequence 2774, Ap
C 434	7	1.9	601	4	US-09-949-016-195681	Sequence 195681,	C 507	7	1.9	987	4	US-09-252-991A-15392	Sequence 15392, A
C 435	7	1.9	601	4	US-09-949-016-195967	Sequence 195967,	C 508	7	1.9	989	3	US-09-128-155-1	Sequence 1, Appl
C 436	7	1.9	601	4	US-09-949-016-196975	Sequence 196975,	C 509	7	1.9	989	3	US-09-446-504-41	Sequence 41, Appl
C 437	7	1.9	601	4	US-09-949-016-199578	Sequence 199578,	C 510	7	1.9	989	3	US-09-712-266-41	Sequence 41, Appl
C 438	7	1.9	601	4	US-09-949-016-199579	Sequence 199579,	C 511	7	1.9	990	4	US-09-327-138C-6	Sequence 6, Appl
C 439	7	1.9	601	4	US-09-949-016-199580	Sequence 199580,	C 512	7	1.9	996	4	US-09-328-352-1213	Sequence 1213, Ap
C 440	7	1.9	601	4	US-09-949-016-199581	Sequence 199581,	C 513	7	1.9	999	3	US-08-870-511-7	Sequence 7, Appl
C 441	7	1.9	601	4	US-09-949-016-199582	Sequence 199582,	C 514	7	1.9	1012	4	US-09-270-767-12677	Sequence 12677, A
C 442	7	1.9	601	4	US-09-949-016-199583	Sequence 199583,	C 515	7	1.9	1014	4	US-09-327-138C-9	Sequence 9, Appl
C 443	7	1.9	601	4	US-09-949-016-199687	Sequence 199687,	C 516	7	1.9	1023	4	US-09-506-286B-1	Sequence 1, Appl
C 444	7	1.9	601	4	US-09-949-016-200040	Sequence 200040,	C 517	7	1.9	1023	4	US-09-762-861B-1	Sequence 1, Appl
C 445	7	1.9	601	4	US-09-949-016-200074	Sequence 200074,	C 518	7	1.9	1023	4	US-09-762-861B-4	Sequence 4, Appl
C 446	7	1.9	601	4	US-09-949-016-200182	Sequence 201892,	C 519	7	1.9	1023	4	US-09-1065-133A-1	Sequence 1, Appl
C 447	7	1.9	601	4	US-09-949-016-202141	Sequence 202141,	C 520	7	1.9	1023	4	US-10-065-133A-4	Sequence 4, Appl
C 448	7	1.9	601	4	US-09-949-016-203231	Sequence 203231,	C 521	7	1.9	1023	4	US-10-065-133A-1	Sequence 1, Appl
C 449	7	1.9	601	4	US-09-949-016-203232	Sequence 203232,	C 522	7	1.9	1023	4	US-10-434-811A-1	Sequence 1, Appl
C 450	7	1.9	601	4	US-09-949-016-204463	Sequence 204463,	C 523	7	1.9	1024	4	US-10-434-811A-4	Sequence 4, Appl
					Sequence 204533,							US-09-327-138C-7	Sequence 7, Appl

c 524	7	1.9	1027	5	PCT-US95-12357A-3	Sequence 3, Appli	c 597	7	1.9	1457	4	US-09-949-016-3988	Sequence 3988, Ap
525	7	1.9	1046	4	US-09-949-016-2992	Sequence 2992, Ap	598	7	1.9	1473	4	US-09-248-796A-5807	Sequence 5807, Ap
526	7	1.9	1062	4	US-09-016-434-1286	Sequence 1286, Ap	c 599	7	1.9	1479	4	US-09-902-540-6689	Sequence 6689, Ap
527	7	1.9	1062	4	US-08-134-231C-33	Sequence 33, Appl	600	7	1.9	1504	3	US-09-010-998-3	Sequence 3, Appli
528	7	1.9	1062	4	US-09-023-655-1327	Sequence 1327, Ap	601	7	1.9	1529	3	US-08-477-451-17	Sequence 17, Appl
529	7	1.9	1062	4	US-08-728-160-33	Sequence 33, Appl	c 602	7	1.9	1529	2	US-08-477-451-21	Sequence 21, Appl
530	7	1.9	1065	4	US-09-348-352-3136	Sequence 3136, Ap	c 603	7	1.9	1529	4	US-09-523-263B-7	Sequence 7, Appli
531	7	1.9	1070	4	US-09-976-594-1062	Sequence 1062, Ap	604	7	1.9	1540	4	US-09-560-761B-3	Sequence 3, Appli
532	7	1.9	1076	4	US-09-660-107-10	Sequence 12, Appl	c 605	7	1.9	1554	4	US-09-252-991A-13880	Sequence 2279, A
c 533	7	1.9	1086	4	US-09-479-040-10	Sequence 10, Appl	c 606	7	1.9	1569	4	US-09-252-991A-13880	Sequence 13880, A
c 534	7	1.9	1088	4	US-09-327-138C-12	Sequence 12, Appl	607	7	1.9	1593	4	US-09-023-655-1498	Sequence 1498, Ap
535	7	1.9	1113	4	US-09-252-991A-8037	Sequence 8037, Ap	608	7	1.9	1594	4	US-08-248-628A-1	Sequence 1, Appli
536	7	1.9	1113	4	US-09-620-312D-406	Sequence 406, App	c 609	7	1.9	1596	4	US-09-023-655-1476	Sequence 1476, Ap
c 537	7	1.9	1113	4	US-09-583-110-744	Sequence 744, App	610	7	1.9	1600	1	US-08-073-384C-12	Sequence 12, Appl
c 538	7	1.9	1113	4	US-09-107-433-1099	Sequence 1099, Ap	611	7	1.9	1600	1	US-08-254-359A-12	Sequence 12, Appl
c 539	7	1.9	1125	3	US-09-436-983-2	Sequence 2, Appli	612	7	1.9	1600	1	US-08-483-043-12	Sequence 12, Appl
c 540	7	1.9	1173	4	US-09-252-991A-9438	Sequence 9438, Ap	613	7	1.9	1600	1	US-08-481-238-12	Sequence 12, Appl
c 541	7	1.9	1182	3	US-09-469-242-1	Sequence 1, Appli	614	7	1.9	1600	2	US-08-471-066B-12	Sequence 12, Appl
c 542	7	1.9	1194	4	US-09-506-286B-21	Sequence 21, Appl	615	7	1.9	1600	2	US-08-484-356-12	Sequence 12, Appl
c 543	7	1.9	1194	4	US-09-506-286B-25	Sequence 25, Appl	616	7	1.9	1600	2	US-08-757-653-12	Sequence 12, Appl
c 544	7	1.9	1194	4	US-09-762-861B-21	Sequence 21, Appl	617	7	1.9	1600	2	US-08-599-491-12	Sequence 12, Appl
c 545	7	1.9	1194	4	US-09-762-861B-25	Sequence 25, Appl	618	7	1.9	1600	2	US-08-756-386-12	Sequence 12, Appl
c 546	7	1.9	1194	4	US-10-065-133A-21	Sequence 21, Appl	619	7	1.9	1600	2	US-08-823-516-12	Sequence 12, Appl
c 547	7	1.9	1194	4	US-10-065-133A-25	Sequence 25, Appl	620	7	1.9	1600	3	US-08-682-853A-12	Sequence 12, Appl
c 548	7	1.9	1194	4	US-10-434-811A-21	Sequence 21, Appl	621	7	1.9	1600	3	US-08-759-038-12	Sequence 12, Appl
c 549	7	1.9	1203	4	US-10-434-811A-25	Sequence 25, Appl	622	7	1.9	1600	3	US-08-758-314-12	Sequence 12, Appl
550	7	1.9	1209	4	US-09-252-991A-9395	Sequence 9395, Ap	623	7	1.9	1600	3	US-09-350-309-12	Sequence 12, Appl
551	7	1.9	1225	4	US-09-489-039A-6373	Sequence 6373, Ap	624	7	1.9	1600	3	US-08-520-946-12	Sequence 12, Appl
552	7	1.9	1225	4	US-09-398-412B-1	Sequence 1, Appli	625	7	1.9	1600	4	US-09-684-938-12	Sequence 12, Appl
553	7	1.9	1226	4	US-09-976-594-1110	Sequence 1110, Ap	626	7	1.9	1600	4	US-09-308-825A-12	Sequence 12, Appl
c 554	7	1.9	1232	4	US-09-506-286B-22	Sequence 22, Appl	627	7	1.9	1600	4	US-09-655-378A-12	Sequence 12, Appl
c 555	7	1.9	1232	4	US-09-506-286B-23	Sequence 23, Appl	628	7	1.9	1600	4	US-09-940-244-12	Sequence 12, Appl
c 556	7	1.9	1232	4	US-09-762-861B-22	Sequence 22, Appl	629	7	1.9	1600	4	US-09-333-145-12	Sequence 12, Appl
c 557	7	1.9	1232	4	US-09-762-861B-19	Sequence 23, Appl	630	7	1.9	1614	4	US-09-252-991A-9387	Sequence 9387, Ap
c 558	7	1.9	1232	4	US-10-065-133A-22	Sequence 22, Appl	c 631	7	1.9	1618	2	US-08-533-669A-9	Sequence 9, Appli
c 559	7	1.9	1232	4	US-10-065-133A-23	Sequence 23, Appl	c 632	7	1.9	1618	2	US-08-607-509-1	Sequence 1, Appli
c 560	7	1.9	1232	4	US-10-434-811A-22	Sequence 22, Appl	c 633	7	1.9	1618	2	US-08-454-036-1	Sequence 1, Appli
c 561	7	1.9	1233	4	US-10-434-811A-23	Sequence 23, Appl	c 634	7	1.9	1618	2	US-08-634-642-1	Sequence 1, Appli
c 562	7	1.9	1233	4	US-09-506-286B-19	Sequence 19, Appl	c 635	7	1.9	1618	3	US-08-989-370-1	Sequence 1, Appli
c 563	7	1.9	1233	4	US-09-762-861B-19	Sequence 19, Appl	c 636	7	1.9	1618	3	US-09-183-861-9	Sequence 9, Appli
c 564	7	1.9	1233	4	US-10-065-133A-19	Sequence 19, Appl	c 637	7	1.9	1618	3	US-09-022-765-9	Sequence 9, Appli
c 565	7	1.9	1233	4	US-10-434-811A-19	Sequence 19, Appl	c 638	7	1.9	1618	4	US-09-551-974A-9	Sequence 9, Appli
c 566	7	1.9	1242	4	US-09-252-991A-12428	Sequence 12428, A	c 639	7	1.9	1618	4	US-09-565-501A-9	Sequence 9, Appli
c 567	7	1.9	1251	4	US-09-205-258-156	Sequence 156, App	c 640	7	1.9	1618	4	US-09-639-206A-9	Sequence 9, Appli
c 568	7	1.9	1251	4	US-09-248-796A-2693	Sequence 2693, Ap	c 641	7	1.9	1618	4	US-09-874-923-9	Sequence 9, Appli
c 569	7	1.9	1253	2	US-08-786-606-6	Sequence 6, Appli	c 642	7	1.9	1618	4	US-09-398-169-1	Sequence 1, Appli
c 570	7	1.9	1253	4	US-09-016-434-5	Sequence 5, Appli	c 643	7	1.9	1618	4	US-08-798-841-9	Sequence 9, Appli
c 571	7	1.9	1254	4	US-09-489-039A-4384	Sequence 4384, Ap	c 644	7	1.9	1618	5	PCT-US95-05064-1	Sequence 1, Appli
c 572	7	1.9	1260	1	US-08-029-404-1	Sequence 1, Appli	c 645	7	1.9	1629	4	US-09-799-451-699	Sequence 699, App
c 573	7	1.9	1260	3	US-08-459-953A-1	Sequence 1, Appli	646	7	1.9	1638	3	US-09-351-224E-2	Sequence 2, Appli
c 574	7	1.9	1260	4	US-09-393-212-1	Sequence 1, Appli	647	7	1.9	1638	4	US-09-677-488A-2	Sequence 2, Appli
c 575	7	1.9	1272	4	US-09-248-796A-1740	Sequence 1740, Ap	648	7	1.9	1638	4	US-09-677-682B-2	Sequence 2, Appli
c 576	7	1.9	1317	3	US-09-457-046B-27	Sequence 27, Appl	649	7	1.9	1638	4	US-09-883-694B-2	Sequence 2, Appli
c 577	7	1.9	1317	4	US-09-023-655-051	Sequence 851, App	650	7	1.9	1660	4	US-09-142-108C-16	Sequence 16, Appl
578	7	1.9	1317	4	US-09-866-570B-27	Sequence 27, Appl	651	7	1.9	1662	1	US-08-565-386-2	Sequence 2, Appli
579	7	1.9	1329	4	US-09-252-991A-12162	Sequence 12162, A	652	7	1.9	1683	4	US-09-912-559-2	Sequence 1, Appli
580	7	1.9	1347	3	US-09-457-046B-55	Sequence 55, Appl	653	7	1.9	1683	4	US-09-912-559-2	Sequence 2, Appli
581	7	1.9	1347	4	US-09-866-570B-55	Sequence 55, Appl	654	7	1.9	1691	3	US-09-351-324E-1	Sequence 1, Appli
582	7	1.9	1367	4	US-09-023-655-971	Sequence 971, App	655	7	1.9	1691	4	US-09-677-488A-1	Sequence 1, Appli
c 583	7	1.9	1368	4	US-09-902-540-4506	Sequence 4506, App	656	7	1.9	1691	4	US-09-677-682B-1	Sequence 1, Appli
584	7	1.9	1381	3	US-08-936-165A-225	Sequence 225, App	c 557	7	1.9	1691	4	US-09-882-694B-1	Sequence 1, Appli
585	7	1.9	1390	2	US-08-683-908-3	Sequence 3, Appli	c 558	7	1.9	1703	3	US-09-135-021-77	Sequence 77, Appli
586	7	1.9	1406	3	US-09-287-097-1	Sequence 1, Appli	c 559	7	1.9	1703	3	US-09-135-020-3	Sequence 3, Appli
c 587	7	1.9	1419	4	US-09-252-991A-15908	Sequence 15908, A	c 660	7	1.9	1703	3	US-09-135-010A-3	Sequence 3, Appli
c 588	7	1.9	1425	4	US-09-252-991A-15878	Sequence 15878, A	c 661	7	1.9	1703	3	US-09-444-871-3	Sequence 3, Appli
c 589	7	1.9	1425	4	US-09-543-681A-2701	Sequence 2701, Ap	c 662	7	1.9	1703	3	US-09-597-735-3	Sequence 3, Appli
c 590	7	1.9	1428	4	US-09-489-039A-3243	Sequence 3243, Ap	c 663	7	1.9	1703	3	US-09-444-295-3	Sequence 3, Appli
c 591	7	1.9	1433	1	US-07-968-971A-11	Sequence 11, Appl	c 664	7	1.9	1703	3	US-09-597-732-3	Sequence 3, Appli
c 592	7	1.9	1433	1	US-08-383-756-5	Sequence 5, Appli	c 665	7	1.9	1703	4	US-09-597-731-3	Sequence 3, Appli
c 593	7	1.9	1433	1	US-08-424-406-2	Sequence 2, Appli	666	7	1.9	1704	4	US-09-023-655-263	Sequence 263, App
c 594	7	1.9	1433	1	US-08-464-523B-8	Sequence 8, Appli	667	7	1.9	1715	3	US-09-023-655-230A-1	Sequence 1, Appli
c 595	7	1.9	1433	2	US-08-460-898-5	Sequence 5, Appli	668	7	1.9	1715	4	US-08-757-230A-1	Sequence 1, Appli
c 596	7	1.9	1439	4	US-09-640-211A-332	Sequence 332, App	669	7	1.9	1715	5	PCT-US95-02315-1	Sequence 1, Appli

670	7	1.9	1737	4	US-09-142-108C-3	Sequence 3, Appli	743	7	1.9	2502	4	US-09-684-938-21	Sequence 21, Appli
c 671	7	1.9	1774	3	US-09-215-252-16	Sequence 16, Appli	744	7	1.9	2502	4	US-09-308-825A-21	Sequence 21, Appli
c 672	7	1.9	1774	4	US-09-970-989A-16	Sequence 16, Appli	745	7	1.9	2502	4	US-09-758-282B-39	Sequence 39, Appli
c 673	7	1.9	1798	3	US-09-797-906-1	Sequence 1, Appli	746	7	1.9	2502	4	US-09-655-378A-21	Sequence 21, Appli
c 674	7	1.9	1803	4	US-09-327-138C-5	Sequence 5, Appli	747	7	1.9	2502	4	US-09-940-244-21	Sequence 21, Appli
c 675	7	1.9	1815	4	US-09-328-352-341	Sequence 341, App	748	7	1.9	2502	4	US-09-333-145-21	Sequence 39, Appli
c 676	7	1.9	1831	4	US-09-799-451-646	Sequence 646, App	749	7	1.9	2502	4	US-09-577-304A-39	Sequence 1, Appli
c 677	7	1.9	1839	4	US-09-774-528-214	Sequence 214, App	750	7	1.9	2508	2	US-08-850-993-1	Sequence 9, Appli
c 678	7	1.9	1855	4	US-09-023-655-856	Sequence 856, App	751	7	1.9	2520	1	US-08-405-254-9	Sequence 917, App
c 679	7	1.9	1866	4	US-09-252-991A-2554	Sequence 2554, App	c 752	7	1.9	2520	4	US-09-023-655-917	Sequence 917, App
c 680	7	1.9	1866	4	US-09-902-540-2398	Sequence 2398, App	753	7	1.9	2540	4	US-09-799-451-463	Sequence 463, App
c 681	7	1.9	1881	4	US-09-248-796A-752	Sequence 752, App	754	7	1.9	2574	4	US-09-902-540-1961	Sequence 1961, App
c 682	7	1.9	1926	4	US-09-328-352-2865	Sequence 2865, App	755	7	1.9	2588	3	US-09-087-465-7	Sequence 7, Appli
c 683	7	1.9	1930	5	PCT-US95-07874-1	Sequence 1, Appli	756	7	1.9	2588	4	US-09-016-434-1145	Sequence 1145, App
c 684	7	1.9	1930	5	PCT-US95-07874-1	Sequence 1, Appli	757	7	1.9	2588	4	US-09-972-800A-7	Sequence 7, Appli
c 685	7	1.9	1950	4	US-09-640-419C-1	Sequence 1, Appli	c 758	7	1.9	2588	4	US-09-023-655-958	Sequence 958, App
c 686	7	1.9	1974	4	US-09-540-236-1239	Sequence 1239, App	759	7	1.9	2606	1	US-08-408-318-1	Sequence 1, Appli
c 687	7	1.9	1991	4	US-09-270-767-14329	Sequence 14329, App	c 760	7	1.9	2606	1	US-08-839-164-1	Sequence 1, Appli
c 688	7	1.9	2017	3	US-09-436-983-1	Sequence 1, Appli	c 761	7	1.9	2628	4	US-09-919-831-1	Sequence 1, Appli
c 689	7	1.9	2028	4	US-10-162-012-28	Sequence 28, Appli	762	7	1.9	2658	3	US-08-727-308-2	Sequence 2, Appli
c 690	7	1.9	2099	4	US-09-800-729-56	Sequence 56, Appli	763	7	1.9	2658	3	US-08-727-308-3	Sequence 3, Appli
c 691	7	1.9	2108	4	US-09-800-729-20	Sequence 20, Appli	764	7	1.9	2730	4	US-09-789-599A-1	Sequence 1, Appli
c 692	7	1.9	2116	3	US-09-000-041A-1	Sequence 1, Appli	c 765	7	1.9	2787	4	US-09-252-991A-9331	Sequence 9331, App
c 693	7	1.9	2116	4	US-09-734-002-1	Sequence 1, Appli	766	7	1.9	2790	4	US-09-252-991A-2632	Sequence 2632, App
c 694	7	1.9	2145	3	US-09-059-584-48	Sequence 48, Appli	c 767	7	1.9	2791	4	US-09-327-138C-4	Sequence 4, Appli
c 695	7	1.9	2147	4	US-09-949-016-3887	Sequence 3887, App	768	7	1.9	2899	4	US-09-270-767-13753	Sequence 13753, A
c 696	7	1.9	2195	1	US-08-915-003-1	Sequence 1, Appli	769	7	1.9	2907	4	US-09-417-197-48	Sequence 48, Appli
c 697	7	1.9	2195	2	US-08-642-247-1	Sequence 1, Appli	770	7	1.9	2913	4	US-09-417-197-66	Sequence 66, Appli
c 698	7	1.9	2196	4	US-09-540-236-124	Sequence 124, App	c 771	7	1.9	2917	2	US-08-624-581-3	Sequence 3, Appli
c 699	7	1.9	2220	4	US-09-489-039A-4703	Sequence 4703, App	c 772	7	1.9	2923	1	US-08-480-449-1	Sequence 1, Appli
c 700	7	1.9	2220	6	5171850-1	Sequence 1, Appli	c 773	7	1.9	2923	2	US-08-660-542-1	Sequence 1, Appli
c 701	7	1.9	2220	6	5171850-1	Patent No. 5171850	c 774	7	1.9	2923	3	US-08-479-603-1	Sequence 1, Appli
c 702	7	1.9	2259	4	US-09-252-991A-13556	Sequence 13556, A	c 775	7	1.9	2923	4	US-08-939-107-1	Sequence 1, Appli
c 703	7	1.9	2277	4	US-09-506-286B-46	Sequence 46, Appli	c 776	7	1.9	2923	4	US-08-931-764-1	Sequence 1, Appli
c 704	7	1.9	2277	4	US-09-506-286B-49	Sequence 49, Appli	c 777	7	1.9	2923	4	US-09-591-992-1	Sequence 1, Appli
c 705	7	1.9	2277	4	US-10-065-133A-46	Sequence 46, Appli	c 778	7	1.9	2923	4	US-09-067-447B-1	Sequence 1, Appli
c 706	7	1.9	2277	4	US-10-065-133A-49	Sequence 49, Appli	c 779	7	1.9	2923	4	US-08-479-620-1	Sequence 1, Appli
c 707	7	1.9	2281	4	US-09-023-655-26	Sequence 26, Appli	c 780	7	1.9	2927	3	US-09-232-878-5	Sequence 5, Appli
c 708	7	1.9	2283	4	US-09-107-532A-1836	Sequence 1836, App	781	7	1.9	2931	3	US-09-151-189-1	Sequence 1, Appli
c 709	7	1.9	2287	3	US-09-059-584-47	Sequence 47, Appli	782	7	1.9	2931	4	US-09-596-794-1	Sequence 1, Appli
c 710	7	1.9	2326	4	US-10-162-012-26	Sequence 26, Appli	783	7	1.9	2931	4	US-09-840-762A-1	Sequence 1, Appli
c 711	7	1.9	2329	1	US-08-455-559-9	Sequence 9, Appli	c 784	7	1.9	2967	4	US-09-902-540-7756	Sequence 7756, App
c 712	7	1.9	2329	3	US-09-145-060-9	Sequence 9, Appli	785	7	1.9	3008	4	US-09-949-016-587	Sequence 587, App
c 713	7	1.9	2329	5	PCT-US94-00657-9	Sequence 9, Appli	786	7	1.9	3013	4	US-09-949-016-4921	Sequence 4921, App
c 714	7	1.9	2341	4	US-09-506-286B-44	Sequence 44, Appli	c 787	7	1.9	3064	4	US-09-620-312D-378	Sequence 378, App
c 715	7	1.9	2341	4	US-09-506-286B-47	Sequence 47, Appli	c 788	7	1.9	3150	4	US-09-489-039A-5843	Sequence 5843, App
c 716	7	1.9	2341	4	US-10-065-133A-44	Sequence 44, Appli	c 789	7	1.9	3236	3	US-08-961-527-222	Sequence 222, App
c 717	7	1.9	2341	4	US-10-065-133A-47	Sequence 47, Appli	c 790	7	1.9	3301	2	US-08-447-430A-42	Sequence 42, Appli
c 718	7	1.9	2372	4	US-09-774-528-362	Sequence 362, App	c 791	7	1.9	3301	4	US-09-342-673-42	Sequence 42, Appli
c 719	7	1.9	2379	4	US-09-134-000C-2490	Sequence 2490, App	c 792	7	1.9	3340	4	US-09-714-948-1	Sequence 1, Appli
c 720	7	1.9	2394	4	US-09-799-451-931	Sequence 931, App	c 793	7	1.9	3372	1	US-07-906-349A-1	Sequence 1, Appli
c 721	7	1.9	2403	4	US-09-949-016-4376	Sequence 4376, App	c 794	7	1.9	3372	1	US-08-167-035-1	Sequence 1, Appli
c 722	7	1.9	2403	4	US-09-949-016-4377	Sequence 4377, App	c 795	7	1.9	3372	1	US-08-167-035-48	Sequence 48, Appli
c 723	7	1.9	2415	4	US-10-029-180-1377	Sequence 137, App	796	7	1.9	3372	1	US-08-208-887A-1	Sequence 1, Appli
c 724	7	1.9	2475	4	US-09-799-451-932	Sequence 932, App	797	7	1.9	3372	2	US-08-539-005-1	Sequence 1, Appli
c 725	7	1.9	2484	3	US-08-961-527-234	Sequence 234, App	c 798	7	1.9	3372	2	US-08-539-005-48	Sequence 48, Appli
c 726	7	1.9	2492	4	US-09-902-540-421	Sequence 421, App	799	7	1.9	3372	3	US-09-344-521-1	Sequence 1, Appli
c 727	7	1.9	2495	4	US-09-949-016-5571	Sequence 5571, App	800	7	1.9	3372	3	US-09-280-598-1	Sequence 1, Appli
c 728	7	1.9	2502	1	US-08-073-384C-21	Sequence 21, Appli	801	7	1.9	3372	4	US-09-963-137-180	Sequence 180, App
c 729	7	1.9	2502	1	US-08-254-359A-21	Sequence 21, Appli	c 802	7	1.9	3423	2	US-08-447-430A-40	Sequence 40, Appli
c 730	7	1.9	2502	1	US-08-483-043-21	Sequence 21, Appli	c 803	7	1.9	3423	3	US-09-485-737B-86	Sequence 86, Appli
c 731	7	1.9	2502	1	US-08-481-238-21	Sequence 21, Appli	c 804	7	1.9	3423	4	US-09-342-673-40	Sequence 40, Appli
c 732	7	1.9	2502	2	US-08-471-066B-21	Sequence 21, Appli	c 805	7	1.9	3423	4	US-10-071-485-86	Sequence 86, Appli
c 733	7	1.9	2502	2	US-08-484-956-21	Sequence 21, Appli	c 806	7	1.9	3474	2	US-08-447-430A-41	Sequence 41, Appli
c 734	7	1.9	2502	2	US-08-757-653-21	Sequence 21, Appli	c 807	7	1.9	3474	2	US-08-318-837-10	Sequence 10, Appli
c 735	7	1.9	2502	2	US-08-599-431-21	Sequence 21, Appli	c 808	7	1.9	3474	3	US-08-122-458D-8	Sequence 8, Appli
c 736	7	1.9	2502	2	US-08-756-386-21	Sequence 21, Appli	c 809	7	1.9	3474	4	US-09-342-673-41	Sequence 41, Appli
c 737	7	1.9	2502	2	US-08-823-516-21	Sequence 21, Appli	c 810	7	1.9	3519	2	US-08-380-403A-1	Sequence 1, Appli
c 738	7	1.9	2502	3	US-08-682-853A-21	Sequence 21, Appli	c 811	7	1.9	3519	3	US-08-895-628-1	Sequence 1, Appli
c 739	7	1.9	2502	3	US-08-759-038-21	Sequence 21, Appli	c 812	7	1.9	3519	3	US-08-895-628-1	Sequence 1, Appli
c 740	7	1.9	2502	3	US-08-758-314-21	Sequence 21, Appli	c 813	7	1.9	3538	4	US-09-902-540-528	Sequence 528, App
c 741	7	1.9	2502	3	US-09-350-309-21	Sequence 21, Appli	c 814	7	1.9	3545	3	US-09-221-017B-468	Sequence 468, App
c 742	7	1.9	2502	3	US-08-520-946-21	Sequence 21, Appli	c 815	7	1.9	3545	2	US-08-553-436A-5	Sequence 5, Appli

C 816	7	1.9	3646	4	US-09-327-138C-36	Sequence 36, Appl	889	7	1.9	4986	3	US-09-338-907-121	Sequence 121, App
C 817	7	1.9	3651	4	US-09-134-000C-1725	Sequence 1725, Ap	890	7	1.9	4986	3	US-09-218-207-121	Sequence 121, App
C 818	7	1.9	3651	4	US-09-583-110-1163	Sequence 1163, Ap	891	7	1.9	4990	3	US-08-776-511-1	Sequence 1, Appl
C 819	7	1.9	3665	4	US-09-327-138C-35	Sequence 35, Appl	C 892	7	1.9	5005	4	US-09-695-437A-60	Sequence 60, Appl
C 820	7	1.9	3675	4	US-09-107-433-1744	Sequence 1744, Ap	893	7	1.9	5009	4	US-09-221-013A-4	Sequence 4, Appl
C 821	7	1.9	3686	4	US-09-327-138C-3	Sequence 3, Appl	894	7	1.9	5020	3	US-09-338-907-120	Sequence 120, App
C 822	7	1.9	3686	4	US-09-327-138C-37	Sequence 37, Appl	895	7	1.9	5020	3	US-09-218-207-120	Sequence 120, App
C 823	7	1.9	3801	4	US-09-640-882-1	Sequence 1, Appl	896	7	1.9	5044	3	US-09-338-907-115	Sequence 115, App
C 824	7	1.9	3937	4	US-09-620-312D-280	Sequence 280, App	897	7	1.9	5044	3	US-09-218-207-115	Sequence 115, App
C 825	7	1.9	3940	4	US-09-327-138C-1	Sequence 1, Appl	898	7	1.9	5057	3	US-09-338-907-123	Sequence 123, App
C 826	7	1.9	3966	3	US-09-215-131-1	Sequence 1, Appl	899	7	1.9	5057	3	US-09-218-207-123	Sequence 123, App
C 827	7	1.9	3966	3	US-09-222-734-1	Sequence 1, Appl	900	7	1.9	5076	4	US-09-991-258-8	Sequence 8, Appl
C 828	7	1.9	4009	2	US-08-500-860A-2	Sequence 2, Appl	C 901	7	1.9	5098	1	US-08-450-257-10	Sequence 10, Appl
C 829	7	1.9	4023	4	US-08-809-513A-8	Sequence 8, Appl	C 902	7	1.9	5098	1	US-08-450-246-10	Sequence 10, Appl
C 830	7	1.9	4108	3	US-08-981-729-8	Sequence 8, Appl	C 903	7	1.9	5098	1	US-08-450-098-10	Sequence 10, Appl
C 831	7	1.9	4108	3	US-08-981-446B-1	Sequence 1, Appl	C 904	7	1.9	5098	1	US-08-451-233-10	Sequence 10, Appl
C 832	7	1.9	4108	3	US-09-613-811-8	Sequence 8, Appl	C 905	7	1.9	5098	1	US-08-450-236-10	Sequence 10, Appl
C 833	7	1.9	4196	4	US-09-453-313-1	Sequence 1, Appl	C 906	7	1.9	5098	3	US-08-235-403-10	Sequence 10, Appl
C 834	7	1.9	4198	4	US-09-949-016-934	Sequence 934, App	907	7	1.9	5100	3	US-09-338-907-122	Sequence 122, App
C 835	7	1.9	4199	3	US-09-204-117B-1	Sequence 1, Appl	908	7	1.9	5100	3	US-09-218-207-122	Sequence 122, App
C 836	7	1.9	4245	2	US-08-929-967-4	Sequence 4, Appl	909	7	1.9	5115	3	US-08-825-852-19	Sequence 19, Appl
C 837	7	1.9	4309	5	PCT-US91-02954-11	Sequence 11, Appl	910	7	1.9	5115	3	US-09-052-888-19	Sequence 19, Appl
C 838	7	1.9	4342	3	US-09-338-907-107	Sequence 107, App	911	7	1.9	5115	4	US-09-723-890-19	Sequence 19, Appl
C 839	7	1.9	4342	3	US-09-218-207-107	Sequence 107, App	912	7	1.9	5115	4	US-09-723-901-19	Sequence 19, Appl
C 840	7	1.9	4352	4	US-09-601-326-77	Sequence 77, Appl	913	7	1.9	5115	4	US-09-723-547-19	Sequence 19, Appl
C 841	7	1.9	4451	3	US-09-303-064-45	Sequence 45, Appl	914	7	1.9	5115	4	US-09-724-127-19	Sequence 19, Appl
C 842	7	1.9	4451	3	US-09-086-503-45	Sequence 45, Appl	915	7	1.9	5115	4	US-09-723-931-19	Sequence 19, Appl
C 843	7	1.9	4481	3	US-08-867-611-1	Sequence 1, Appl	916	7	1.9	5115	4	US-09-723-873-19	Sequence 19, Appl
C 844	7	1.9	4481	3	US-09-690-359-1	Sequence 1, Appl	917	7	1.9	5115	4	US-09-724-114-19	Sequence 19, Appl
C 845	7	1.9	4481	5	PCT-US92-06965A-6	Sequence 6, Appl	918	7	1.9	5115	4	US-09-723-913-19	Sequence 19, Appl
C 846	7	1.9	4529	1	US-08-565-386-1	Sequence 1, Appl	919	7	1.9	5115	4	US-09-723-912-19	Sequence 19, Appl
C 847	7	1.9	4582	3	US-09-338-907-118	Sequence 118, App	920	7	1.9	5115	4	US-09-724-095-19	Sequence 19, Appl
C 848	7	1.9	4582	3	US-09-218-207-118	Sequence 118, App	921	7	1.9	5115	4	US-09-724-157-19	Sequence 19, Appl
C 849	7	1.9	4593	3	US-08-801-344-1	Sequence 1, Appl	922	7	1.9	5115	4	US-09-724-062-19	Sequence 19, Appl
C 850	7	1.9	4593	3	US-09-498-599-1	Sequence 1, Appl	923	7	1.9	5115	4	US-09-724-065-19	Sequence 19, Appl
C 851	7	1.9	4612	4	US-09-626-301-1	Sequence 1, Appl	924	7	1.9	5148	3	US-09-338-907-112	Sequence 112, App
C 852	7	1.9	4642	4	US-09-626-301-3	Sequence 3, Appl	925	7	1.9	5148	3	US-09-218-207-112	Sequence 112, App
C 853	7	1.9	4686	3	US-09-338-907-117	Sequence 117, App	926	7	1.9	5197	3	US-09-293-170-6	Sequence 6, Appl
C 854	7	1.9	4686	3	US-09-218-207-117	Sequence 117, App	C 927	7	1.9	5201	4	US-09-640-882-2	Sequence 2, Appl
C 855	7	1.9	4775	3	US-09-303-064-37	Sequence 37, Appl	C 928	7	1.9	5201	4	US-09-640-882-3	Sequence 3, Appl
C 856	7	1.9	4775	3	US-09-086-503-37	Sequence 37, Appl	929	7	1.9	5227	2	US-08-996-306-3	Sequence 3, Appl
C 857	7	1.9	4819	1	US-08-450-257-20	Sequence 20, Appl	930	7	1.9	5234	3	US-09-338-907-113	Sequence 113, App
C 858	7	1.9	4819	1	US-08-450-246-20	Sequence 20, Appl	931	7	1.9	5234	3	US-09-218-207-113	Sequence 113, App
C 859	7	1.9	4819	1	US-08-450-098-20	Sequence 20, Appl	C 932	7	1.9	5238	6	5453363-1	Patent No. 5453363
C 860	7	1.9	4819	1	US-08-451-233-20	Sequence 20, Appl	C 933	7	1.9	5238	6	5453363-1	Patent No. 5453363
C 861	7	1.9	4819	1	US-08-450-236-20	Sequence 20, Appl	C 934	7	1.9	5241	4	US-08-809-513A-1	Sequence 1, Appl
C 862	7	1.9	4819	3	US-08-235-403-20	Sequence 20, Appl	C 935	7	1.9	5241	4	US-08-809-513A-2	Sequence 2, Appl
C 863	7	1.9	4875	3	US-09-338-907-114	Sequence 114, App	C 936	7	1.9	5245	3	US-09-338-907-3	Sequence 3, Appl
C 864	7	1.9	4875	3	US-09-218-207-114	Sequence 114, App	937	7	1.9	5245	3	US-09-218-207-3	Sequence 3, Appl
C 865	7	1.9	4910	1	US-08-450-257-11	Sequence 11, Appl	C 938	7	1.9	5245	4	US-09-949-016-4210	Sequence 4210, Ap
C 866	7	1.9	4910	1	US-08-450-246-11	Sequence 11, Appl	939	7	1.9	5249	1	US-08-688-649-3	Sequence 3, Appl
C 867	7	1.9	4910	1	US-08-450-098-11	Sequence 11, Appl	C 940	7	1.9	5249	1	US-08-688-649-3	Sequence 3, Appl
C 868	7	1.9	4910	1	US-08-451-233-11	Sequence 11, Appl	941	7	1.9	5249	1	US-08-688-649-4	Sequence 4, Appl
C 869	7	1.9	4910	1	US-08-450-236-11	Sequence 11, Appl	942	7	1.9	5250	3	US-09-338-907-69	Sequence 69, Appl
C 870	7	1.9	4910	3	US-09-303-064-40	Sequence 40, Appl	943	7	1.9	5250	3	US-09-218-207-69	Sequence 69, Appl
C 871	7	1.9	4910	3	US-08-235-403-11	Sequence 11, Appl	C 944	7	1.9	5252	4	US-09-949-016-338	Sequence 338, App
C 872	7	1.9	4936	4	US-09-086-503-40	Sequence 40, Appl	945	7	1.9	5252	4	US-09-303-064-48	Sequence 48, Appl
C 873	7	1.9	4954	4	US-09-573-080A-329	Sequence 329, App	946	7	1.9	5258	3	US-09-086-503-48	Sequence 48, Appl
C 874	7	1.9	4954	4	US-09-949-016-4527	Sequence 4527, Ap	947	7	1.9	5290	3	US-09-338-907-119	Sequence 119, App
C 875	7	1.9	4958	3	US-09-338-907-116	Sequence 116, App	948	7	1.9	5290	3	US-09-218-207-119	Sequence 119, App
C 876	7	1.9	4958	3	US-09-218-207-116	Sequence 116, App	949	7	1.9	5326	3	US-09-338-907-124	Sequence 124, App
C 877	7	1.9	4977	1	US-08-450-257-14	Sequence 14, Appl	C 950	7	1.9	5326	3	US-09-218-207-124	Sequence 124, App
C 878	7	1.9	4977	1	US-08-450-257-17	Sequence 17, Appl	C 951	7	1.9	5418	3	US-09-949-016-14328	Sequence 14328, A
C 879	7	1.9	4977	1	US-08-450-246-14	Sequence 14, Appl	952	7	1.9	5438	3	US-08-809-326A-25	Sequence 25, Appl
C 880	7	1.9	4977	1	US-08-450-246-17	Sequence 17, Appl	953	7	1.9	5438	4	US-09-689-914A-25	Sequence 25, Appl
C 881	7	1.9	4977	1	US-08-450-098-14	Sequence 14, Appl	954	7	1.9	5438	4	US-09-689-913A-25	Sequence 25, Appl
C 882	7	1.9	4977	1	US-08-450-098-17	Sequence 17, Appl	955	7	1.9	5438	4	US-09-689-916A-25	Sequence 25, Appl
C 883	7	1.9	4977	1	US-08-451-233-14	Sequence 14, Appl	C 956	7	1.9	5446	4	US-09-338-907-124	Sequence 124, App
C 884	7	1.9	4977	1	US-08-451-233-17	Sequence 17, Appl	C 957	7	1.9	5552	3	US-08-155-888-1	Sequence 1, Appl
C 885	7	1.9	4977	1	US-08-450-236-14	Sequence 14, Appl	C 958	7	1.9	5574	1	US-08-450-257-22	Sequence 22, Appl
C 886	7	1.9	4977	1	US-08-450-236-17	Sequence 17, Appl	C 959	7	1.9	5574	1	US-08-450-246-22	Sequence 22, Appl
C 887	7	1.9	4977	3	US-08-235-403-14	Sequence 14, Appl	C 960	7	1.9	5574	1	US-08-450-098-22	Sequence 22, Appl
C 888	7	1.9	4977	3	US-08-235-403-17	Sequence 17, Appl	C 961	7	1.9	5574	1	US-08-451-233-22	Sequence 22, Appl

c 962 7 1.9 5574 1 US-08-450-236-22
c 963 7 1.9 5574 3 US-08-235-403-22
964 7 1.9 5574 3 US-08-867-611-3
965 7 1.9 5600 4 US-09-690-359-3
966 7 1.9 5600 5 PCT-US92-06965A-8
967 7 1.9 5658 3 US-08-809-326A-10
968 7 1.9 5658 4 US-09-689-913A-10
969 7 1.9 5658 4 US-09-689-913A-10
970 7 1.9 5674 3 US-09-293-170-3
971 7 1.9 5674 3 US-09-293-170-3
972 7 1.9 5688 3 US-09-293-170-7
973 7 1.9 5727 5 PCT-US91-02954-13
974 7 1.9 5734 3 US-09-293-170-5
c 975 7 1.9 5836 3 US-09-453-702B-253
976 7 1.9 5838 2 US-08-850-880-3
977 7 1.9 5838 2 US-08-944-916-3
978 7 1.9 5838 2 US-08-814-877-3
979 7 1.9 5838 3 US-09-272-432A-3
980 7 1.9 5856 3 US-09-293-170-1
981 7 1.9 5857 3 US-09-293-170-4
982 7 1.9 6151 5 PCT-US91-02954-12
983 7 1.9 6166 3 US-08-591-632-51
984 7 1.9 6166 3 US-09-611-451-51
985 7 1.9 6226 3 US-08-542-363-1
986 7 1.9 6226 3 US-09-100-089-1
987 7 1.9 6226 3 US-09-670-827-1
988 7 1.9 6226 4 US-09-827-949-1
c 989 7 1.9 6312 1 US-08-531-601-3
c 990 7 1.9 6312 2 US-08-859-032-3
991 7 1.9 6361 3 US-08-646-538-7
992 7 1.9 6361 3 US-09-503-222-7
993 7 1.9 6446 3 US-09-293-170-2
c 994 7 1.9 6479 4 US-09-949-016-15251
995 7 1.9 6550 3 US-09-422-712B-1
996 7 1.9 6550 3 US-09-607-756-1
997 7 1.9 6563 3 US-09-027-449-61
998 7 1.9 6563 3 US-08-804-444A-61
999 7 1.9 6563 3 US-09-026-985-61
1000 7 1.9 6563 3 US-09-121-952A-61

ALIGNMENTS

RESULT 1
US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-492B-2

Alignment Scores:
Pred. No.: 0 Length: 1133
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-054-492B-2 (1-1133)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAACACAGAGATGCTTTCCTGTTGGAAAGCGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGTTTATAGTTACCGTA 240
Qy 81 LysAlaHisProLysTrpLeuSerCysIleAlaLysSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCAAAATACTTGGATTGTATTGCAATCAGCTGTTTTTCTTAGCTGCCAAG 300
Qy 101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAGGTATTGGCAAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAGAAATGGAGAGAAATTAATCTGGATAGTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCATTTGATTTTCTTCATATTTTCCATGTCATTCAGTGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCACTACTTCACTGTATGGCTGCACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTCTCTGGCCATGGTTAGTCTGAAATGAGAAACTCATTCCTGATGCTGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAATTGAACCTTCAGAAAGACAGATGATAGTCCCGATGTCATTCATTCGCG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGAGCTCTCCCTGCTCTGAAATTCGTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGGTACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAenSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCAGACTTCTCCAGAGACACACAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGGAATGGAAGTGATGACTTCTATGATGGGAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGCTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCTTTCGTCTGTCATG 1131

RESULT 2

US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-08-969-106-5

Alignment Scores:

Pred. No.: 0 Length: 1260

Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-1 (1-377) x US-08-969-106-5 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCTTTGGAAAACACAGAGATTGCTTCTCTGTTGGAAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAAATGCCCTTCAAAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATAACTTGGAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGAGACAGTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATTTCTGGATAAGTGAATTTGG 420
Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGGATTTTCTCATATTTTCCATGCCATTGCCAGTGA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTGATTGGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGATTGATCCATTGTCGG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTCTACTCTGCAGTCTTCCCTGCCTCTGAAATTCGGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTCGTGCACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCACAGACTTCTCCAGAGACACACAGCCAGAGTGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLeuArgLeu 340

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; US-09-023-655-899

Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-023-655-899 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAAACAGAGATTGCTTTCTGTTGGAAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTplysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCAGACATGTGGAAAGTGAATGTGGCGAAAATGCCCTTCAAAATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATTCAATGGCTGGCCAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80

Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGTTTGTAGTACCCTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAAATACCTTGAAGTGTATTGCAATCAGCTGTTTCTTCTAGTCCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGAAAGATGAGAAATCCAGTACTAAAGATATTGGCAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTGAGANTGAGAGAAATATTCTGGATAGTTGAATTGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACCATTTGATTTCTTCATATTTTCCATGCAATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTTACCAGCAACTTACTTCTGATGGCTGCAACCACTTTCGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTGGCCATGTTAGTCTGGAATGAGAAACTCATTTCTGATTTGCTTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTTACAAATTGAATGCTTTCAGAAAGCAGATGATAGTCTCCAGATTTGATTCGG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACAATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTCTGTCACCTGTGCACAAAGAGTTCAGATTACAT 840
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCCTCTCTGTCCAGGCCCCAGACTTCTCCAAGACACACAGCAGCAGAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAACAGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGCATGCTTCCCTTGTCCACTTTGAGCCCTTTGAGCCCTGTTCTGTGCTAG 1131

RESULT 5

US-09-513-999C-1907
; Sequence 1907, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.V.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961

```
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1907
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 52..444
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 10
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-1907

Alignment Scores:
Pred. No.: 3,47e-138 Length: 444
Score: 144.00 Matches: 144
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 38.20% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-1907 (1-444)

Qy 117 AspSerPheCysGlyCysSerSerSerGluLeuArgMetGluArgIleLeuAsp 136
Db 13 GACAGTCTCTGGGATGTTCTCTCATCTGAAATTTTGAGATGGAGAAATATTCTGGAT 72

Qy 137 LysLeuAenTpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAla 156
Db 73 AAGTTGAATTGGGATCTTCACAGCCACACATGGATTTCTCATATTATTTTCCATGCC 132

Qy 157 IleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGln 176
Db 133 ATTGAGGTGCAACTAGGCTCAGTTACTTTTCAGTTTGCCCAATTTGAGCCCATCTCAA 192

Qy 177 HisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGln 196
Db 193 CATTTGGCAGTCCTTACCAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAA 252

Qy 197 PheArgGlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIlePro 216
Db 253 TTCAGAGATTCATGCTTGCTCTGGCCATGTTAGTCTGGAAATGGAGAACTCATTCCT 312

Qy 217 AspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeu 236
Db 313 GATTGGCTTCTCTTACAAATTTGAATGCTTTCAGAAAGCACAGATGATGCTCCAGTTG 372

Qy 237 IleHisCysArgGluLeuValAlaHisIleSerThrLeuGlnSerSerLeuProLeu 256
Db 373 ATCAATTCGGGAGCTTGGGCACATCACCTTTCTACTCTGCAGTCTTCCCTCCCTCTG 432

Qy 257 AsnSerValTyr 260
Db 433 AATCCGTTTAT 444

RESULT 6
US-09-513-999C-29894
; Sequence 1, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
```

```
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 29894
; LENGTH: 304
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 230
; OTHER INFORMATION: m=a or c
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 231
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 268
; OTHER INFORMATION: w=a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 1.23e-25 Length: 304
Score: 34.00 Matches: 34
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.02% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-29894 (1-304)

Qy 344 AspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGly 363
Db 2 GATAATCTCTCAGAAATGTTGGTTCGTGTGTGGCACTGATTATCAAGACAGAGGGA 61

Qy 364 HisAlaSerProCysProProLeuGlnProValSerValMet 377
Db 62 CATGCTTCCCTTGTCACCTTTGCAGCCGTTCCTGTCATG 103

RESULT 7
US-09-129-112-1
; Sequence 1, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; TITLE OF INVENTION: The Regents of the University of California
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: US 08/907,226
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1643
; TYPE: DNA
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (51)..(1439)
; OTHER INFORMATION: NEP46 (DB46) No. 6465716 factor binding lectin
; NAME/KEY: mat_peptide
; LOCATION: (195)..(1436)
US-09-129-112-1
```

Alignment Scores:
Pred. No.: 26.8 Length: 1643
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.39% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-129-112-1 (1-1643)

Qy 165 LeuLeuPheSerLeuProLysLeuSer 173
Db 108 CTACTCTTCTCATTCGCCAAACTTCT 134

RESULT 8
US-09-129-112-3
; Sequence 3, Application US/09129112
; Patent No. 6465716
; GENERAL INFORMATION:
; APPLICANT: Etzler, Marilyn E.
; APPLICANT: Murphy, Judith B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: A No. 6465716 Factor Binding Protein From Legume Roots
; FILE REFERENCE: 023070-079810US
; CURRENT APPLICATION NUMBER: US/09/129,112
; CURRENT FILING DATE: 1998-08-04
; PRIOR FILING DATE: 1997-08-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 6265
; TYPE: DNA
; ORGANISM: Dolichos biflorus
; FEATURE:
; NAME/KEY: exon
; LOCATION: (633)..(944)
; NAME/KEY: intron
; LOCATION: (945)..(1022)
; NAME/KEY: exon
; LOCATION: (1023)..(1151)
; NAME/KEY: intron
; LOCATION: (1152)..(1559)
; NAME/KEY: exon
; LOCATION: (1560)..(1616)
; NAME/KEY: intron
; LOCATION: (1617)..(1697)
; NAME/KEY: exon
; LOCATION: (1698)..(1790)
US-09-129-112-3

Alignment Scores:
Pred. No.: 99.8 Length: 6265
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.39% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-1 (1-377) x US-09-129-112-3 (1-6265)

Qy 165 LeuLeuPheSerLeuProLysLeuSer 173
Db 732 CTACTCTTCTCATTCGCCAAACTTCT 758

RESULT 9
US-09-313-294A-98
; Sequence 98, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.

; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 98
; LENGTH: 277
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: incyte ID No. 6476212 700548521H1
; NAME/KEY: unsure
; LOCATION: 57, 79, 106, 202, 275
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-98

Alignment Scores:
Pred. No.: 49.2 Length: 277
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-313-294A-98 (1-277)

Qy 172 LeuSerProSerGlnHisLeuAla 179
Db 2 CTATCCCATCGCAGCATCTGCC 25

RESULT 10
US-09-513-999C-32630/c
; Sequence 32630, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 32630
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 139
; OTHER INFORMATION: n=a, g, c or t
; NAME/KEY: misc_feature
; LOCATION: 221
; OTHER INFORMATION: k=g or t
; NAME/KEY: misc_feature
; LOCATION: 252
; OTHER INFORMATION: m=a or c
US-09-513-999C-32630

Alignment Scores:
Pred. No.: 49.6 Length: 279
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-513-999C-32630 (1-279)

Qy 203 AlaleuAlaMetValSerLeuGlu 210
Db 130 GCTTTGGCTATGTCAGCCTTGAG 107

RESULT 11

US-09-270-767-26393
; Sequence 26393, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26393
; LENGTH: 382
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-26393

Alignment Scores:
Pred. No.: 67.5 Length: 382
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-270-767-26393 (1-382)

Qy 180 ValLeuThrLysGlnLeuLeuHis 187
Db 235 GTTCTTACCAACACATTTCAT 258

RESULT 12

US-08-956-171E-1529
; Sequence 1529, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956.171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 1529:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1529:
US-08-956-171E-1529

Alignment Scores:
Pred. No.: 70.7 Length: 400
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-08-956-171E-1529 (1-400)

Qy 165 LeuLeuPheSerLeuProLysLeu 172
Db 130 CTACTTTTCTCTTCCAAATTA 153

RESULT 13

US-08-781-986A-1529
; Sequence 1529, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1529:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-781-986A-1529

Alignment Scores:
Pred. No.: 70.7 Length: 400
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-08-781-986A-1529 (1-400)

Qy 165 LeuLeuPheSerLeuProLysLeu 172
Db 130 CTACTTTTCTCTTCCAAATTA 153

RESULT 14

US-09-767-8308
; Sequence 8308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8308
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8308

Alignment Scores:
Pred. No.: 90.1 Length: 512
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-270-767-8308 (1-512)

Qy 219 LeuSerLeuThrIleGluLeuLeu 226
Db 215 CTCTCACTTACTATAGAGCTGCTA 238

RESULT 15

US-09-270-767-23590
; Sequence 23590, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23590
; LENGTH: 512
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23590

Alignment Scores:
Pred. No.: 90.1 Length: 512
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.12% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x US-09-270-767-23590 (1-512)

Qy 219 LeuSerLeuThrIleGluLeuLeu 226
Db 215 CTCTCACTTACTATAGAGCTGCTA 238

Search completed: February 11, 2005, 14:37:22
Job time : 320.864 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 12:22:06 ; Search time 987.335 Seconds
(without alignments)
2253.008 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFGPLENORLSFLEKAI.....LSRQGHASPCPPQPVSVM 377

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 295022984 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10747261

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154944_20748/app_query_fasta_1.718
-DB=Published_applications NA -QFMT=fastap -SUFFIX=oligo.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USAR=US09736250 @CGN 1.1.582 @runat_07022005_154944_20748
-NCPU=6 -ICPU=3 -NO_WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DRV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FPGAPOP=6 -FPGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/1/pubna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/1/pubna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/1/pubna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubna/US10C_PUBCOMB.seq.*
16: /cgn2_6/ptodata/1/pubna/US10D_PUBCOMB.seq.*
17: /cgn2_6/ptodata/1/pubna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/1/pubna/US10F_PUBCOMB.seq.*
19: /cgn2_6/ptodata/1/pubna/US11_NEW_PUB.seq.*
20: /cgn2_6/ptodata/1/pubna/US11_PUB.seq.*
21: /cgn2_6/ptodata/1/pubna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/1/pubna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	377	100.0	1134	12	US-09-736-250-2	Sequence 2, Appli
2	377	100.0	1260	17	US-10-172-118-1326	Sequence 1326, Ap
3	377	100.0	1260	17	US-10-342-887-1326	Sequence 1326, Ap
4	377	100.0	1260	17	US-10-641-643-899	Sequence 899, App
5	377	100.0	1889	9	US-09-867-701-10907	Sequence 10907, A
6	266	70.6	2755	10	US-09-814-353-21586	Sequence 21586, A
7	139	36.9	444	17	US-10-242-535A-16032	Sequence 16032, A
8	139	36.9	444	17	US-10-085-783A-16032	Sequence 16032, A
9	133	35.3	490	17	US-10-242-535A-30212	Sequence 30212, A
10	133	35.3	490	17	US-10-085-783A-30212	Sequence 30212, A
11	123	32.6	2146	10	US-09-814-353-21294	Sequence 21294, A
12	118	31.3	389	17	US-10-242-535A-6834	Sequence 6834, Ap
13	118	31.3	389	17	US-10-085-783A-6834	Sequence 6834, Ap
14	112	29.7	369	17	US-10-242-535A-33391	Sequence 33391, A
15	112	29.7	369	17	US-10-085-783A-33391	Sequence 33391, A
16	77	20.4	350	17	US-10-242-535A-20816	Sequence 20816, A
17	77	20.4	350	17	US-10-085-783A-20816	Sequence 20816, A
18	75	19.9	486	10	US-09-814-353-17297	Sequence 17297, A
19	70	18.6	387	9	US-09-796-692-3935	Sequence 3935, Ap
20	70	18.6	387	14	US-10-040-862-3935	Sequence 3935, Ap
21	70	18.6	387	17	US-10-057-475B-3935	Sequence 3935, Ap
22	70	18.6	387	17	US-10-154-884B-3935	Sequence 3935, Ap
23	70	18.6	387	18	US-10-764-324-3935	Sequence 3935, Ap
24	65	17.2	447	9	US-09-777-564-1252	Sequence 1252, Ap
25	65	17.2	447	14	US-10-015-219-1252	Sequence 1252, Ap
26	62	16.4	889	9	US-09-867-701-10906	Sequence 10906, A
27	49	13.0	426	10	US-09-814-353-4614	Sequence 4614, Ap
28	49	13.0	426	10	US-09-814-353-10913	Sequence 10913, A
29	41	10.9	288	17	US-10-242-535A-57578	Sequence 57578, A
30	41	10.9	288	17	US-10-085-783A-57578	Sequence 57578, A
31	40	10.6	477	10	US-09-814-353-5374	Sequence 5374, Ap
32	40	10.6	477	10	US-09-814-353-11661	Sequence 11661, A
33	40	10.6	516	10	US-09-814-353-18045	Sequence 18045, A
34	37	9.8	444	9	US-09-920-300A-1413	Sequence 1413, Ap
35	37	9.8	444	13	US-10-033-528-1413	Sequence 1413, Ap
36	37	9.8	444	16	US-10-099-926-1413	Sequence 1413, Ap
37	34	9.0	308	17	US-10-242-535A-41781	Sequence 41781, A
38	34	9.0	308	17	US-10-085-783A-41781	Sequence 41781, A
39	30	8.0	247	9	US-09-998-598-2340	Sequence 2340, Ap
40	25	6.6	469	10	US-09-918-995-13873	Sequence 13873, A
41	24	6.4	244	17	US-10-242-535A-58868	Sequence 58868, A
42	24	6.4	244	17	US-10-085-783A-58868	Sequence 58868, A
43	24	6.4	420	9	US-09-960-352-9810	Sequence 9810, Ap
44	20	5.3	200	17	US-10-242-535A-5568	Sequence 5568, Ap
45	20	5.3	200	17	US-10-085-783A-5568	Sequence 5568, Ap
46	19	5.0	60	10	US-09-908-975-12858	Sequence 12858, A
47	18	4.8	348	9	US-09-728-445-666	Sequence 666, App
48	18	4.8	666	17	US-10-240-425-64	Sequence 64, Appl
49	15	4.0	251	17	US-10-242-535A-34894	Sequence 34894, A
50	15	4.0	251	17	US-10-085-783A-34894	Sequence 34894, A
51	14	3.7	65	10	US-09-908-975-28496	Sequence 28496, A
52	12	3.2	183	17	US-10-242-535A-48968	Sequence 48968, A
53	12	3.2	183	17	US-10-085-783A-48968	Sequence 48968, A
54	10	2.7	50	17	US-10-131-827-740	Sequence 740, App
55	9	2.4	431	13	US-10-027-632-21884	Sequence 21884, A
56	9	2.4	431	17	US-10-027-632-21884	Sequence 21884, A
57	9	2.4	1643	9	US-09-129-112-1	Sequence 1, Appli
58	9	2.4	6265	9	US-09-129-112-3	Sequence 3, Appli
59	9	2.4	163382	18	US-10-367-094-179	Sequence 179, App
60	8	2.1	25	19	US-10-719-900-297656	Sequence 297656, A
61	8	2.1	25	19	US-10-719-900-297657	Sequence 297657, A
62	8	2.1	25	19	US-10-719-900-570691	Sequence 570691, A
63	8	2.1	25	19	US-10-719-900-712383	Sequence 712383, A
64	8	2.1	25	19	US-10-719-900-765056	Sequence 765056, A
65	8	2.1	156	18	US-10-437-963-31670	Sequence 31670, A
66	8	2.1	201	18	US-10-741-601-18231	Sequence 18231, A
67	8	2.1	201	18	US-10-741-601-18232	Sequence 18232, A
68	8	2.1	201	18	US-10-741-601-49334	Sequence 49334, A
69	8	2.1	201	19	US-10-741-600-49335	Sequence 49335, A

c 70	8	2.1	267	9	US-09-923-876-331	Sequence 331, App	c 143	8	2.1	825	13	US-10-027-632-156599	Sequence 156599,
c 71	8	2.1	267	10	US-09-923-876-331	Sequence 331, App	c 144	8	2.1	825	13	US-10-027-632-156600	Sequence 156600,
c 72	8	2.1	311	18	US-10-425-115-138356	Sequence 138356,	c 145	8	2.1	825	13	US-10-027-632-156598	Sequence 156598,
c 73	8	2.1	342	18	US-10-425-115-175287	Sequence 175287,	c 146	8	2.1	825	17	US-10-027-632-156599	Sequence 156599,
c 74	8	2.1	400	8	US-08-781-986A-1529	Sequence 1529, Ap	c 147	8	2.1	825	17	US-10-027-632-156600	Sequence 156600,
c 75	8	2.1	400	17	US-10-329-624-1529	Sequence 1529, Ap	c 148	8	2.1	846	18	US-10-425-115-164850	Sequence 164850,
c 76	8	2.1	433	18	US-10-425-115-72890	Sequence 72890, A	c 149	8	2.1	855	13	US-10-027-632-157373	Sequence 157373,
c 77	8	2.1	437	17	US-10-424-599-95269	Sequence 95269, A	c 150	8	2.1	855	17	US-10-027-632-157373	Sequence 157373,
c 78	8	2.1	454	18	US-10-425-115-2103	Sequence 2103, Ap	c 151	8	2.1	865	13	US-10-027-632-157329	Sequence 157329,
c 79	8	2.1	465	17	US-10-424-599-102869	Sequence 102869, A	c 152	8	2.1	865	17	US-10-027-632-157329	Sequence 157329,
c 80	8	2.1	487	17	US-10-424-599-68700	Sequence 68700, A	c 153	8	2.1	871	18	US-10-767-795-4424	Sequence 4424, Ap
c 81	8	2.1	494	18	US-10-021-323-10833	Sequence 10833, A	c 154	8	2.1	901	17	US-10-425-114-29891	Sequence 29891, A
c 82	8	2.1	496	18	US-10-425-115-163797	Sequence 163797,	c 155	8	2.1	903	17	US-10-424-599-54004	Sequence 54004, A
c 83	8	2.1	501	18	US-10-425-115-5892	Sequence 5892, Ap	c 156	8	2.1	907	17	US-10-425-114-19888	Sequence 19888, A
c 84	8	2.1	508	18	US-10-425-115-68144	Sequence 68144, A	c 157	8	2.1	912	9	US-09-891-641-75	Sequence 75, Appl
c 85	8	2.1	527	17	US-10-425-114-7572	Sequence 7572, Ap	c 158	8	2.1	912	17	US-10-602-747A-75	Sequence 75, Appl
c 86	8	2.1	547	13	US-10-027-632-246125	Sequence 246125,	c 159	8	2.1	912	17	US-10-275-191-75	Sequence 75, Appl
c 87	8	2.1	547	17	US-10-027-632-246125	Sequence 246125,	c 160	8	2.1	999	17	US-10-424-599-85830	Sequence 85830, A
c 88	8	2.1	551	17	US-10-264-049-1871	Sequence 1871, Ap	c 161	8	2.1	1088	13	US-10-027-632-101341	Sequence 101341,
c 89	8	2.1	568	13	US-10-027-632-298827	Sequence 298827,	c 162	8	2.1	1088	13	US-10-027-632-101342	Sequence 101342,
c 90	8	2.1	568	17	US-10-027-632-298827	Sequence 298827,	c 163	8	2.1	1088	17	US-10-027-632-101341	Sequence 101341,
c 91	8	2.1	573	18	US-10-425-115-175290	Sequence 175290,	c 164	8	2.1	1088	17	US-10-027-632-101342	Sequence 101342,
c 92	8	2.1	585	13	US-10-027-632-225673	Sequence 225673,	c 165	8	2.1	1089	9	US-09-866-562-60	Sequence 60, Appl
c 93	8	2.1	585	13	US-10-027-632-225674	Sequence 225674,	c 166	8	2.1	1106	17	US-10-425-114-29284	Sequence 29284, A
c 94	8	2.1	585	17	US-10-027-632-225673	Sequence 225673,	c 167	8	2.1	1110	17	US-10-282-122A-32544	Sequence 32544, A
c 95	8	2.1	585	17	US-10-027-632-225674	Sequence 225674,	c 168	8	2.1	1119	17	US-10-240-425-1330	Sequence 1330, Ap
c 96	8	2.1	610	13	US-10-027-632-197848	Sequence 197848,	c 169	8	2.1	1140	18	US-10-437-963-43099	Sequence 43099, A
c 97	8	2.1	610	17	US-10-027-632-197848	Sequence 197848,	c 170	8	2.1	1176	9	US-09-866-562-59	Sequence 59, Appl
c 98	8	2.1	611	13	US-10-027-632-190099	Sequence 190099,	c 171	8	2.1	1309	18	US-10-425-115-150303	Sequence 150303,
c 99	8	2.1	611	13	US-10-027-632-190100	Sequence 190100,	c 172	8	2.1	1345	18	US-10-739-930-1384	Sequence 1384, Ap
c 100	8	2.1	611	13	US-10-027-632-190101	Sequence 190101,	c 173	8	2.1	1353	13	US-10-027-632-250414	Sequence 250414,
c 101	8	2.1	611	13	US-10-027-632-190102	Sequence 190102,	c 174	8	2.1	1353	17	US-10-027-632-250414	Sequence 250414,
c 102	8	2.1	611	17	US-10-027-632-190099	Sequence 190099,	c 175	8	2.1	1356	17	US-10-236-192-91	Sequence 91, Appl
c 103	8	2.1	611	17	US-10-027-632-190100	Sequence 190100,	c 176	8	2.1	1374	10	US-09-934-455-429	Sequence 429, App
c 104	8	2.1	611	17	US-10-027-632-190101	Sequence 190101,	c 177	8	2.1	1401	17	US-10-369-493-43536	Sequence 43536, A
c 105	8	2.1	612	13	US-10-027-632-190102	Sequence 190102,	c 178	8	2.1	1410	17	US-10-425-114-1192	Sequence 1192, Ap
c 106	8	2.1	612	13	US-10-027-632-193498	Sequence 193498,	c 179	8	2.1	1521	18	US-10-425-115-47751	Sequence 47751, A
c 107	8	2.1	612	17	US-10-027-632-193498	Sequence 193498,	c 180	8	2.1	1550	18	US-09-814-353-20781	Sequence 20781, A
c 108	8	2.1	623	18	US-10-425-115-122212	Sequence 122212,	c 181	8	2.1	1557	18	US-10-491-733-59	Sequence 59, Appl
c 109	8	2.1	637	17	US-10-425-114-15520	Sequence 15520, A	c 182	8	2.1	1559	17	US-10-425-114-30121	Sequence 30121, A
c 110	8	2.1	649	13	US-10-027-632-221754	Sequence 221754,	c 183	8	2.1	1638	17	US-10-424-599-53838	Sequence 53838, A
c 111	8	2.1	649	13	US-10-027-632-221755	Sequence 221755,	c 184	8	2.1	1703	17	US-10-264-237-952	Sequence 952, App
c 112	8	2.1	649	13	US-10-027-632-221756	Sequence 221756,	c 185	8	2.1	1715	17	US-09-397-945-87	Sequence 87, Appl
c 113	8	2.1	649	13	US-10-027-632-221757	Sequence 221757,	c 186	8	2.1	1715	17	US-10-653-595-87	Sequence 595, A
c 114	8	2.1	649	13	US-10-027-632-221758	Sequence 221758,	c 187	8	2.1	1722	18	US-10-424-599-11538	Sequence 11538, A
c 115	8	2.1	649	13	US-10-027-632-221759	Sequence 221759,	c 188	8	2.1	1722	18	US-10-437-963-515	Sequence 515, App
c 116	8	2.1	649	13	US-10-027-632-221760	Sequence 221760,	c 189	8	2.1	1781	17	US-10-424-599-13029	Sequence 13029, A
c 117	8	2.1	649	13	US-10-027-632-221761	Sequence 221761,	c 190	8	2.1	1790	18	US-10-723-860-359	Sequence 359, App
c 118	8	2.1	649	17	US-10-027-632-221754	Sequence 221754,	c 191	8	2.1	1848	18	US-10-767-701-12892	Sequence 12892, A
c 119	8	2.1	649	17	US-10-027-632-221755	Sequence 221755,	c 192	8	2.1	1907	18	US-10-437-963-24686	Sequence 24686, A
c 120	8	2.1	649	17	US-10-027-632-221756	Sequence 221756,	c 193	8	2.1	1936	17	US-10-425-114-33720	Sequence 33720, A
c 121	8	2.1	649	17	US-10-027-632-221757	Sequence 221757,	c 194	8	2.1	1957	18	US-10-437-963-9811	Sequence 9811, A
c 122	8	2.1	649	17	US-10-027-632-221758	Sequence 221758,	c 195	8	2.1	1962	17	US-10-369-493-31804	Sequence 31804, A
c 123	8	2.1	649	17	US-10-027-632-221759	Sequence 221759,	c 196	8	2.1	1986	17	US-10-282-122A-8409	Sequence 8409, Ap
c 124	8	2.1	649	17	US-10-027-632-221760	Sequence 221760,	c 197	8	2.1	1993	13	US-10-027-632-98093	Sequence 98093, A
c 125	8	2.1	649	17	US-10-027-632-221761	Sequence 221761,	c 198	8	2.1	1993	17	US-10-027-632-98093	Sequence 98093, A
c 126	8	2.1	650	17	US-10-424-599-53835	Sequence 53835, A	c 199	8	2.1	2004	18	US-10-437-963-24687	Sequence 24687, A
c 127	8	2.1	650	13	US-10-027-632-49333	Sequence 49333, A	c 200	8	2.1	2007	9	US-09-815-242-4207	Sequence 4207, Ap
c 128	8	2.1	657	17	US-10-027-632-49333	Sequence 49333, A	c 201	8	2.1	2010	9	US-09-815-242-8236	Sequence 8236, Ap
c 129	8	2.1	674	18	US-10-767-701-25591	Sequence 25591, A	c 202	8	2.1	2010	17	US-10-282-122A-8189	Sequence 8189, Ap
c 130	8	2.1	708	13	US-10-027-632-268871	Sequence 268871,	c 203	8	2.1	2021	17	US-09-974-300-1157	Sequence 1157, Ap
c 131	8	2.1	708	17	US-10-027-632-268871	Sequence 268871,	c 204	8	2.1	2041	18	US-10-425-115-26537	Sequence 26537, A
c 132	8	2.1	738	17	US-10-172-118-2378	Sequence 2378, Ap	c 205	8	2.1	2114	17	US-10-264-049-714	Sequence 714, App
c 133	8	2.1	738	17	US-10-342-887-2378	Sequence 2378, Ap	c 206	8	2.1	2161	11	US-09-997-722-101	Sequence 101, App
c 134	8	2.1	747	13	US-10-027-632-12227	Sequence 12227, A	c 207	8	2.1	2165	9	US-09-866-562-58	Sequence 58, Appl
c 135	8	2.1	747	17	US-10-027-632-12227	Sequence 12227, A	c 208	8	2.1	2165	18	US-10-643-795A-60	Sequence 60, Appl
c 136	8	2.1	749	18	US-10-425-115-134444	Sequence 134444,	c 209	8	2.1	2235	18	US-10-767-701-14511	Sequence 14511, A
c 137	8	2.1	779	17	US-10-424-599-115803	Sequence 115803,	c 210	8	2.1	2304	17	US-10-276-774-746	Sequence 746, App
c 138	8	2.1	791	18	US-10-363-345A-23639	Sequence 23639, A	c 211	8	2.1	2393	17	US-10-425-115-85772	Sequence 85772, A
c 139	8	2.1	791	18	US-10-363-345A-23640	Sequence 23640, A	c 212	8	2.1	2464	17	US-10-276-774-467	Sequence 467, App
c 140	8	2.1	796	18	US-10-363-345A-20749	Sequence 20749, A	c 213	8	2.1	2490	18	US-10-425-115-174924	Sequence 174924, A
c 141	8	2.1	796	18	US-10-363-345A-20750	Sequence 20750, A	c 214	8	2.1	2497	18	US-10-739-930-5364	Sequence 5364, Ap
c 142	8	2.1	825	13	US-10-027-632-156598	Sequence 156598,	c 215	8	2.1	2508	18	US-10-425-115-174920	Sequence 174920,

C 216	8	2.1	2532	18	US-10-437-963-14825	Sequence 14825, A	289	7	1.9	25	18	US-10-765-672-34	Sequence 34, Appl
C 217	8	2.1	2800	14	US-10-300-834-5	Sequence 5, Appl	290	7	1.9	25	19	US-10-719-900-204432	Sequence 204432, A
C 218	8	2.1	2790	17	US-10-108-260A-23	Sequence 23, Appl	C 291	7	1.9	25	19	US-10-719-900-275167	Sequence 275167, A
C 219	8	2.1	3275	18	US-10-357-930-23833	Sequence 23833, A	C 292	7	1.9	25	19	US-10-719-900-307773	Sequence 307773, A
C 220	8	2.1	3381	18	US-10-425-115-101082	Sequence 101082, A	C 293	7	1.9	25	19	US-10-719-900-379090	Sequence 379090, A
C 221	8	2.1	3387	18	US-10-661-809-14	Sequence 14, Appl	C 294	7	1.9	25	19	US-10-719-900-479965	Sequence 479965, A
C 222	8	2.1	3416	18	US-10-425-115-69463	Sequence 69463, A	C 295	7	1.9	25	19	US-10-719-900-492311	Sequence 492311, A
C 223	8	2.1	3432	14	US-10-300-834-4	Sequence 4, Appl	C 296	7	1.9	25	19	US-10-719-900-827583	Sequence 827583, A
C 224	8	2.1	3486	18	US-10-473-126-20	Sequence 20, Appl	C 297	7	1.9	25	19	US-10-719-900-938778	Sequence 938778, A
C 225	8	2.1	4003	18	US-10-723-860-5060	Sequence 5060, A	C 298	7	1.9	25	19	US-10-719-900-956705	Sequence 956705, A
C 226	8	2.1	4434	17	US-10-282-122A-10150	Sequence 10150, A	C 299	7	1.9	25	19	US-10-719-900-956706	Sequence 956706, A
C 227	8	2.1	4750	11	US-09-968-007A-685	Sequence 686, App	C 300	7	1.9	25	19	US-10-719-900-973233	Sequence 973233, A
C 228	8	2.1	4938	18	US-10-425-115-79300	Sequence 79300, A	C 301	7	1.9	25	19	US-10-719-900-973234	Sequence 973234, A
C 229	8	2.1	5793	18	US-10-437-963-35838	Sequence 35838, A	C 302	7	1.9	33	12	US-09-736-250-3	Sequence 3, Appl
C 230	8	2.1	6657	17	US-10-062-674-1937	Sequence 1937, A	C 303	7	1.9	35	9	US-09-484-704-38	Sequence 38, Appl
C 231	8	2.1	6669	15	US-10-311-455-166	Sequence 166, App	C 304	7	1.9	35	18	US-10-765-672-38	Sequence 38, Appl
C 232	8	2.1	6669	17	US-10-240-589C-6	Sequence 6, Appl	C 305	7	1.9	41	17	US-10-035-833A-1348	Sequence 1348, A
C 233	8	2.1	8285	9	US-09-732-025-3	Sequence 3, Appl	C 306	7	1.9	41	17	US-10-035-833A-4136	Sequence 4136, A
C 234	8	2.1	8285	16	US-10-153-317-3	Sequence 3, Appl	C 307	7	1.9	65	10	US-09-508-975-26809	Sequence 26809, A
C 235	8	2.1	8522	9	US-09-817-181-3	Sequence 3, Appl	C 308	7	1.9	65	10	US-10-741-849-3212	Sequence 3212, A
C 236	8	2.1	8522	14	US-10-300-828-3	Sequence 3, Appl	C 309	7	1.9	82	13	US-10-027-632-177870	Sequence 177870, A
C 237	8	2.1	9224	13	US-10-108-605-254	Sequence 254, App	C 310	7	1.9	82	17	US-10-027-632-177870	Sequence 177870, A
C 238	8	2.1	9299	15	US-10-311-455-1697	Sequence 1697, A	C 311	7	1.9	110	9	US-09-969-373-149	Sequence 149, App
C 239	8	2.1	9352	15	US-10-311-455-76	Sequence 76, Appl	C 312	7	1.9	117	18	US-10-437-963-3743	Sequence 3743, A
C 240	8	2.1	11827	9	US-09-733-455-3	Sequence 3, Appl	C 313	7	1.9	129	18	US-10-425-115-43161	Sequence 43161, A
C 241	8	2.1	11827	16	US-10-153-319-3	Sequence 3, Appl	C 314	7	1.9	135	9	US-09-864-761-24101	Sequence 24101, A
C 242	8	2.1	17000	18	US-10-837-624-3	Sequence 3, Appl	C 315	7	1.9	138	18	US-10-466-894-18	Sequence 18, Appl
C 243	8	2.1	17934	15	US-10-311-455-1691	Sequence 1691, A	C 316	7	1.9	149	17	US-10-424-599-48325	Sequence 48325, A
C 244	8	2.1	21840	13	US-10-087-192-310	Sequence 310, App	C 317	7	1.9	154	10	US-09-754-853A-234	Sequence 234, App
C 245	8	2.1	24617	18	US-10-741-601-5765	Sequence 5765, A	C 318	7	1.9	156	9	US-09-864-761-23900	Sequence 23900, A
C 246	8	2.1	24617	19	US-10-741-600-17967	Sequence 17967, A	C 319	7	1.9	159	17	US-10-424-599-71839	Sequence 71839, A
C 247	8	2.1	26071	18	US-10-322-281-575	Sequence 575, App	C 320	7	1.9	167	17	US-10-424-599-19075	Sequence 19075, A
C 248	8	2.1	27310	13	US-10-087-192-1162	Sequence 1162, A	C 321	7	1.9	171	18	US-10-425-115-164623	Sequence 164623, A
C 249	8	2.1	32220	9	US-09-764-877-3933	Sequence 3933, A	C 322	7	1.9	186	15	US-10-156-761-5741	Sequence 5741, A
C 250	8	2.1	32220	17	US-10-242-515-3933	Sequence 3933, A	C 323	7	1.9	187	18	US-10-425-115-17741	Sequence 17741, A
C 251	8	2.1	36176	13	US-10-087-192-1918	Sequence 1918, A	C 324	7	1.9	189	17	US-10-425-535A-46879	Sequence 46879, A
C 252	8	2.1	39443	17	US-10-085-117-313	Sequence 313, App	C 325	7	1.9	189	17	US-10-085-783A-46879	Sequence 46879, A
C 253	8	2.1	39827	17	US-10-041-018-399	Sequence 399, App	C 326	7	1.9	193	17	US-10-242-535A-30452	Sequence 30452, A
C 254	8	2.1	40394	18	US-10-741-601-5774	Sequence 5774, A	C 327	7	1.9	193	17	US-10-085-783A-30452	Sequence 30452, A
C 255	8	2.1	40394	19	US-10-741-600-17987	Sequence 17987, A	C 328	7	1.9	195	18	US-10-425-115-109444	Sequence 109444, A
C 256	8	2.1	48680	13	US-10-087-192-2044	Sequence 2044, A	C 329	7	1.9	198	18	US-10-674-1248-6137	Sequence 6137, A
C 257	8	2.1	50781	13	US-10-087-192-769	Sequence 769, App	C 330	7	1.9	201	18	US-10-741-601-11909	Sequence 11909, A
C 258	8	2.1	55996	11	US-09-997-722-7	Sequence 7, Appl	C 331	7	1.9	201	18	US-10-741-601-19718	Sequence 19718, A
C 259	8	2.1	56339	17	US-10-085-117-280	Sequence 280, App	C 332	7	1.9	201	18	US-10-719-993-5389	Sequence 5389, A
C 260	8	2.1	61718	19	US-10-741-600-17743	Sequence 17743, A	C 333	7	1.9	201	18	US-10-719-993-5395	Sequence 5395, A
C 261	8	2.1	67097	17	US-10-085-117-88	Sequence 88, Appl	C 334	7	1.9	201	18	US-10-719-993-5396	Sequence 5396, A
C 262	8	2.1	67126	18	US-10-741-601-5691	Sequence 5691, A	C 335	7	1.9	201	18	US-10-719-993-5402	Sequence 5402, A
C 263	8	2.1	67126	19	US-10-741-600-17762	Sequence 17762, A	C 336	7	1.9	201	18	US-10-719-993-5403	Sequence 5403, A
C 264	8	2.1	70768	13	US-10-135-322-13	Sequence 13, Appl	C 337	7	1.9	201	18	US-10-719-993-5409	Sequence 5409, A
C 265	8	2.1	96592	11	US-09-997-722-88	Sequence 88, Appl	C 338	7	1.9	201	18	US-10-719-993-6654	Sequence 6654, A
C 266	8	2.1	115780	18	US-10-367-094-96	Sequence 96, Appl	C 339	7	1.9	201	18	US-10-719-993-6655	Sequence 6655, A
C 267	8	2.1	119211	17	US-10-672-787-40	Sequence 40, Appl	C 340	7	1.9	201	18	US-10-719-993-22664	Sequence 22664, A
C 268	8	2.1	119472	19	US-10-741-600-17865	Sequence 17865, A	C 341	7	1.9	201	18	US-10-719-993-28333	Sequence 28333, A
C 269	8	2.1	129710	13	US-10-027-632-178902	Sequence 178902, A	C 342	7	1.9	201	18	US-10-719-993-28428	Sequence 28428, A
C 270	8	2.1	129710	13	US-10-027-632-178902	Sequence 178902, A	C 343	7	1.9	201	18	US-10-719-993-28430	Sequence 28430, A
C 271	8	2.1	130207	13	US-10-087-192-1372	Sequence 1372, A	C 344	7	1.9	201	18	US-10-719-993-29247	Sequence 29247, A
C 272	8	2.1	133632	13	US-10-087-192-1810	Sequence 1810, A	C 345	7	1.9	201	18	US-10-719-993-29247	Sequence 29247, A
C 273	8	2.1	166910	17	US-10-292-337-11	Sequence 11, Appl	C 346	7	1.9	201	18	US-10-719-993-31264	Sequence 31264, A
C 274	8	2.1	176930	18	US-10-741-601-5679	Sequence 5679, A	C 347	7	1.9	201	18	US-10-719-993-33571	Sequence 33571, A
C 275	8	2.1	176930	19	US-10-741-600-17725	Sequence 17725, A	C 348	7	1.9	201	18	US-10-719-993-36604	Sequence 36604, A
C 276	8	2.1	203127	19	US-10-741-601-5654	Sequence 5654, A	C 349	7	1.9	201	18	US-10-719-993-36629	Sequence 36629, A
C 277	8	2.1	203127	19	US-10-741-600-17666	Sequence 17666, A	C 350	7	1.9	201	18	US-10-719-993-38502	Sequence 38502, A
C 278	8	2.1	312477	18	US-10-317-883A-12	Sequence 12, Appl	C 351	7	1.9	201	18	US-10-719-993-39622	Sequence 39622, A
C 279	8	2.1	339234	18	US-10-322-696-73	Sequence 73, Appl	C 352	7	1.9	201	18	US-10-719-993-39623	Sequence 39623, A
C 280	8	2.1	2140405	13	US-10-027-632-76212	Sequence 76212, A	C 353	7	1.9	201	18	US-10-719-993-39674	Sequence 39674, A
C 281	8	2.1	2140405	17	US-10-027-632-76212	Sequence 76212, A	C 354	7	1.9	201	18	US-10-719-993-41624	Sequence 41624, A
C 282	8	2.1	2256646	18	US-10-470-565-1	Sequence 1, Appl	C 355	7	1.9	201	18	US-10-719-993-41626	Sequence 41626, A
C 283	7	1.9	22	14	US-10-175-225-14	Sequence 14, Appl	C 356	7	1.9	201	18	US-10-719-993-43908	Sequence 43908, A
C 284	7	1.9	25	9	US-09-484-704-31	Sequence 31, Appl	C 357	7	1.9	201	18	US-10-719-993-43909	Sequence 43909, A
C 285	7	1.9	25	9	US-09-484-704-31	Sequence 31, Appl	C 358	7	1.9	201	18	US-10-719-993-49159	Sequence 49159, A
C 286	7	1.9	25	15	US-10-098-263B-29901	Sequence 29901, A	C 359	7	1.9	201	18	US-10-719-993-49167	Sequence 49167, A
C 287	7	1.9	25	18	US-10-775-169-4005	Sequence 4005, App	C 360	7	1.9	201	18	US-10-719-993-49168	Sequence 49168, A
C 288	7	1.9	25	18	US-10-765-672-31	Sequence 31, Appl	C 361	7	1.9	201	18	US-10-719-993-49983	Sequence 49983, A

C 362	7	1.9	201	18	US-10-719-993-49989	Sequence 49989, A	435	7	1.9	283	10	US-09-237-183A-1543	Sequence 1543, Ap
C 363	7	1.9	201	18	US-10-719-993-50004	Sequence 50004, A	436	7	1.9	283	11	US-09-987-899-3752	Sequence 3752, Ap
C 364	7	1.9	201	18	US-10-719-993-53130	Sequence 53130, A	437	7	1.9	283	11	US-10-424-599-6605	Sequence 6605, A
C 365	7	1.9	201	18	US-10-719-993-53132	Sequence 53132, A	438	7	1.9	283	18	US-10-674-124A-21549	Sequence 21549, A
C 366	7	1.9	201	18	US-10-719-993-54108	Sequence 54108, A	439	7	1.9	287	18	US-10-357-930-59715	Sequence 59715, A
C 367	7	1.9	201	19	US-10-741-600-22208	Sequence 22208, A	440	7	1.9	290	17	US-10-242-535A-1743	Sequence 1743, Ap
C 368	7	1.9	201	19	US-10-741-600-22217	Sequence 22217, A	441	7	1.9	290	17	US-10-425-114-12429	Sequence 12429, A
C 369	7	1.9	201	19	US-10-741-600-42497	Sequence 42497, A	442	7	1.9	290	17	US-10-085-783A-1743	Sequence 1743, Ap
C 370	7	1.9	201	19	US-10-741-600-48813	Sequence 48813, A	443	7	1.9	291	9	US-09-294-093B-1050	Sequence 1050, Ap
C 371	7	1.9	201	19	US-10-741-600-49418	Sequence 49418, A	444	7	1.9	291	17	US-10-282-122A-3720	Sequence 3720, A
C 372	7	1.9	201	19	US-10-741-600-52817	Sequence 52817, A	445	7	1.9	291	17	US-10-425-115-112494	Sequence 112494, A
C 373	7	1.9	201	19	US-10-741-600-54662	Sequence 54662, A	446	7	1.9	292	13	US-10-001-843-84	Sequence 84, Appl
C 374	7	1.9	201	19	US-10-741-600-56642	Sequence 56642, A	447	7	1.9	292	17	US-10-242-535A-3803	Sequence 3803, Ap
C 375	7	1.9	201	19	US-10-741-600-62224	Sequence 62224, A	448	7	1.9	292	17	US-10-085-783A-3803	Sequence 3803, Ap
C 376	7	1.9	201	19	US-10-741-600-66878	Sequence 66878, A	449	7	1.9	293	9	US-09-294-093B-295	Sequence 295, App
C 377	7	1.9	201	19	US-10-741-600-69849	Sequence 69849, A	450	7	1.9	293	9	US-09-294-093B-2025	Sequence 2025, Ap
C 378	7	1.9	201	19	US-10-741-600-69882	Sequence 69882, A	451	7	1.9	293	9	US-09-764-860-115	Sequence 115, App
C 379	7	1.9	201	19	US-10-741-600-69856	Sequence 69856, A	452	7	1.9	293	14	US-10-074-095-115	Sequence 115, App
C 380	7	1.9	201	19	US-10-741-600-71518	Sequence 71518, A	453	7	1.9	293	17	US-10-212-872-115	Sequence 115, App
C 381	7	1.9	203	17	US-10-424-599-61988	Sequence 61988, A	454	7	1.9	293	18	US-10-723-860-2410	Sequence 2410, Ap
C 382	7	1.9	206	18	US-09-510-332-104	Sequence 104, App	455	7	1.9	294	18	US-10-425-115-970	Sequence 970, App
C 383	7	1.9	206	18	US-10-770-127-104	Sequence 104, App	456	7	1.9	299	17	US-10-369-493-29158	Sequence 29158, A
C 384	7	1.9	210	17	US-10-335-977-2450	Sequence 2450, App	457	7	1.9	299	17	US-10-424-599-99283	Sequence 99283, A
C 385	7	1.9	213	17	US-10-335-977-2451	Sequence 2451, App	458	7	1.9	300	9	US-09-294-093B-1644	Sequence 1644, Ap
C 386	7	1.9	213	18	US-10-425-115-111306	Sequence 111306, A	459	7	1.9	300	18	US-10-425-115-33626	Sequence 33626, A
C 387	7	1.9	216	19	US-10-472-928-2619	Sequence 2619, Ap	460	7	1.9	300	18	US-10-357-930-59696	Sequence 59696, A
C 388	7	1.9	225	18	US-10-674-124A-10379	Sequence 10379, A	461	7	1.9	303	18	US-10-425-115-43372	Sequence 43372, A
C 389	7	1.9	231	9	US-09-878-178-1620	Sequence 1620, Ap	462	7	1.9	304	18	US-10-437-963-83772	Sequence 83772, A
C 390	7	1.9	231	13	US-10-046-935-1620	Sequence 1620, Ap	463	7	1.9	306	18	US-10-425-115-156390	Sequence 156390, A
C 391	7	1.9	231	14	US-10-146-502-1620	Sequence 1620, Ap	464	7	1.9	307	9	US-09-983-965-4120	Sequence 4120, Ap
C 392	7	1.9	232	18	US-10-357-930-59891	Sequence 59891, A	465	7	1.9	308	18	US-10-357-930-2243	Sequence 2243, Ap
C 393	7	1.9	232	18	US-10-674-124A-20391	Sequence 20391, A	466	7	1.9	313	11	US-09-864-408A-991	Sequence 991, App
C 394	7	1.9	235	17	US-10-424-599-115635	Sequence 115635, A	467	7	1.9	313	18	US-10-425-115-19000	Sequence 19000, A
C 395	7	1.9	240	11	US-09-864-408A-1789	Sequence 1789, Ap	468	7	1.9	314	18	US-10-425-115-59582	Sequence 59582, A
C 396	7	1.9	242	17	US-10-424-599-81355	Sequence 81355, A	469	7	1.9	315	9	US-09-867-550-1573	Sequence 1573, Ap
C 397	7	1.9	245	10	US-09-237-183A-1542	Sequence 1542, Ap	470	7	1.9	317	10	US-09-814-353-4071	Sequence 4071, Ap
C 398	7	1.9	245	11	US-09-987-899-3751	Sequence 3751, Ap	471	7	1.9	317	10	US-09-814-353-10378	Sequence 10378, A
C 399	7	1.9	246	10	US-09-918-995-31236	Sequence 31236, A	472	7	1.9	317	14	US-10-091-572-15	Sequence 15, Appl
C 400	7	1.9	246	17	US-10-424-599-469	Sequence 469, App	473	7	1.9	324	14	US-10-424-599-20982	Sequence 20982, A
C 401	7	1.9	248	9	US-09-867-701-5528	Sequence 5528, Ap	474	7	1.9	324	18	US-10-437-963-100969	Sequence 100969, A
C 402	7	1.9	249	18	US-10-425-115-106663	Sequence 106663, A	475	7	1.9	325	17	US-10-242-535A-21858	Sequence 21858, A
C 403	7	1.9	250	18	US-10-425-115-137000	Sequence 137000, A	476	7	1.9	325	17	US-10-085-783A-21858	Sequence 21858, A
C 404	7	1.9	252	18	US-10-425-115-134187	Sequence 134187, A	477	7	1.9	327	18	US-10-425-115-102926	Sequence 102926, A
C 405	7	1.9	253	18	US-10-425-115-78037	Sequence 78037, A	478	7	1.9	330	10	US-09-814-353-4168	Sequence 4168, Ap
C 406	7	1.9	255	10	US-09-930-213-344	Sequence 344, App	479	7	1.9	330	10	US-09-814-353-10474	Sequence 10474, A
C 407	7	1.9	255	17	US-10-424-599-40897	Sequence 40897, A	480	7	1.9	330	17	US-10-424-599-48625	Sequence 48625, A
C 408	7	1.9	256	11	US-09-922-293-3289	Sequence 3289, Ap	481	7	1.9	330	17	US-10-152-319A-818	Sequence 818, App
C 409	7	1.9	257	18	US-10-437-963-8593	Sequence 8593, Ap	482	7	1.9	332	18	US-10-914-037-560	Sequence 560, App
C 410	7	1.9	260	18	US-10-437-963-8590	Sequence 8590, Ap	483	7	1.9	333	9	US-09-796-692-5826	Sequence 5826, Ap
C 411	7	1.9	260	18	US-09-864-761-23833	Sequence 10353, A	484	7	1.9	333	14	US-10-040-862-5826	Sequence 5826, Ap
C 412	7	1.9	261	9	US-09-864-761-23833	Sequence 23833, A	485	7	1.9	333	17	US-10-057-475B-5826	Sequence 5826, Ap
C 413	7	1.9	261	17	US-10-424-599-16138	Sequence 16138, A	486	7	1.9	333	17	US-10-154-884B-5826	Sequence 5826, Ap
C 414	7	1.9	261	18	US-10-437-963-67368	Sequence 67368, A	487	7	1.9	333	18	US-10-764-324-5826	Sequence 5826, Ap
C 415	7	1.9	262	18	US-10-425-115-19440	Sequence 19440, A	488	7	1.9	335	17	US-10-242-535A-12432	Sequence 12432, A
C 416	7	1.9	262	18	US-10-357-930-56952	Sequence 56952, A	489	7	1.9	335	17	US-10-085-783A-12432	Sequence 12432, A
C 417	7	1.9	266	18	US-10-425-115-184183	Sequence 184183, A	490	7	1.9	336	9	US-09-969-373-379	Sequence 379, App
C 418	7	1.9	266	14	US-10-082-830-11	Sequence 11, Appl	491	7	1.9	339	18	US-10-425-115-89865	Sequence 89865, A
C 419	7	1.9	266	18	US-10-425-115-39917	Sequence 39917, A	492	7	1.9	339	18	US-10-856-499-420	Sequence 420, App
C 420	7	1.9	268	10	US-09-237-183A-1546	Sequence 1546, Ap	493	7	1.9	339	17	US-10-242-535A-20460	Sequence 20460, A
C 421	7	1.9	268	11	US-09-987-899-3755	Sequence 3755, Ap	494	7	1.9	340	17	US-10-085-783A-20460	Sequence 20460, A
C 422	7	1.9	269	17	US-10-424-599-39933	Sequence 39933, A	495	7	1.9	342	17	US-10-243-552-20	Sequence 20, Appl
C 423	7	1.9	269	18	US-10-674-124A-10378	Sequence 10378, A	496	7	1.9	342	17	US-10-335-977-4117	Sequence 4117, Ap
C 424	7	1.9	271	18	US-10-425-115-22091	Sequence 22091, A	497	7	1.9	343	17	US-10-381-813-118	Sequence 118, App
C 425	7	1.9	272	18	US-10-425-115-15307	Sequence 15307, A	498	7	1.9	343	17	US-10-381-813-119	Sequence 119, App
C 426	7	1.9	273	9	US-09-933-797-230	Sequence 230, App	499	7	1.9	345	17	US-10-335-977-4116	Sequence 4116, Ap
C 427	7	1.9	273	18	US-10-425-115-5786	Sequence 5786, Ap	500	7	1.9	345	17	US-10-381-813-111	Sequence 111, App
C 428	7	1.9	273	18	US-10-357-930-60047	Sequence 60047, A	501	7	1.9	347	9	US-09-880-107-2217	Sequence 2217, Ap
C 429	7	1.9	274	9	US-09-969-708-528	Sequence 528, App	502	7	1.9	348	9	US-09-860-352-5894	Sequence 5894, Ap
C 430	7	1.9	274	9	US-09-880-107-313	Sequence 313, App	503	7	1.9	348	10	US-09-814-353-667	Sequence 667, App
C 431	7	1.9	274	17	US-10-424-599-21697	Sequence 21697, A	504	7	1.9	351	10	US-09-814-353-7043	Sequence 7043, Ap
C 432	7	1.9	276	18	US-10-437-963-38765	Sequence 38765, A	505	7	1.9	351	11	US-09-864-408A-667	Sequence 667, App
C 433	7	1.9	281	13	US-10-027-632-77053	Sequence 77053, A	506	7	1.9	352	17	US-10-170-385-194	Sequence 194, App
C 434	7	1.9	281	17	US-10-027-632-77053	Sequence 77053, A	507	7	1.9	353	17	US-10-424-599-76487	Sequence 76487, A

508	7	1.9	355	9	US-09-960-352-5460	Sequence 5460, Ap	c 581	7	1.9	417	17	US-10-282-122A-13640	Sequence 13640, A
509	7	1.9	356	18	US-10-425-115-57347	Sequence 57347, A	582	7	1.9	419	18	US-10-425-115-183688	Sequence 183688, A
510	7	1.9	357	17	US-10-424-599-38756	Sequence 38756, A	583	7	1.9	421	13	US-10-027-632-48577	Sequence 48577, A
511	7	1.9	357	18	US-10-437-963-87453	Sequence 87453, A	584	7	1.9	421	17	US-10-027-632-48577	Sequence 48577, A
c 512	7	1.9	363	17	US-10-335-977-4118	Sequence 4118, Ap	585	7	1.9	421	17	US-10-276-774-58	Sequence 58, Appl
513	7	1.9	364	18	US-10-357-930-6775	Sequence 6775, Ap	586	7	1.9	421	18	US-10-425-115-167481	Sequence 167481, A
514	7	1.9	365	17	US-10-424-599-130146	Sequence 130146, Ap	c 587	7	1.9	423	9	US-09-983-965-2637	Sequence 2637, Ap
515	7	1.9	366	17	US-10-260-238-1403	Sequence 1403, Ap	c 588	7	1.9	423	18	US-10-357-930-607	Sequence 607, App
516	7	1.9	366	18	US-10-425-115-182292	Sequence 182292, A	589	7	1.9	424	13	US-10-027-632-96967	Sequence 96967, A
517	7	1.9	367	18	US-10-357-930-3376	Sequence 3376, Ap	590	7	1.9	424	13	US-10-027-632-306400	Sequence 306400, A
c 518	7	1.9	369	17	US-10-369-493-23853	Sequence 23853, A	591	7	1.9	424	17	US-10-027-632-96967	Sequence 96967, A
519	7	1.9	372	9	US-09-960-352-3227	Sequence 3227, Ap	592	7	1.9	424	17	US-10-027-632-306400	Sequence 306400, A
520	7	1.9	373	9	US-09-962-832-16	Sequence 16, Appl	593	7	1.9	424	17	US-10-424-599-4396	Sequence 4396, Ap
521	7	1.9	373	9	US-09-954-456-177	Sequence 177, App	594	7	1.9	424	18	US-10-767-701-5537	Sequence 5537, Ap
522	7	1.9	374	17	US-10-424-599-17137	Sequence 17137, A	c 595	7	1.9	425	18	US-10-424-599-68649	Sequence 68649, A
c 523	7	1.9	374	17	US-10-425-114-18037	Sequence 18037, A	596	7	1.9	425	18	US-10-357-930-9776	Sequence 9776, Ap
524	7	1.9	378	18	US-10-674-124A-21328	Sequence 21328, A	597	7	1.9	427	9	US-09-864-761-3626	Sequence 3626, Ap
525	7	1.9	379	18	US-10-425-115-184122	Sequence 184122, A	c 598	7	1.9	429	9	US-09-983-965-4102	Sequence 4102, Ap
526	7	1.9	380	18	US-10-425-115-184122	Sequence 184122, A	599	7	1.9	429	10	US-09-764-891-9485	Sequence 9485, Ap
c 527	7	1.9	381	9	US-09-960-352-12211	Sequence 12211, A	600	7	1.9	429	10	US-09-764-891-9486	Sequence 9486, Ap
c 528	7	1.9	383	10	US-09-918-995-18831	Sequence 18831, A	601	7	1.9	429	10	US-09-764-891-9487	Sequence 9487, Ap
529	7	1.9	383	18	US-10-425-115-166430	Sequence 166430, A	602	7	1.9	429	13	US-10-001-887-73	Sequence 73, Appl
530	7	1.9	384	18	US-10-357-930-15267	Sequence 15267, A	603	7	1.9	429	13	US-10-027-632-180838	Sequence 180838, A
c 531	7	1.9	385	17	US-10-242-535A-6746	Sequence 6746, Ap	604	7	1.9	429	15	US-10-205-428-865	Sequence 865, App
c 532	7	1.9	385	17	US-10-085-783A-6746	Sequence 6746, Ap	605	7	1.9	429	15	US-10-205-428-867	Sequence 867, App
c 533	7	1.9	386	9	US-09-770-791-75	Sequence 75, Appl	606	7	1.9	429	15	US-10-205-428-868	Sequence 868, App
c 534	7	1.9	386	17	US-10-641-643-692	Sequence 692, App	607	7	1.9	429	17	US-10-027-632-180838	Sequence 180838, A
535	7	1.9	388	17	US-10-191-803-820	Sequence 820, App	c 608	7	1.9	432	10	US-09-918-995-34514	Sequence 34514, A
c 536	7	1.9	390	14	US-10-066-543-1320	Sequence 1320, Ap	609	7	1.9	432	13	US-10-027-632-43681	Sequence 43681, A
c 537	7	1.9	390	17	US-10-260-238-5295	Sequence 5295, Ap	610	7	1.9	433	13	US-10-027-632-72860	Sequence 72860, A
538	7	1.9	390	18	US-10-425-115-132416	Sequence 132416, A	611	7	1.9	433	13	US-10-027-632-72860	Sequence 72860, A
539	7	1.9	394	17	US-10-424-599-50246	Sequence 50246, A	612	7	1.9	433	17	US-10-027-632-43681	Sequence 43681, A
c 540	7	1.9	395	9	US-09-783-590-6434	Sequence 6434, Ap	613	7	1.9	433	17	US-10-027-632-72860	Sequence 72860, A
c 541	7	1.9	395	17	US-10-424-599-98673	Sequence 98673, A	614	7	1.9	433	17	US-10-027-632-312826	Sequence 312826, A
542	7	1.9	398	18	US-10-425-115-79190	Sequence 79190, A	615	7	1.9	433	18	US-10-674-124A-16331	Sequence 16331, A
543	7	1.9	399	9	US-09-960-352-6868	Sequence 6868, Ap	616	7	1.9	433	18	US-10-357-930-32584	Sequence 32584, A
c 544	7	1.9	399	10	US-09-814-353-16858	Sequence 16858, A	617	7	1.9	433	18	US-10-357-930-41510	Sequence 41510, A
c 545	7	1.9	400	8	US-08-781-986A-852	Sequence 852, App	c 618	7	1.9	434	18	US-10-767-701-22247	Sequence 22247, A
546	7	1.9	400	10	US-09-814-353-16762	Sequence 16762, A	c 619	7	1.9	435	18	US-10-437-963-63636	Sequence 63636, A
c 547	7	1.9	400	17	US-10-424-599-130022	Sequence 130022, A	620	7	1.9	436	18	US-10-674-124A-5265	Sequence 5265, Ap
c 548	7	1.9	400	17	US-10-329-624-852	Sequence 852, App	621	7	1.9	437	10	US-09-764-891-2251	Sequence 2251, Ap
c 549	7	1.9	400	18	US-10-425-115-121967	Sequence 121967, A	622	7	1.9	437	15	US-10-205-428-179	Sequence 179, App
550	7	1.9	401	13	US-10-027-632-75873	Sequence 75873, A	c 623	7	1.9	437	17	US-10-424-599-127046	Sequence 127046, A
551	7	1.9	401	17	US-10-027-632-75873	Sequence 75873, A	624	7	1.9	439	9	US-09-924-035A-382	Sequence 382, App
c 552	7	1.9	402	11	US-08-781-986A-1282	Sequence 1282, Ap	625	7	1.9	439	18	US-10-767-701-2816	Sequence 2816, Ap
c 553	7	1.9	402	18	US-09-732-627A-2239	Sequence 2239, Ap	626	7	1.9	441	10	US-09-918-995-36870	Sequence 36870, A
c 554	7	1.9	402	17	US-10-329-624-1282	Sequence 1282, Ap	627	7	1.9	441	17	US-10-424-599-85815	Sequence 85815, A
c 555	7	1.9	403	17	US-10-424-599-70666	Sequence 70666, A	628	7	1.9	443	10	US-09-918-995-37067	Sequence 37067, A
556	7	1.9	404	9	US-09-867-701-4500	Sequence 4500, Ap	c 629	7	1.9	443	13	US-10-027-632-183309	Sequence 183309, A
c 557	7	1.9	404	10	US-09-918-995-18751	Sequence 18751, A	630	7	1.9	443	13	US-10-027-632-183310	Sequence 183310, A
c 558	7	1.9	406	13	US-10-027-632-301592	Sequence 301592, A	631	7	1.9	443	17	US-10-027-632-183310	Sequence 183310, A
559	7	1.9	406	16	US-10-181-447A-31	Sequence 31, Appl	c 632	7	1.9	443	17	US-10-027-632-183310	Sequence 183310, A
c 560	7	1.9	406	17	US-10-027-632-301592	Sequence 301592, A	633	7	1.9	443	17	US-10-424-599-22068	Sequence 22068, A
c 561	7	1.9	407	9	US-09-864-761-17101	Sequence 17101, A	634	7	1.9	444	17	US-10-424-599-132964	Sequence 132964, A
562	7	1.9	407	18	US-10-425-115-177335	Sequence 177335, A	c 635	7	1.9	444	18	US-10-767-701-30768	Sequence 30768, A
c 563	7	1.9	408	13	US-10-095-407-10	Sequence 10, Appl	636	7	1.9	445	18	US-10-357-930-11412	Sequence 11412, A
c 564	7	1.9	408	18	US-10-437-963-13286	Sequence 13286, A	637	7	1.9	448	17	US-10-425-114-20465	Sequence 20465, A
565	7	1.9	408	18	US-10-674-124A-768	Sequence 768, App	638	7	1.9	449	9	US-09-864-761-2168	Sequence 2168, Ap
c 566	7	1.9	408	18	US-10-425-115-105713	Sequence 105713, A	639	7	1.9	450	17	US-10-131-827-8406	Sequence 8406, Ap
c 567	7	1.9	410	18	US-10-425-115-44036	Sequence 44036, A	c 640	7	1.9	451	10	US-09-918-995-15275	Sequence 15275, A
568	7	1.9	411	9	US-09-922-217-180	Sequence 180, App	641	7	1.9	452	9	US-09-864-761-11355	Sequence 11355, A
c 569	7	1.9	411	9	US-09-833-263-180	Sequence 180, App	642	7	1.9	452	17	US-10-424-599-84528	Sequence 84528, A
570	7	1.9	411	13	US-10-025-380-180	Sequence 180, App	643	7	1.9	452	18	US-10-856-499-63	Sequence 63, Appl
c 571	7	1.9	411	17	US-10-242-535A-44077	Sequence 44077, A	644	7	1.9	453	11	US-09-969-034-18822	Sequence 18822, Ap
c 572	7	1.9	411	17	US-10-424-599-117379	Sequence 117379, A	645	7	1.9	453	18	US-10-425-115-71694	Sequence 71694, A
c 573	7	1.9	411	17	US-10-085-783A-44077	Sequence 44077, A	646	7	1.9	454	13	US-10-027-632-89646	Sequence 89646, A
c 574	7	1.9	411	18	US-10-437-963-41061	Sequence 41061, A	647	7	1.9	454	17	US-10-027-632-89646	Sequence 89646, A
575	7	1.9	412	10	US-09-918-995-3007	Sequence 3007, Ap	c 648	7	1.9	455	10	US-09-918-995-21800	Sequence 21800, A
c 576	7	1.9	412	13	US-10-027-632-309030	Sequence 309030, A	649	7	1.9	455	18	US-10-674-124A-6999	Sequence 6999, Ap
c 577	7	1.9	412	17	US-10-027-632-309030	Sequence 309030, A	650	7	1.9	456	10	US-09-918-995-26925	Sequence 26925, A
c 578	7	1.9	413	9	US-09-983-965-407	Sequence 407, App	651	7	1.9	456	18	US-10-425-115-34555	Sequence 34555, A
579	7	1.9	413	14	US-10-198-846-7400	Sequence 7400, Ap	c 652	7	1.9	458	10	US-09-918-995-28818	Sequence 28818, A
c 580	7	1.9	416	10	US-09-918-995-73390	Sequence 73390, A	c 653	7	1.9	459	10	US-09-918-995-27189	Sequence 27189, A

c 654	7	1.9	460	9	US-09-770-444-432	Sequence 432, App	727	7	1.9	495	13	US-10-027-632-193912	Sequence 193912, A
c 655	7	1.9	460	18	US-10-283-975A-598	Sequence 598, App	728	7	1.9	495	17	US-10-027-632-193912	Sequence 193912, A
c 656	7	1.9	460	18	US-10-357-930-9628	Sequence 9628, App	729	7	1.9	496	18	US-10-357-930-9628	Sequence 9628, App
c 657	7	1.9	460	18	US-10-357-930-36089	Sequence 36089, A	730	7	1.9	496	18	US-10-027-632-93416	Sequence 93416, A
c 658	7	1.9	461	9	US-09-770-444-442	Sequence 442, App	731	7	1.9	497	13	US-10-027-632-307754	Sequence 307754, A
c 659	7	1.9	461	18	US-10-357-930-30830	Sequence 30830, A	732	7	1.9	497	13	US-10-027-632-93416	Sequence 93416, A
c 660	7	1.9	461	18	US-10-357-930-39799	Sequence 39799, A	733	7	1.9	497	17	US-10-027-632-307754	Sequence 307754, A
c 661	7	1.9	462	15	US-10-156-761-7438	Sequence 7438, App	734	7	1.9	497	18	US-10-027-632-307754	Sequence 307754, A
c 662	7	1.9	462	17	US-10-425-114-18774	Sequence 18774, A	c 735	7	1.9	498	10	US-10-357-930-59631	Sequence 59631, A
c 663	7	1.9	464	9	US-09-864-761-5412	Sequence 5412, App	c 736	7	1.9	498	10	US-09-318-995-2826	Sequence 2826, App
c 664	7	1.9	464	17	US-10-242-535A-55966	Sequence 55966, A	c 737	7	1.9	500	10	US-09-991-936-662	Sequence 662, App
c 665	7	1.9	464	18	US-10-085-783A-55966	Sequence 55966, A	c 738	7	1.9	501	9	US-09-867-701-2998	Sequence 2998, App
c 666	7	1.9	464	18	US-10-437-963-55501	Sequence 55501, A	c 739	7	1.9	501	13	US-09-814-353-14349	Sequence 14349, A
c 667	7	1.9	466	13	US-10-027-632-95025	Sequence 95025, A	740	7	1.9	501	18	US-10-095-407-6	Sequence 6, Appli
c 668	7	1.9	466	13	US-10-027-632-305639	Sequence 305639, A	741	7	1.9	502	17	US-10-767-701-29192	Sequence 29192, A
c 669	7	1.9	466	17	US-10-027-632-95025	Sequence 95025, A	c 742	7	1.9	503	17	US-10-424-599-64863	Sequence 64863, A
c 670	7	1.9	466	17	US-10-027-632-305639	Sequence 305639, A	743	7	1.9	503	17	US-09-770-961-376	Sequence 376, App
c 671	7	1.9	467	18	US-10-357-930-30977	Sequence 30977, A	744	7	1.9	504	9	US-10-424-599-58265	Sequence 58265, A
c 672	7	1.9	468	9	US-09-864-761-6081	Sequence 6081, App	c 745	7	1.9	504	13	US-09-878-178-1058	Sequence 1058, App
c 673	7	1.9	468	9	US-09-864-761-6081	Sequence 6081, App	c 746	7	1.9	504	13	US-10-046-935-1058	Sequence 1058, App
c 674	7	1.9	469	17	US-10-242-535A-39422	Sequence 39422, A	747	7	1.9	504	13	US-10-027-632-47671	Sequence 47671, A
c 675	7	1.9	469	17	US-10-085-783A-39422	Sequence 39422, A	748	7	1.9	504	13	US-10-027-632-214204	Sequence 214204, A
c 676	7	1.9	469	18	US-10-425-115-120294	Sequence 120294, A	c 749	7	1.9	504	14	US-10-027-632-214205	Sequence 214205, A
c 677	7	1.9	470	11	US-09-732-627A-3406	Sequence 3406, App	c 750	7	1.9	504	17	US-10-146-502-1058	Sequence 1058, App
c 678	7	1.9	471	18	US-10-674-124A-3252	Sequence 3252, App	c 751	7	1.9	504	17	US-10-027-632-47671	Sequence 47671, A
c 679	7	1.9	471	18	US-10-425-115-15821	Sequence 15821, A	752	7	1.9	504	17	US-10-027-632-214204	Sequence 214204, A
c 680	7	1.9	472	17	US-10-424-599-24967	Sequence 24967, A	c 753	7	1.9	505	9	US-09-998-598-1092	Sequence 1092, App
c 681	7	1.9	473	13	US-10-027-632-34455	Sequence 34455, A	754	7	1.9	505	13	US-10-027-632-88655	Sequence 88655, A
c 682	7	1.9	473	13	US-10-027-632-34456	Sequence 34456, A	755	7	1.9	505	13	US-10-027-632-317058	Sequence 317058, A
c 683	7	1.9	473	17	US-10-027-632-34456	Sequence 34456, A	756	7	1.9	505	13	US-10-027-632-88655	Sequence 88655, A
c 684	7	1.9	473	17	US-10-027-632-34456	Sequence 34456, A	757	7	1.9	505	17	US-10-027-632-317058	Sequence 317058, A
c 685	7	1.9	474	10	US-09-918-995-443	Sequence 443, App	c 758	7	1.9	505	17	US-10-425-114-15825	Sequence 15825, A
c 686	7	1.9	474	10	US-09-918-995-21887	Sequence 21887, A	c 759	7	1.9	507	17	US-10-424-599-31226	Sequence 31226, A
c 687	7	1.9	474	10	US-09-918-995-25135	Sequence 25135, A	c 760	7	1.9	507	18	US-10-437-963-23170	Sequence 23170, A
c 688	7	1.9	474	10	US-09-876-790-7	Sequence 7, Appli	c 761	7	1.9	507	18	US-10-437-963-86776	Sequence 86776, A
c 689	7	1.9	474	18	US-10-888-918-7	Sequence 7, Appli	c 762	7	1.9	509	18	US-10-425-115-13553	Sequence 13553, A
c 690	7	1.9	474	18	US-10-888-918-7	Sequence 7, Appli	c 763	7	1.9	509	18	US-10-425-115-13553	Sequence 13553, A
c 691	7	1.9	474	19	US-10-888-867-7	Sequence 7, Appli	c 764	7	1.9	510	18	US-10-425-115-62975	Sequence 62975, A
c 692	7	1.9	474	19	US-10-888-867-7	Sequence 7, Appli	c 765	7	1.9	511	18	US-10-767-701-5525	Sequence 5525, App
c 693	7	1.9	474	19	US-10-888-931-7	Sequence 7, Appli	c 766	7	1.9	512	14	US-10-198-846-9282	Sequence 9282, App
c 694	7	1.9	476	18	US-10-425-115-165935	Sequence 165935, A	c 767	7	1.9	513	13	US-10-027-632-134701	Sequence 134701, A
c 695	7	1.9	477	9	US-09-740-668A-23	Sequence 23, Appli	c 768	7	1.9	513	13	US-10-027-632-194004	Sequence 194004, A
c 696	7	1.9	477	10	US-09-918-995-26538	Sequence 26538, A	c 769	7	1.9	513	17	US-10-027-632-134701	Sequence 134701, A
c 697	7	1.9	480	18	US-10-357-930-59691	Sequence 59691, A	c 770	7	1.9	513	17	US-10-027-632-194004	Sequence 194004, A
c 698	7	1.9	481	10	US-09-918-995-32827	Sequence 32827, A	c 771	7	1.9	513	17	US-10-424-599-69416	Sequence 69416, A
c 699	7	1.9	481	13	US-10-027-632-90999	Sequence 90999, A	c 772	7	1.9	513	18	US-10-437-963-86804	Sequence 86804, A
c 700	7	1.9	481	13	US-10-027-632-317604	Sequence 317604, A	c 773	7	1.9	514	17	US-10-341-961A-188	Sequence 188, App
c 701	7	1.9	481	17	US-10-027-632-90999	Sequence 90999, A	c 774	7	1.9	514	18	US-10-481-179-31	Sequence 31, Appli
c 702	7	1.9	481	17	US-10-027-632-317604	Sequence 317604, A	c 775	7	1.9	515	16	US-10-029-386-8536	Sequence 8536, App
c 703	7	1.9	482	9	US-09-867-701-10792	Sequence 10792, A	c 776	7	1.9	517	13	US-10-027-632-86724	Sequence 86724, A
c 704	7	1.9	483	17	US-10-424-599-102232	Sequence 102232, A	c 777	7	1.9	517	13	US-10-027-632-86725	Sequence 86725, A
c 705	7	1.9	484	18	US-10-425-115-82025	Sequence 82025, A	c 778	7	1.9	517	17	US-10-027-632-86724	Sequence 86724, A
c 706	7	1.9	486	17	US-10-424-599-133264	Sequence 133264, A	c 779	7	1.9	517	17	US-10-027-632-86725	Sequence 86725, A
c 707	7	1.9	486	18	US-10-767-701-27673	Sequence 27673, A	c 780	7	1.9	518	17	US-10-424-599-13584	Sequence 13584, A
c 708	7	1.9	487	11	US-09-732-627A-551	Sequence 551, App	c 781	7	1.9	519	9	US-09-734-017A-29	Sequence 29, Appli
c 709	7	1.9	488	10	US-09-918-995-27044	Sequence 27044, A	c 782	7	1.9	519	10	US-09-770-961-55	Sequence 55, Appli
c 710	7	1.9	488	13	US-10-027-632-85966	Sequence 85966, A	c 783	7	1.9	519	17	US-10-424-599-24575	Sequence 24575, A
c 711	7	1.9	488	13	US-10-027-632-238139	Sequence 238139, A	c 784	7	1.9	519	18	US-10-021-323-10093	Sequence 10093, A
c 712	7	1.9	488	13	US-10-027-632-316237	Sequence 316237, A	c 785	7	1.9	520	16	US-09-918-995-28356	Sequence 28356, A
c 713	7	1.9	488	17	US-10-027-632-85966	Sequence 85966, A	c 786	7	1.9	520	16	US-10-029-386-10852	Sequence 10852, A
c 714	7	1.9	488	17	US-10-027-632-238139	Sequence 238139, A	c 787	7	1.9	520	18	US-10-767-701-15904	Sequence 15904, A
c 715	7	1.9	488	17	US-10-027-632-316237	Sequence 316237, A	c 788	7	1.9	521	13	US-10-027-632-265935	Sequence 265935, A
c 716	7	1.9	491	13	US-10-027-632-304334	Sequence 304334, A	c 789	7	1.9	521	17	US-10-027-632-265935	Sequence 265935, A
c 717	7	1.9	491	17	US-10-027-632-304334	Sequence 304334, A	c 790	7	1.9	521	17	US-10-424-599-91106	Sequence 91106, A
c 718	7	1.9	492	9	US-09-867-701-5958	Sequence 5958, App	c 791	7	1.9	522	9	US-09-974-300-6617	Sequence 6617, App
c 719	7	1.9	493	17	US-10-424-599-47714	Sequence 47714, A	c 792	7	1.9	523	10	US-09-764-891-1863	Sequence 1863, App
c 720	7	1.9	493	18	US-10-425-115-10108	Sequence 10108, A	c 793	7	1.9	523	11	US-09-732-627A-522	Sequence 522, App
c 721	7	1.9	494	10	US-09-318-995-38027	Sequence 38027, A	c 794	7	1.9	523	13	US-10-027-632-191086	Sequence 191086, A
c 722	7	1.9	494	13	US-10-027-632-245898	Sequence 245898, A	c 795	7	1.9	523	17	US-10-027-632-191086	Sequence 191086, A
c 723	7	1.9	494	17	US-10-027-632-245898	Sequence 245898, A	c 796	7	1.9	523	18	US-10-767-795-2981	Sequence 2981, App
c 724	7	1.9	494	18	US-10-425-115-40738	Sequence 40738, A	c 797	7	1.9	523	18	US-10-425-115-183364	Sequence 183364, A
c 725	7	1.9	495	9	US-09-822-830A-565	Sequence 565, App	c 798	7	1.9	524	18	US-10-021-323-14636	Sequence 14636, A
c 726	7	1.9	495	10	US-09-814-353-13428	Sequence 13428, A	c 799	7	1.9	525	14	US-10-198-846-11871	Sequence 11871, A

800	7	1.9	525	18	US-10-021-323-10401	Sequence 10401, A	c 873	7	1.9	551	9	US-09-764-860-741	Sequence 741, App
801	7	1.9	525	18	US-10-767-701-26508	Sequence 26508, A	c 874	7	1.9	551	9	US-09-764-860-742	Sequence 742, App
802	7	1.9	529	9	US-09-864-761-7378	Sequence 7378, Ap	c 875	7	1.9	551	14	US-10-074-095-741	Sequence 741, App
803	7	1.9	529	18	US-10-021-323-14399	Sequence 14399, A	c 876	7	1.9	551	14	US-10-074-095-742	Sequence 742, App
804	7	1.9	530	18	US-10-021-323-14680	Sequence 14680, A	c 877	7	1.9	551	15	US-10-106-698-2550	Sequence 2550, Ap
805	7	1.9	531	10	US-09-814-353-13041	Sequence 13041, A	c 878	7	1.9	551	17	US-10-212-872-741	Sequence 741, App
806	7	1.9	531	10	US-09-814-353-19269	Sequence 19269, A	c 879	7	1.9	551	17	US-10-212-872-742	Sequence 742, App
807	7	1.9	531	13	US-10-027-632-90686	Sequence 90686, A	c 880	7	1.9	552	13	US-10-027-632-308834	Sequence 308834, App
808	7	1.9	531	13	US-10-027-632-317484	Sequence 317484, A	c 881	7	1.9	552	17	US-10-027-632-308834	Sequence 308834, App
809	7	1.9	531	17	US-10-027-632-90686	Sequence 90686, A	c 882	7	1.9	552	17	US-10-260-238-4263	Sequence 4263, Ap
810	7	1.9	531	17	US-10-027-632-317484	Sequence 317484, A	c 883	7	1.9	552	18	US-10-437-963-83509	Sequence 83509, A
811	7	1.9	533	13	US-10-027-632-92528	Sequence 92528, A	c 884	7	1.9	553	13	US-10-027-632-226732	Sequence 226732, App
812	7	1.9	533	13	US-10-027-632-128968	Sequence 128968, A	c 885	7	1.9	553	13	US-10-027-632-226733	Sequence 226733, App
813	7	1.9	533	13	US-10-027-632-234056	Sequence 234056, A	c 886	7	1.9	553	13	US-10-027-632-226734	Sequence 226734, App
814	7	1.9	533	13	US-10-027-632-307628	Sequence 307628, A	c 887	7	1.9	553	13	US-10-027-632-226735	Sequence 226735, App
815	7	1.9	533	17	US-10-027-632-92528	Sequence 92528, A	c 888	7	1.9	553	17	US-10-027-632-226733	Sequence 226733, App
816	7	1.9	533	17	US-10-027-632-128968	Sequence 128968, A	c 889	7	1.9	553	17	US-10-027-632-226733	Sequence 226733, App
817	7	1.9	533	17	US-10-027-632-234056	Sequence 234056, A	c 890	7	1.9	553	17	US-10-027-632-226734	Sequence 226734, App
818	7	1.9	533	17	US-10-027-632-307628	Sequence 307628, A	c 891	7	1.9	553	17	US-10-027-632-226735	Sequence 226735, App
819	7	1.9	534	13	US-10-095-407-3	Sequence 3, Appli	c 892	7	1.9	553	18	US-10-647-628A-46	Sequence 46, Appli
820	7	1.9	535	18	US-10-021-323-1524	Sequence 1524, Ap	c 893	7	1.9	554	18	US-10-425-115-58000	Sequence 58000, A
821	7	1.9	535	18	US-10-767-701-28329	Sequence 28329, A	c 894	7	1.9	554	18	US-10-027-632-87364	Sequence 87364, A
822	7	1.9	535	18	US-10-425-115-158988	Sequence 158988, A	c 895	7	1.9	555	13	US-10-027-632-87365	Sequence 87365, A
823	7	1.9	536	13	US-10-027-632-130786	Sequence 130786, A	c 896	7	1.9	555	13	US-10-027-632-269719	Sequence 269719, App
824	7	1.9	536	13	US-10-027-632-193388	Sequence 193388, A	c 897	7	1.9	555	13	US-10-027-632-269720	Sequence 269720, App
825	7	1.9	536	13	US-10-027-632-193389	Sequence 193389, A	c 898	7	1.9	555	13	US-10-027-632-269721	Sequence 269721, App
826	7	1.9	536	13	US-10-027-632-193390	Sequence 193390, A	c 899	7	1.9	555	13	US-10-027-632-303587	Sequence 303587, App
827	7	1.9	536	13	US-10-027-632-193391	Sequence 193391, A	c 900	7	1.9	555	13	US-10-027-632-303588	Sequence 303588, App
828	7	1.9	536	17	US-10-027-632-130786	Sequence 130786, A	c 901	7	1.9	555	17	US-10-027-632-87364	Sequence 87364, A
829	7	1.9	536	17	US-10-027-632-193388	Sequence 193388, A	c 902	7	1.9	555	17	US-10-027-632-87365	Sequence 87365, A
830	7	1.9	536	17	US-10-027-632-193389	Sequence 193389, A	c 903	7	1.9	555	17	US-10-027-632-269719	Sequence 269719, App
831	7	1.9	536	17	US-10-027-632-193390	Sequence 193390, A	c 904	7	1.9	555	17	US-10-027-632-269720	Sequence 269720, App
832	7	1.9	536	17	US-10-027-632-193391	Sequence 193391, A	c 905	7	1.9	555	17	US-10-027-632-269721	Sequence 269721, App
833	7	1.9	537	13	US-10-027-632-181646	Sequence 181646, A	c 906	7	1.9	555	17	US-10-027-632-303587	Sequence 303587, App
834	7	1.9	537	13	US-10-027-632-318797	Sequence 318797, A	c 907	7	1.9	555	17	US-10-027-632-303588	Sequence 303588, App
835	7	1.9	537	13	US-10-027-632-318798	Sequence 318798, A	c 908	7	1.9	557	10	US-09-918-995-26912	Sequence 26912, A
836	7	1.9	537	17	US-10-027-632-181646	Sequence 181646, A	c 909	7	1.9	557	10	US-09-814-353-267	Sequence 267, App
837	7	1.9	537	17	US-10-027-632-318797	Sequence 318797, A	c 910	7	1.9	558	18	US-09-814-353-6656	Sequence 6656, Ap
838	7	1.9	537	17	US-10-027-632-318798	Sequence 318798, A	c 911	7	1.9	558	18	US-10-425-115-11233	Sequence 11233, A
839	7	1.9	538	18	US-10-767-701-28179	Sequence 28179, A	c 912	7	1.9	559	9	US-09-864-761-16511	Sequence 16511, A
840	7	1.9	538	18	US-10-767-795-4828	Sequence 4828, Ap	c 913	7	1.9	559	18	US-10-425-115-124033	Sequence 124033, App
841	7	1.9	539	16	US-10-029-386-10882	Sequence 10882, A	c 914	7	1.9	559	18	US-10-425-115-124033	Sequence 124033, App
842	7	1.9	542	9	US-09-974-300-4868	Sequence 4868, Ap	c 915	7	1.9	559	18	US-10-425-115-158315	Sequence 158315, App
843	7	1.9	542	13	US-10-027-632-299072	Sequence 299072, A	c 916	7	1.9	560	13	US-10-027-632-108918	Sequence 108918, App
844	7	1.9	542	13	US-10-027-632-306625	Sequence 306625, A	c 917	7	1.9	560	13	US-10-027-632-313290	Sequence 313290, App
845	7	1.9	542	13	US-10-027-632-306626	Sequence 306626, A	c 918	7	1.9	560	17	US-10-027-632-108918	Sequence 108918, App
846	7	1.9	542	17	US-10-027-632-299072	Sequence 299072, A	c 919	7	1.9	561	17	US-10-027-632-313290	Sequence 313290, App
847	7	1.9	542	17	US-10-027-632-306625	Sequence 306625, A	c 920	7	1.9	561	17	US-10-027-632-74099	Sequence 74099, A
848	7	1.9	542	17	US-10-027-632-306626	Sequence 306626, A	c 921	7	1.9	561	18	US-10-021-323-16973	Sequence 16973, A
849	7	1.9	543	18	US-10-767-701-27086	Sequence 27086, A	c 922	7	1.9	561	18	US-10-021-323-16973	Sequence 16973, A
850	7	1.9	543	18	US-10-027-632-289460	Sequence 289460, A	c 923	7	1.9	563	13	US-10-425-115-94301	Sequence 94301, A
851	7	1.9	544	17	US-10-027-632-289460	Sequence 289460, A	c 924	7	1.9	563	17	US-10-027-632-45651	Sequence 45651, A
852	7	1.9	545	13	US-10-027-632-40156	Sequence 40156, A	c 925	7	1.9	563	17	US-10-027-632-45651	Sequence 45651, A
853	7	1.9	545	17	US-10-027-632-40156	Sequence 40156, A	c 926	7	1.9	563	17	US-10-369-493-30010	Sequence 30010, A
854	7	1.9	546	17	US-10-424-599-88281	Sequence 88281, A	c 927	7	1.9	563	18	US-10-021-323-16691	Sequence 16691, A
855	7	1.9	547	10	US-09-997-003-18	Sequence 18, Appli	c 928	7	1.9	564	13	US-10-425-115-149027	Sequence 149027, App
856	7	1.9	547	13	US-10-027-632-116133	Sequence 116133, A	c 929	7	1.9	564	13	US-10-027-632-92940	Sequence 92940, A
857	7	1.9	547	13	US-10-027-632-253039	Sequence 253039, A	c 930	7	1.9	564	13	US-10-027-632-92941	Sequence 92941, A
858	7	1.9	547	17	US-10-027-632-116133	Sequence 116133, A	c 931	7	1.9	564	13	US-10-027-632-137712	Sequence 137712, App
859	7	1.9	547	17	US-10-027-632-253039	Sequence 253039, A	c 932	7	1.9	564	17	US-10-027-632-217638	Sequence 217638, App
860	7	1.9	547	17	US-10-027-632-253039	Sequence 253039, A	c 933	7	1.9	564	17	US-10-027-632-217639	Sequence 217639, App
861	7	1.9	547	18	US-10-357-930-21420	Sequence 21420, A	c 934	7	1.9	564	17	US-10-424-599-32561	Sequence 32561, A
862	7	1.9	547	18	US-10-357-930-27261	Sequence 27261, A	c 935	7	1.9	564	18	US-10-425-115-63698	Sequence 63698, A
863	7	1.9	548	18	US-10-425-115-136172	Sequence 136172, A	c 936	7	1.9	564	17	US-10-027-632-92941	Sequence 92941, A
864	7	1.9	549	13	US-10-027-632-283605	Sequence 283605, A	c 937	7	1.9	564	17	US-10-027-632-137712	Sequence 137712, App
865	7	1.9	549	16	US-10-029-386-8947	Sequence 8947, Ap	c 938	7	1.9	564	17	US-10-027-632-217639	Sequence 217639, App
866	7	1.9	549	16	US-10-029-386-3008	Sequence 3008, Ap	c 939	7	1.9	564	17	US-10-027-632-217639	Sequence 217639, App
867	7	1.9	549	17	US-10-027-632-283605	Sequence 283605, A	c 940	7	1.9	564	18	US-10-425-115-63698	Sequence 63698, A
868	7	1.9	549	17	US-10-260-238-5635	Sequence 5635, Ap	c 941	7	1.9	565	9	US-10-357-930-60527	Sequence 60527, A
869	7	1.9	550	13	US-10-027-632-130449	Sequence 130449, A	c 942	7	1.9	565	9	US-09-864-761-9830	Sequence 9830, Ap
870	7	1.9	550	17	US-10-027-632-130449	Sequence 130449, A	c 943	7	1.9	566	13	US-10-027-632-93735	Sequence 93735, A
871	7	1.9	550	18	US-10-425-115-23805	Sequence 23805, A	c 944	7	1.9	566	13	US-10-027-632-318293	Sequence 318293, App
872	7	1.9	550	18	US-10-425-115-150227	Sequence 150227, A	c 945	7	1.9	566	17	US-10-027-632-93735	Sequence 93735, A

```
946 7 1.9 566 17 US-10-027-632-318293, Sequence 318293,
947 7 1.9 566 17 US-10-242-535A-46367, Sequence 46367, A
948 7 1.9 566 17 US-10-085-783A-46367, Sequence 46367, A
949 7 1.9 566 18 US-10-357-930-50406, Sequence 50406, A
950 7 1.9 567 17 US-10-369-493-29136, Sequence 29136, A
951 7 1.9 567 17 US-10-424-599-57070, Sequence 57070, A
952 7 1.9 567 18 US-10-425-115-102573, Sequence 102573, A
953 7 1.9 568 17 US-10-424-599-27796, Sequence 27796, A
954 7 1.9 569 9 US-09-864-761-12731, Sequence 12731, A
955 7 1.9 569 14 US-10-181-642-17, Sequence 17, Appl
956 7 1.9 569 17 US-10-257-294-70, Sequence 70, Appl
957 7 1.9 569 17 US-10-257-294-71, Sequence 71, Appl
958 7 1.9 569 18 US-10-809-654-17, Sequence 17, Appl
959 7 1.9 569 18 US-10-809-655-17, Sequence 17, Appl
960 7 1.9 570 18 US-10-425-115-110416, Sequence 110416, A
961 7 1.9 571 13 US-10-027-632-81980, Sequence 81980, A
962 7 1.9 571 17 US-10-027-632-81990, Sequence 81990, A
963 7 1.9 571 18 US-10-653-047-3969, Sequence 3969, Ap
964 7 1.9 572 13 US-10-027-632-220249, Sequence 220249, A
965 7 1.9 572 13 US-10-027-632-320963, Sequence 320963, A
966 7 1.9 572 17 US-10-027-632-220249, Sequence 220249, A
967 7 1.9 572 17 US-10-027-632-320963, Sequence 320963, A
968 7 1.9 573 13 US-10-002-344A-28, Sequence 28, Appl
969 7 1.9 573 13 US-10-027-632-192226, Sequence 19226, A
970 7 1.9 573 17 US-10-027-632-19226, Sequence 19226, A
971 7 1.9 574 9 US-09-864-761-7102, Sequence 7102, Ap
972 7 1.9 574 16 US-10-029-386-6596, Sequence 6596, Ap
973 7 1.9 574 17 US-10-424-599-83722, Sequence 83722, A
974 7 1.9 574 18 US-10-425-115-119468, Sequence 119468, A
975 7 1.9 575 17 US-10-424-599-105472, Sequence 105472, A
976 7 1.9 575 18 US-10-437-963-86588, Sequence 86588, A
977 7 1.9 576 9 US-09-778-320-146, Sequence 146, App
978 7 1.9 576 9 US-09-770-152-215, Sequence 215, App
979 7 1.9 576 9 US-09-864-761-7169, Sequence 7169, Ap
980 7 1.9 576 9 US-09-910-689-146, Sequence 146, App
981 7 1.9 576 13 US-10-010-742-146, Sequence 146, App
982 7 1.9 576 18 US-10-714-389-146, Sequence 146, App
983 7 1.9 576 18 US-10-717-296-146, Sequence 146, App
984 7 1.9 577 13 US-10-027-632-213527, Sequence 213527, A
985 7 1.9 577 13 US-10-027-632-213528, Sequence 213528, A
986 7 1.9 577 17 US-10-027-632-213527, Sequence 213527, A
987 7 1.9 577 17 US-10-027-632-213528, Sequence 213528, A
988 7 1.9 578 13 US-10-027-632-198019, Sequence 198019, A
989 7 1.9 578 13 US-10-027-632-225913, Sequence 225913, A
990 7 1.9 578 16 US-10-029-386-12911, Sequence 12911, A
991 7 1.9 578 17 US-10-027-632-198019, Sequence 198019, A
992 7 1.9 578 17 US-10-027-632-225913, Sequence 225913, A
993 7 1.9 579 10 US-09-876-790-1, Sequence 45179, A
994 7 1.9 579 10 US-09-876-790-1, Sequence 45179, A
995 7 1.9 579 17 US-10-282-122A-37838, Sequence 37838, A
996 7 1.9 579 18 US-10-425-115-112778, Sequence 112778, A
997 7 1.9 579 18 US-10-888-918-1, Sequence 1, Appli
998 7 1.9 579 19 US-10-888-918-1, Sequence 1, Appli
999 7 1.9 579 19 US-10-888-918-1, Sequence 1, Appli
1000 7 1.9 579 19 US-10-888-918-1, Sequence 1, Appli
```

ALIGNMENTS

```
RESULT 1
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JF96/02905
```

```
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 0 Length: 1134
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-1 (1-377) x US-09-736-250-2 (1-1134)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAGACACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCATATCAGAAATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAATTAATTCATGGTGCCAAACCTCAAGTACCAATTC AAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTGGCTAGCAGATCTTTGGATAGGTTTGTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATATCTTGGATTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGTAATTGGCAGACAGACAGTTCTGT 360
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGGAGAAATTTCTGGATAAGTTGAAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGGATTTCCTCATATTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCCTCAGTTACTTTTTCAGTTTCCCAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTCATGTCCTGCAACCAACTCTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAAATCTCATTTCTGTTGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACAATTCAGATGCTTCAGAAAGACAGATGATGATGATGATGATGATGATGATGATG 720
Qy 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTCACATCATCCCTTTCTACTCTGAGTCTTCTCCCTGCTCTGAAATTCGTTAT 780
```

```
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACACCTCGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCAGGCCAGACTTCTCCAGAGNCAACAGCAAGCCAGAGTGCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACTTCTATGATGGAAATCAAAACGGGTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGTTTCAGAAATGTGGTCTGTGTGGACATGATTTATCAAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCCTGTTCTGTCTCATG 1131
RESULT 2
US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 17 Gaps: 0
US-09-736-250-1 (1-377) x US-10-172-118-1326 (1-1260)
QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGCGCTTTGGAAACACAGAGATTGTCTTCTCTGTGGAAAGGCAATC 60
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGAAGCACAGATGTGGAAGTGAATGTGCGGAAATGCCCTTCAATCAGAAATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 1131 TATATGAGATATATGTTTCAGAAATGTGGTCTGTGTGGACATGATTTATCAAGA 1080
```

```
Db 121 TCTCCATCCCGAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
QY 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCGTA 240
QY 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAAGTTGATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGGAGAGATGAGAGATTCAGACTACTAAAGTATTTGGCAGAGACAGTTTCTGT 360
QY 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTTCAGAAATGAGAGAAATTAATTCGGATAAGTTGAATGG 420
QY 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTACACAGCCACCATTCGATTTCTTCATATTTTCCATGTCATTTGCAAGTGTCA 480
QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTACTGTATGGCTTGCACCAACCAACTCTGCAATTTGAGGATCC 600
QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGTCTCGCCATGGTTAGTCTGGAATGAGAAACTCATTTCTGATGGCTTTCT 660
QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACATTTGACTGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTCATTCATTTGTCGG 720
QY 241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACCTTTTACTCTGCAGTCTTCCCTGCTCTGAAATTCGTTTAT 780
QY 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
QY 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTCCAGGCCACAGACTTCTCCAGAGCAACAGCAAGCCAGAGTGCAGTC 900
QY 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTGCAGTGGGTGCAAGCAGACCTCT 960
QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysArgLeu 340
Db 961 ACTAAACCAAGTAGAGAAATGGAAGTGAATGATGATGATGGAATCAAAACGGGTC 1020
QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATATGAGATATATGTTTCAGAAATGTGGTCTGTGTGGACATGATTTATCAAGA 1080
QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTCAGCCCTGTTCTGTCTCATG 1131
RESULT 3
US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
```

APPLICANT: Linsley, Peter S.
APPLICANT: Mao, Mao
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
PRIORITY FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1326
LENGTH: 1260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:
Pred. No.: 0
Score: 377.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
Indels: 0
Gaps: 17

US-09-736-250-1 (1-377) x US-10-342-887-1326 (1-1260)

QY 1 MetLysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATTGTTCTTCTGTTGGAAAGCCAAATC 60

QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGGAAAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT 120

QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAATCAATGGCTGGCCAAACTCAAGTACCAATTCAC 180

QY 61 LeuTyTrpGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTGCTCTGGCTAGCAGTCTTTTGGATAGTTTTCAGTACCGTA 240

QY 81 LysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGAGTTGTATTGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

QY 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGACAGATTCTGT 360

QY 121 GlyCysSerSerSerGluLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAAGTTCAATTGG 420

QY 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACCAATGGATTTCTTCATATTTTCCATGTCATGTCAGTGTCA 480

QY 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTACTTTTCAGTTTGGCCAAATTTGAGCCCACTCAACATTTGGCAGTC 540

QY 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600

QY 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTTAGTCTGAAATGGAGAACTCATCTCTGATTGCTTCT 660

QY 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 661 CTTACAAATTGAATGCTTCAGAAAGCACAGATGATAGTCCCAAGTTGATCCATTGTCGG 720

QY 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyTrp 260
Db 721 GAGCTTGTGGCACAATCACTTTTACTCTGAGTCTTCCCTGCTCTGAATTCGGTTTAT 780

QY 261 ValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGTGTGACCTGTGACAAAGAGGTTCAGATTACAT 840

QY 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGTCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTCCAGTC 900

QY 301 ArgGlyThrAlaAlaPheTyTrpHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGTACAGAGCCCTTTTACCACATCTCCAGCTGCCAGTGGGTGCAAGACACTCT 960

QY 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyTrpAspGlyIleLysArgLeu 340
Db 961 ACTAAACGCAAGGTAGAGGAAATGGAAATGGATGACTTCTATGATGGAATCAACGGCTC 1020

QY 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1021 TATAATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGTGCACTGATTTATCAAGA 1080

QY 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1081 CAAGAGGAGACATGCTTCCCTTTGTCACCTTTGAGCCCTGTTTCTGTGTCATG 1131

RESULT 4

US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 899:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1260 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK

; CLONE: g1183161

; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :

US-10-641-643-899

Alignment Scores:

Pred. No.:	0	Length:	1260
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	17	Gaps:	0

US-09-736-250-1 (1-377) x US-10-641-643-899 (1-1260)

Qy	1	MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle	20
Db	1	ATGAAGTTTCAGGGCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC	60
Qy	21	ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal	40
Db	61	ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT	120
Qy	41	SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn	60
Db	121	TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATCAAC	180
Qy	61	LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal	80
Db	181	CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTA	240
Qy	81	LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys	100
Db	241	AAGGCTCATCCAAATACTTGAAGTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG	300
Qy	101	ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys	120
Db	301	ACTGTGAGGAAGATGAGAGAAATCCAGTACTAAGGTATTGGCAAGACAGATTTCTGT	360
Qy	121	GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp	140
Db	361	GGATGTTCTCATCTGAATTTTGGAAATGGAGAGAAATATTCTGGATAAGTTGAATGG	420
Qy	141	AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer	160
Db	421	GATCTTCACAGCCACACACCATGATGATTTTCTCATATTTTCCATGCTCCATGCAATG	480
Qy	161	ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal	180
Db	481	ACTAGGCTCTAGTTACTTTTCAAGTTTGGCCAAATGGAGCCCATCTCAACATTTGGCAGTC	540
Qy	181	LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer	200
Db	541	CTTACCAGCAACTACTTCTCATGTATGGCTGGCAACCAACTTCTGCAATTCAGAGATCC	600
Qy	201	MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer	220
Db	601	ATGCTTGCTCTGGCCATGTTAGTCTGGAATGGAGAAACTCATTTCTGATTTGCTTCT	660
Qy	221	LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg	240
Db	661	CTTCAATTTGAATGCTTTTCAAGAAAGCACAGATGGATAGCTCCCAATTCATTTGTCGG	720
Qy	241	GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr	260
Db	721	GAGCTTGGGCACATCACCTTTTCTACTCTGCAGTCTTCCCTGCTGCAATTCGTTAT	780

Qy	261	ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis	280
Db	781	GTCTACCGTCCCTCTCAAGCACACCCCTGTGACCTGTGACAAAGAGTGTTCAGATTACAT	840
Qy	281	ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal	300
Db	841	CCCTCCTCTGTCCAGGCCAGACTTCTCCAGGACCAACAGCAAGCCAGAGTCCAGTC	900
Qy	301	ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer	320
Db	901	AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGTGCAGACACCTCT	960
Qy	321	ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu	340
Db	961	ACTAAACGCAAGTAGAGGAATGGAAAGTGGATGACTTCTATGATGGAATCAAACGGCTC	1020
Qy	341	TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg	360
Db	1021	TATAATGAAGATATATGCTCAGAAATGTGGTCTGTGTGGCACTGATTTATCAAGA	1080
Qy	361	GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet	377
Db	1081	CAAGAGGACATGCTTCCCTTGTCCACCTTGCAGCCTGTTTCTGTCTATG 1131	

RESULT 5

US-09-867-701-10907

; Sequence 10907, Application US/09867701

; Patent No. US20020132237A1

; GENERAL INFORMATION:

; APPLICANT: Aglate, Paul A.

; APPLICANT: Jones, Robert

; APPLICANT: Harlocker, Susan L.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.497

; CURRENT APPLICATION NUMBER: US/09/867,701

; CURRENT FILING DATE: 2001-05-29

; NUMBER OF SEQ ID NOS: 10912

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 10907

; LENGTH: 1889

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-867-701-10907

Alignment Scores:

Pred. No.:	0	Length:	1889
Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-736-250-1 (1-377) x US-09-867-701-10907 (1-1889)

Qy	1	MethLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle	20
Db	544	ATGAAGTTTCAGGGCCTTGGAAACACAGAGATTGCTTTCCTGTTGGAAAGGCAATC	603
Qy	21	ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal	40
Db	604	ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT	663
Qy	41	SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn	60
Db	664	TCTCCATCCAGAGAGATGAAGTAAATTCATGCTGGCCAAACTCAAGTACCAATTCAC	723
Qy	61	LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal	80
Db	724	CTTTACCAGAAACATTTGCTCTGCTGCTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTA	783
Qy	81	LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys	100

```
Db 784 AAGGCTCATCCAAATACCTGAGTGTATTGCAATCAGCTGTTTCTAGCTGCCAAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAAGATGAGAGAATCCAGTAAAGGATTATGCGAAGACAGACTTCTGT 903
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 904 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGATTAATCTGGATAGTTGAATGG 963
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGCCACACCATGATGATTTCTTCATATTTCCATGTCATTCAGTGTC 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGGCCCAATCTCAACATTTGGCAGTC 1083
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 1084 CTTACCAAGCACTACTTCACTGTATGGCTGCAACCACTCTGCAATTCAGAGGATCC 1143
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 1144 ATGCTTGCTCTGGCCATGGTGTAGTCTGGAATGAGAAACTCAITCTCTGATGGCTTCT 1203
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTACATTTGAATGCTCTCAGAACAGCAGATGGATAGTCTCCAGTTGATCCATGTCGG 1263
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db 1264 GAGCTGTGGCAGATCACCTTTCTACTCTGCAGTCTTCCCTGCCTCTGAAATTCGTTAT 1323
Qy 261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTCAACGACACCCCTGGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCCTCTCTGTCGCGCCGAGACTTCTCCAGAGACACACAGCAAGCCAGAGTCCAGTC 1443
Qy 301 ArgGlyThrAlaAlaPheTyHisLeuProAlaSerGlyCysLysGlnThrSer 320
Db 1444 AGAGTACAGCAGCGCTTTTACCATCATCTCCAGCTGCGCAGTGGGTGCAAGCAGACTCT 1503
Qy 321 ThrLysArgLysValGluGluMetGluValAspPhePheTrpAspGlyIleLysArgLeu 340
Db 1504 ACTAACCAGAGTAGAGAAATGGAATGGAGTGATGACTTCTATGATGGAATCAACAGGCTC 1563
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1564 TATAATGAAGATATGCTCAGAAATGTGGTCTCTGTGTGGCATGATTTATCAAGA 1623
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1624 CAAGAGGACATGCTTCCCTTGTCCACCTTTGAGGCTGTTTCTGTCTATG 1674
```

RESULT 6

```
US-09-814-353-21586
; Sequence 21586, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
```

```
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21586
; LENGTH: 2155
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21586
```

Alignment Scores:

```
Pred. No.: 3,73e-263 Length: 2755
Score: 266.00 Matches: 266
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 70.56% Indels: 0
DB: 10 Gaps: 0
```

US-09-736-250-1 (1-377) x US-09-814-353-21586 (1-2755)

```
Qy 103 GluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
Db 1099 GAGGAGATGAGAGATTTCCAGTACTAAAGTATTTGGCAGAGACAGTTTCTGTGATGT 1158
Qy 123 SerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeu 142
Db 1159 TCCTCATCTCAAAATTTTGAGATGGAGAAATATTCTGATAAAGTTGAATGGATCTT 1218
Qy 143 HisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArg 162
Db 1219 CACACAGCCACACATTTGGATTTTCTCATATTTTTCATGCCAATTCAGTGTCAACTAGG 1278
Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThr 182
Db 1279 CCTCAGTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTCTTACC 1338
Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeu 202
Db 1339 AAGCAACTACTTCACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTT 1398
Qy 203 AlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThr 222
Db 1399 GCTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATCTCTGATTTGGCTTCTCTTACA 1458
Qy 223 IleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGlyLeu 242
Db 1459 ATTGAATCTGCTTCAGAAAGCACAGATGGATAGTCTCCAGTTGATCCATTTGTCGGAGCTT 1518
Qy 243 ValAlaHisIleLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrpValTrp 262
Db 1519 GTGGCATCATCCTTTCTACTCTGCGAGTCTTCCCTGCCCTCTGAAATTCGATTTATGTCTAC 1578
Qy 263 ArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSer 282
Db 1579 CGTCCCTCCAGCAGACACCTTGGTGGCTGTGACAAAGAGTGTTCAGATTACATCCCTCC 1638
Qy 283 SerValProGlyProAspPheSerLysAspAsnSerLysProGluValProValArgGly 302
Db 1639 TCTGTCCCGAGCCAGACTTCTCCAGGAGCAACAGCAAGCAGAGTCCAGTCCAGAGGT 1698
Qy 303 ThrAlaAlaPheTyHisIleLeuProAlaAlaSerGlyCysLysGlnThrSerThrLys 322
Db 1699 ACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGGTGCAGAGCAGACCTCTACTAAA 1758
```


Qy 323 ArgLysValGluGluMetGluValAspPheTyrAspGlyLeuLysArgLeuTyrAsn 342
Db 1759 CGCAAGTAGAGGAATGGAATGGATGACTTCTATGATGGAATCAACGGCTCTATAAT 1818
Qy 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
Db 1819 GAAGATAATGCTCAGAAATGTTGGTCTGTGTGGCACTGATTTATCAAGACAAGAG 1878
Qy 363 GlyHisAlaSerProCys 368
Db 1879 GGACATGCTTCCCTTGT 1896

RESULT 7

US-10-242-535A-16032
; Sequence 16032, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-16032

Alignment Scores:

Pred. No.: 3,84e-133 Length: 444
Score: 139.00 Matches: 139
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.87% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-16032 (1-444)

Qy 124 SerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGGAGAGAAATTTCTGGATAAGTTGAAATGGATCTTCAC 62
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTCTTCATATTTTCCATGCAATTCGAGTAGTCAACTAGGCGCT 122
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCACTTCTGCAATTCAGAGGATCCATGCTTAC 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAACTACTTCACTGTATGGCCCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCATGGTTAGTCTGGAAATGGAGAAATCTCATTTCTGATTTGGCTTTCTTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 303 GAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTGATCCATTTGTCGGAGGCTTGTG 362

Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 363 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTTATGTCTAC 419

RESULT 8

US-10-085-783A-16032
; Sequence 16032, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16032
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-16032

Alignment Scores:

Pred. No.: 3,84e-133 Length: 444
Score: 139.00 Matches: 139
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 36.87% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-16032 (1-444)

Qy 124 SerSerGluLeuLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHis 143
Db 3 TCATCTGAAATTTTGAGAAATGGAGAGAAATTTCTGGATAAGTTGAAATGGATCTTCAC 62
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 63 ACAGCCACACCATTTGGATTTCTTCATATTTTCCATGCAATTCGAGTAGTCAACTAGGCGCT 122
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 123 CAGTTACTTTTCAGTTTGGCCCAATTTGAGCCCACTTCAACATTTTGGCAGTCTTACCAAG 182
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAla 203
Db 183 CAACTACTTCACTGTATGGCCCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTTGT 242
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 243 CTGGCCATGGTTAGTCTGGAAATGGAGAAATCTCATTTCTGATTTGGCTTTCTTACAAAT 302
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 303 GAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTGATCCATTTGTCGGAGGCTTGTG 362
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
Db 363 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGGTTTATGTCTAC 419

RESULT 9

US-10-242-535A-30212
; Sequence 30212, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:


```

; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-30212

Alignment Scores:
Pred. No.: 6,34e-127 Length: 490
Score: 133.00 Matches: 133
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.28% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-30212 (1-490)
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 91 ACAGCCACACCATGGATTTCTTCATATTTTCCATGCCATTCAGTGCCTCACTAGGCT 150
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 151 CAGTTACTTTTTCAGTTTGCCTGAAATGGAGCAATCTCAACATTTGGCAGTCTTACCAAG 210
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeuAla 203
Db 211 CAACATCTTCACTGTATGGCTGCAACCACTTCGCAATTCAGAGATCCATGCTGCT 270
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 271 CTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTGATTCGCTTCTTACCAATT 330
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 331 GAACCTGCTTCAGAAAGCACAGATGATGATCCAGTTGATCCATTCGCGGAGCTTGTG 390
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 391 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATCCGTTTATGCTACCGT 450
Qy 264 ProLeuLysHisThrLeuValThrCysAspLysGlyVal 276
Db 451 CCCCTCAAGCACACCCCTGGTGGACCTGTGACAAAGAGTG 489

RESULT 10
US-10-085-783A-30212
; Sequence 30212, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13

```

```

; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 30212
; LENGTH: 490
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-30212

Alignment Scores:
Pred. No.: 6,34e-127 Length: 490
Score: 133.00 Matches: 133
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.28% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-30212 (1-490)
Qy 144 ThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgPro 163
Db 91 ACAGCCACACCATGGATTTCTTCATATTTTCCATGCCATTCAGTGCCTCACTAGGCT 150
Qy 164 GlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLys 183
Db 151 CAGTTACTTTTTCAGTTTGCCTGAAATGGAGCAATCTCAACATTTGGCAGTCTTACCAAG 210
Qy 184 GlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlySerMetLeuAla 203
Db 211 CAACATCTTCACTGTATGGCTGCAACCACTTCGCAATTCAGAGATCCATGCTGCT 270
Qy 204 LeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIle 223
Db 271 CTGGCCATGGTTAGTCTGGAATGGAGAACTCATCTGATTCGCTTCTTACCAATT 330
Qy 224 GluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuVal 243
Db 331 GAACCTGCTTCAGAAAGCACAGATGATGATCCAGTTGATCCATTCGCGGAGCTTGTG 390
Qy 244 AlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArg 263
Db 391 GCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATCCGTTTATGCTACCGT 450
Qy 264 ProLeuLysHisThrLeuValThrCysAspLysGlyVal 276
Db 451 CCCCTCAAGCACACCCCTGGTGGACCTGTGACAAAGAGTG 489

RESULT 11
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661

```

```
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294

Alignment Scores:
Pred. No.: 5,01e-116 Length: 2146
Score: 123.00 Matches: 149
Percent Similarity: 98.68% Conservative: 0
Best Local Similarity: 98.68% Mismatches: 0
Query Match: 32.63% Indels: 2
DB: 10 Gaps: 0

US-09-736-250-1 (1-377) x US-09-814-353-21294 (1-2146)
Qy 229 AlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisHisLeuSer 248
Db 869 GCCCAGATGGATAGCTCCAGCTTGATCCATTGTGCGGAGCTTGTGGCACAATCACTTTCT 928
Qy 249 ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLeuHisThr 268
Db 929 ACTCTGCAGTCTTCCCTGCTCTGAATTCCTGTTATGTCTACCGTCCCTCAAGCACACC 988
Qy 269 LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp 288
Db 989 CTGTGTACCTGTGCAAGAGGAGTGTTCAGATTACATCCCTCTCTGTCCCGAGCCAGAC 1048
Qy 289 PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis 308
Db 1049 TTCTCCAGGACAACAGCAGACGAGAGTGCCAGTCAGAGGTACAGAGCCTTTTACCAT 1108
Qy 309 HisLeuProAlaAla-SerGlyCysLysGlnThrSer-ThrLysArgLysValGluLum 328
Db 1109 CATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTTACTAAACGCCAAAGTAGAGGAAA 1168
Qy 328 etGluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerG 348
Db 1169 TGAAGTGGATGACTTCTATCATGGAATCAACAGCGCTCTATAATGAAGATTAATGTCTCAG 1228
Qy 348 luAsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProC 368
Db 1229 AAAATGTGGTCTGTGTGGCACTGATTTATCAAGACAGAGGGACATGCTTCCCTT 1288
Qy 368 ysProProLeuGlnProValSerValMet 377
Db 1289 GTCCACCTTTGCAGCCTGTTTCTGTCTCATG 1317

RESULT 12
US-10-242-535A-6834
; Sequence 6834, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
; US-085-783A-6834

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-242-535A-6834

Alignment Scores:
Pred. No.: 1.42e-111 Length: 389
Score: 118.00 Matches: 118
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.30% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-6834 (1-389)
Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 2 AAGTTTCCAGGGCCTTTGGAAACCCACAGATTGTCTTCTCTTGGAAAGGCAATCACT 61
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 62 AGGGAAGCACAGATGTGGAAGTGAATGTGCGGAAAAATGCCCTTCAAAATCAGAAATGTTTCT 121
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 122 CCATCCAGAGAGATGAAGTAATTCATGGCTGCCCAACTCAAGTACCAATCAACCTT 181
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 182 TACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGTAGGTTTTAGCTACCGTAAAG 241
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
Db 242 GCTCATCCAAAATACTTGAAGTTGATTGCAATCAGCTGTTTTTCTCTAGCTGCCAAGACT 301
Qy 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPhe 119
Db 302 GTTGAGGAAGATGAGAGAAATTCAGTAGTAAAGGATTGGCAAGAGACAGATTTC 355

RESULT 13
US-10-085-783A-6834
; Sequence 6834, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085.783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6834
; LENGTH: 389
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (358)..(358)
; OTHER INFORMATION: n is a, c, g, or t
; US-085-783A-6834
```

```
Alignment Scores:
Pred. No.: 1.42e-111 Length: 389
Score: 118.00 Matches: 118
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 31.30% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-6834 (1-389)

QY 2 LysPheProGluProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
DB 2 AAGTTTCCAGGGCCCTTTGGAAAACAGAGATTGTCTTCTCCTGTTGGAAAAGGCAATCACT 61

QY 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
DB 62 AGGGAAGACACAGATGTGGAAAGTGAATGTGGGAAATGCCCTTCAAATCAAGATGTTTCT 121

QY 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrglnPheAsnLeu 61
DB 122 CCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCACCTT 181

QY 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
DB 182 TACCCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGTGTTTTACCTACCGTAAAG 241

QY 82 AlaHisProLysTyrglnSerCysIleAlaIleSerCysPhePheLeuAlaLysThr 101
DB 242 GCTCATCCAAATATCTTGAGTGTGATTCATCAATCAGCTGTTTTTCTAGCTGCCAAGACT 301

QY 102 ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspPhe 119
DB 302 GTTGAAGAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGATTTC 355

RESULT 14
US-10-242-535A-33391
; Sequence 33391, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; PRIOR FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-33391

Alignment Scores:
Pred. No.: 2.03e-105 Length: 369
Score: 112.00 Matches: 112
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.71% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-33391 (1-369)

Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.71% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-242-535A-33391 (1-369)

QY 216 ProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGln 235
DB 28 CCGATTGGCTTTCTCTTACAATTGAATGCTTCAGAAAGCACAGATGGATAGCTCCAG 87

QY 236 LeuIleHisCysArgGluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuPro 255
DB 88 TTGATTCATTGTCGGAGCTTGTGGACATCACCTTTCTACTCTGCAGTCTTCCCTGCT 147

QY 256 LeuAsnSerValTyrglnArgProLeuLysHisThrLeuValThrCysAspLysGly 275
DB 148 CTGAATTCGCTTTATGTCTACCGTCCCTCAAGCACACCTGTGGTGTGACCTGTGACAAAGGA 207

QY 276 ValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLys 295
DB 208 GTGTTCAATTACATCTCTCTGTCAGGCCAGCTTCTCCAAAGGACACAGCAAG 267

QY 296 ProGluValProValArgGlyThrAlaAlaPheTyrglnHisLeuProAlaAlaSerGly 315
DB 268 CCAGAAGTGCAGTACAGGTACAGAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGG 327

QY 316 CysLysGlnThrSerThrLysArgLysValGluGlu 327
DB 328 TGCAAGCAGACCTCTACTAAACGCAAGTAGAGGAA 363

RESULT 15
US-10-085-783A-33391
; Sequence 33391, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 33391
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(2)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (25)..(25)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-085-783A-33391

Alignment Scores:
Pred. No.: 2.03e-105 Length: 369
Score: 112.00 Matches: 112
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 29.71% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-1 (1-377) x US-10-085-783A-33391 (1-369)
```

```
Qy 216 ProAspTrpLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGln 235
Db 28 CCTGATTGGCTTTCTCTTACAATTGAACTGCTTCAGAAAGCACAGATGGATAGCTCCAG 87
Qy 236 LeuIleHisCysArgGluLeuValAlaHisIleLeuSerThrLeuGlnSerSerLeuPro 255
Db 88 TTGATCCATTGTGGGAGCTTGTGGCAGATCACCTTTCTACTCTGCAGTCTTCCCTGCCT 147
Qy 256 LeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAspLysGly 275
Db 148 CTGAATTCGGTTTATGTTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGACAAAGGA 207
Qy 276 ValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLys 295
Db 208 GTGTTTCAGATTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGACAAAGCAAG 267
Qy 296 ProGluValProValArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGly 315
Db 268 CCAGAGTCCAGTCAGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGG 327
Qy 316 CysLysGlnThrSerThrLysArgLysValGluGlu 327
Db 328 TGCAAGCAGACCTCTACTATAACGCAAAAGTAGAGGAA 363
```

Search completed: February 11, 2005, 17:09:05
Job time : 1020.34 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:42:20 ; Search time 5874.84 Seconds
(without alignments)
2442.660 Million cell updates/sec

Title: US-09-736-250-1
Perfect score: 377
Sequence: 1 MKFPGPLENQLSLLEKAI.....LSROEGHASPCLPQPVSVM 377

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 1

Total number of hits satisfying chosen parameters: 68477535

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154942_20659/app.query.fasta_1.718
-DB=EST -QFMT=fastap -SUPFIX=oligo.rst -MINMATCH=0.1 -LGOPL=0 -LGOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DNCALIGN=200 -THR SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 4385 @runat_07022005_154942_20659 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : EST:
1: gb_est1:*
2: gb_est2:*
3: gb_hcc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gsa1:*
9: gb_gsa2:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length	Description
1	261	69.2	903	BU956287 AGENCOURT
2	253	67.1	918	BQ673252 AGENCOURT
3	252	66.8	899	CD358716 AGENCOURT
4	249	66.0	775	BM016042 603642469
5	249	66.0	890	BI858571 603389030
6	246	65.3	764	CB962746 AGENCOURT
7	246	65.3	936	BU501311 AGENCOURT
8	246	65.3	963	BU538306 AGENCOURT
9	244	64.7	920	BQ673277 AGENCOURT

10	243	64.5	862	5	BU149962
11	241	63.9	830	5	EX437607
12	236	62.6	853	5	BU159699
13	235	62.3	764	4	BG205510 RST24889
14	235	62.3	767	4	BG189523 RST8568 A
15	235	62.3	844	4	BG215999 RST35685
16	235	62.3	889	6	CD358161
17	235	62.3	891	5	BU151205
18	233	61.8	946	5	BU558083
19	232	61.5	865	5	BU188239
20	230	61.0	912	5	BQ670517 AGENCOURT
21	226	59.9	884	5	BU188938
22	223	59.2	670	6	CB115197
23	223	59.2	767	4	BG202878
24	221	58.6	751	5	EX422046
25	221	58.6	753	4	BI859488
26	221	58.6	849	4	BG758079
27	221	58.6	959	4	BF972370
28	220	58.4	662	4	BG830200
29	220	58.4	803	5	BQ071740
30	220	58.4	920	5	BU528295
31	218	57.8	752	6	CB998866
32	218	57.8	932	5	BQ669046
33	217	57.6	914	5	BQ894247
34	216	57.3	933	7	CO048817
35	216	57.3	934	7	CN801970
36	216	57.3	946	7	CN647001
37	216	57.3	963	7	CN803219
38	216	57.3	966	7	CN643780
39	216	57.3	978	4	BM463752
40	216	57.3	978	7	CN641931
41	216	57.3	983	7	CN646807
42	215	57.0	674	7	CN403758
43	213	56.5	674	7	CN403761
44	212	56.2	639	7	CV026068
45	209	55.4	790	4	BG198062
46	208	55.2	640	6	CD698834
47	208	55.2	819	5	BU945610
48	208	55.2	960	5	BQ930674
49	207	54.9	661	6	CD689640
50	207	54.9	1023	4	BM423081
51	206	54.6	801	4	BG253045
52	206	54.6	810	5	EX461980
53	206	54.6	841	7	CF552849
54	206	54.6	885	5	BQ671998
55	204	54.1	909	5	BU975546
56	204	54.1	992	7	CO646424
57	203	53.8	615	5	BU078994
58	202	53.6	852	7	CF243019
59	202	53.6	888	5	EX433245
60	201	53.3	733	6	CB555746
61	200	53.1	716	2	BE880600
62	200	53.1	773	4	BG208600
63	200	53.1	957	5	BU956183
64	195	51.7	587	6	CB154620
65	195	51.7	863	4	BG429609
66	195	51.7	906	6	CD107527
67	195	51.7	921	7	CF264864
68	194	51.5	584	6	CB164677
69	194	51.5	726	6	CD642135
70	194	51.5	736	2	BE876700
71	194	51.5	801	5	BQ645542
72	194	51.5	931	5	BU501596
73	194	51.5	959	7	CN803488
74	193	51.2	581	5	BP372621
75	193	51.2	686	7	CR559762
76	193	51.2	706	4	BG924737
77	193	51.2	1060	4	BI758594
78	193	51.2	1142	4	BM466858
79	192	50.9	579	7	CN403760
80	192	50.9	684	6	CB269635
81	192	50.9	878	4	BI159881
82	191	50.7	956	5	BQ672234

BU149962	AGENCOURT
EX437607	EX437607
BU159699	AGENCOURT
BG205510	RST24889
BG189523	RST8568 A
BG215999	RST35685
CD358161	AGENCOURT
BU151205	AGENCOURT
BU558083	AGENCOURT
BU188239	AGENCOURT
BQ670517	AGENCOURT
BU188938	AGENCOURT
CB115197	K-EST0159
BG202878	RST22246
EX422046	EX422046
BI859488	603385338
BG758079	602712239
BF972370	602240689
BG830200	602764779
BQ071740	AGENCOURT
BU528295	AGENCOURT
CB998866	AGENCOURT
BQ669046	AGENCOURT
BQ894247	AGENCOURT
CO048817	ILLUMIGEN
CN801970	ILLUMIGEN
CN647001	ILLUMIGEN
CN803219	ILLUMIGEN
CN643780	ILLUMIGEN
BM463752	AGENCOURT
CN641931	ILLUMIGEN
CN646807	ILLUMIGEN
CN403758	170005325
CN403761	170006000
CV026068	3899 Full
BG198062	RST17446
CD698834	EST16358
BU945610	AGENCOURT
BQ930674	AGENCOURT
CD689640	EST1613 h
BM423081	PLATE1 H1
BG253045	602365568
EX461980	AGENCOURT
CF552849	AGENCOURT
BQ671998	AGENCOURT
BU975546	AGENCOURT
CO646424	ILLUMIGEN
BU078994	im69c04 Y
CF243019	AGENCOURT
EX433245	EX433245
CB555746	MMSPO001
BE880600	601511562
BG208600	RST28103
BU956183	AGENCOURT
CB154620	K-EST0212
BG429609	602501290
CD107527	AGENCOURT
CF264864	AGENCOURT
CB164677	K-EST0225
CD642135	AGENCOURT
BE876700	601488265
BQ645542	AGENCOURT
BU501596	AGENCOURT
CN803488	ILLUMIGEN
BP372621	BP372621
CR559762	DKF2D459J
BG924737	HNC29-1-D
BI758594	603027253
BM466858	AGENCOURT
CN403760	170004237
CB269635	1008542 H
BI159881	602863704
BQ672234	AGENCOURT

83	190	50.4	570	2	BE297106	601177785	156	160	42.4	485	1	AA417175	AA417175	zui3b07.r
c	84	190	50.4	682	2	BF220183	601296732	157	160	42.4	608	2	BM015005	603640960
	85	190	50.4	774	5	BUI501374	AGENCOURT	c	158	42.4	617	2	AW249490	2821433.3
	86	190	50.4	863	4	BG777471	602664794	159	160	42.4	893	4	BI257270	602967201
	87	189	50.1	568	1	AU280181	AU280181	c	160	42.4	893	5	BQ773620	UI-H-EZ1-
	88	189	50.1	913	5	BQ674754	AGENCOURT	161	159	42.2	681	6	CD642085	AGENCOURT
	89	188	49.9	565	4	BM825480	K-EST0097	162	158	41.9	486	5	BU785709	AGENCOURT
	90	188	49.9	682	2	BE383076	601298885	163	158	41.9	547	4	BM857824	id45c04.y
	91	188	49.9	766	4	BG208089	RST27579	164	157	41.9	784	4	BG337639	id45c03.y
	92	188	49.9	841	6	CD520278	AGENCOURT	165	157	41.6	506	6	CA868199	id45c03.y
	93	188	49.9	899	6	CD522597	AGENCOURT	166	157	41.6	567	5	BF259087	id45c03.y
	94	187	49.6	563	6	CB162617	K-EST0223	167	157	41.6	578	5	BP258271	BP259087
	95	187	49.6	596	7	CB162617	K-EST0223	168	155	41.1	516	5	AA310922	BP258271
	96	186	49.3	569	6	CB115210	K-EST05313	169	155	41.1	691	2	BF337048	BP258271
	97	186	49.3	587	5	BP205055	BP205055	c	170	41.1	724	4	BI761713	602034442
	98	186	49.3	629	6	CB381894	TGEST2y2	171	154	40.8	463	2	BE382365	603046583
	99	186	49.3	851	2	BP569230	602185591	172	154	40.8	470	1	AI350283	601298668
	100	185	49.1	563	2	AW612887	h30e12.x	173	154	40.8	522	1	AA310005	60329a05.x
	101	184	48.8	553	6	CB149851	K-EST0206	174	154	40.8	522	1	AA310005	EST181072
	102	184	48.8	577	5	BP255708	BP255708	c	175	40.8	982	5	BQ708698	AGENCOURT
	103	184	48.8	786	2	BE885933	601507564	176	153	40.6	497	1	AA088548	z189c07.r
	104	184	48.8	858	4	BG112293	602282442	c	177	40.6	674	5	BM994615	UI-H-DUO-
	105	183	48.5	552	4	BF971793	602240073	c	178	40.6	782	4	EG193628	UI-H-DUO-
	106	183	48.5	552	5	BF971793	602240073	178	153	40.6	896	4	EG193628	RST12762
	107	183	48.5	561	2	BE369831	BP369831	179	153	40.6	1134	9	AY412158	RST40363
	108	183	48.5	568	7	CB149851	K-EST0206	180	153	40.6	1134	9	AY412158	RST40363
	109	182	48.3	714	2	BE294585	601176160	c	181	40.3	535	5	BQ345444	MR4-NT014
	110	182	48.3	767	6	CD520815	AGENCOURT	c	182	40.3	670	5	BM997732	UI-H-DIO-
	111	181	48.0	748	6	CB963441	AGENCOURT	c	183	40.3	672	5	BM970544	UI-H-DIO-
	112	181	48.0	757	4	BG201812	RST21154	c	184	40.3	672	5	BM970544	UI-H-DIO-
	113	181	48.0	768	4	BG201812	RST21154	c	185	40.3	672	5	BM970544	UI-H-DIO-
	114	180	47.7	629	6	CD675866	602740208	c	186	40.3	770	2	BF036200	601458271
	115	179	47.5	746	2	BE515271	601236040	c	187	40.3	1047	7	BN641956	ILLUMIGEN
	116	179	47.5	746	2	BE515271	601236040	c	188	40.1	663	4	BI9148410	6034c09.x
	117	179	47.5	970	2	BE899429	601682204	c	189	40.1	663	4	BI9148410	6034c09.x
	118	178	47.2	538	6	CB156885	K-EST0215	c	190	40.1	892	4	BG213298	RST32904
	119	178	47.2	766	4	BG767215	602740208	c	191	39.8	541	4	BM312319	IG41H09.y
	120	178	47.2	911	2	BE747713	601578166	c	192	39.8	596	6	CD671336	IG41H09.y
	121	177	46.9	654	1	AI832925	at73e05.x	c	193	39.8	664	5	BU679866	IG41H09.y
	122	177	46.9	818	4	BG686132	602638411	c	194	39.8	775	4	BG219146	RST38899
	123	177	46.9	909	4	BG199730	RST19024	c	195	39.5	520	2	BF110854	7n41b06.x
	124	177	46.9	1068	5	BM923007	AGENCOURT	c	196	39.5	722	2	BF110854	7n41b06.x
	125	176	46.7	754	4	BM479270	AGENCOURT	c	197	39.3	470	1	AA213687	zq2h06.r
	126	175	46.4	722	6	CD640899	AGENCOURT	c	198	39.0	443	6	CB121958	K-EST0169
	127	175	46.4	889	6	CD517935	AGENCOURT	c	199	39.0	492	4	BM509658	IG92e01.y
	128	174	46.2	876	6	BG209664	RST29190	c	200	39.0	586	2	AW411227	fh1b01.y
	129	173	45.9	756	6	CD623343	602638411	c	201	39.0	636	7	CN483826	hw38g08.y
	130	172	45.6	736	4	B1861437	603386664	c	202	39.0	648	7	CN403762	170004245
	131	172	45.6	1109	4	BM462171	AGENCOURT	c	203	39.0	654	2	BF792283	602252801
	132	171	45.4	607	1	AL044648	DKF2p434P	c	204	38.7	592	5	BP307165	BP307165
	133	171	45.4	938	4	BG387910	602412932	c	205	38.7	667	6	CA441829	UI-H-ED0-
	134	170	45.1	625	5	BU069684	im22f05.y	c	206	38.7	694	6	CA441829	UI-H-ED0-
	135	170	45.1	818	2	BE885777	601508992	c	207	38.7	967	7	CN647834	ILLUMIGEN
	136	170	45.1	839	4	BG397722	602438783	c	208	38.5	444	1	AI348472	Q030a09.x
	137	170	45.1	889	4	BF979086	602147596	c	209	38.5	672	6	CB551872	MSP0028
	138	169	44.8	515	6	CA948213	IG19c12.y	c	210	38.5	787	6	CB551872	MSP0028
	139	169	44.8	735	4	BG199251	RST18532	c	211	38.2	642	5	BU784337	AGENCOURT
	140	169	44.3	535	5	BQ188175	UI-E-E31-	c	212	38.2	644	2	BF794011	602254657
	141	166	44.0	570	1	AA525154	n51a08.s	c	213	38.2	830	4	BI667676	603293024
	142	166	44.0	694	1	AA703243	z170e05.s	c	214	38.2	904	4	BG185256	7n41b06.y
	143	165	43.8	534	6	CA867868	ir82d01.y	c	215	37.9	769	4	BG214935	RST4195.A
	144	164	43.5	500	7	CF135196	UI-HF-CB0	c	216	37.9	751	4	BG192091	RST11198
	145	164	43.5	582	7	BP301192	BP301192	c	217	37.9	973	5	BQ650937	AGENCOURT
	146	164	43.5	872	5	BU542568	AGENCOURT	c	218	37.7	453	4	BF999436	CM3-GN007
	147	164	43.5	1214	5	BU539034	AGENCOURT	c	219	37.7	556	2	BG656173	ib37h12.y
	148	163	43.2	842	2	BE885524	601508717	c	220	37.7	568	2	AW409690	fh01d06.y
	149	162	43.0	767	4	BG213835	RST13455	c	221	37.7	609	7	CF363598	833489.MA
	150	162	43.0	866	4	BG393996	602416893	c	222	37.4	562	1	AA664175	ac04h04.s
	151	162	43.0	887	4	BG182156	RST1020.A	c	223	37.4	644	2	AW972885	EST384980
	152	162	43.0	914	4	BM451072	AGENCOURT	c	224	37.4	664	1	BU603028	AGENCOURT
	153	162	42.7	928	7	BN801922	ILLUMIGEN	c	225	37.4	666	1	AA218918	z102c03.s
	154	161	42.7	673	2	AW409798	fh02d12.x	c	226	37.1	976	4	BG392121	602410213
	155	161	42.7	1241	4	BG746028	602723467	c	227	36.9	421	7	CR525159	DKF2p4590
								228			619	4	BM539941	hb16b08.9

C 229	139	36.9	533	5	BM991335	UI-H-DT0-	BM991335	UI-H-DT0-	C 302	123	32.6	658	1	AI719868	AI719868	as47a04.x
C 230	139	36.9	710	2	BE270121	601185927	BE270121	601185927	303	123	32.6	899	1	BF245597	BF245597	601863527
C 231	138	36.6	535	1	AA215707	zr197h07.r	AA215707	zr197h07.r	304	122	32.4	445	1	AA084885	AA084885	znl3g01.r
C 232	138	36.6	561	4	BF975395	602245924	BF975395	602245924	C 305	122	32.4	562	2	BF437208	BF437208	7p67h12.x
C 233	138	36.6	581	5	BP258977	BP258977	BP258977	BP258977	C 306	122	32.4	635	2	BF594792	BF594792	7o55d03.x
C 234	138	36.6	611	2	BE223082	hu47a07.x	BE223082	hu47a07.x	C 307	122	32.4	920	2	BE300217	BE300217	600944220
C 235	138	36.6	744	6	CD522104	AGENCOURT	CD522104	AGENCOURT	C 308	121	32.1	370	2	AW020950	AW020950	df16g08.y
C 236	138	36.6	775	4	BG214936	RST34591	BG214936	RST34591	C 309	121	32.1	388	2	BF851047	BF851047	CM3-EN00Y
C 237	138	36.6	776	5	BK925342	BK925342	BK925342	BK925342	C 310	121	32.1	475	1	AI302360	AI302360	qm08h11.x
C 238	138	36.6	906	5	BQ673816	AGENCOURT	BQ673816	AGENCOURT	C 311	121	32.1	581	1	AW162274	AW162274	au75h05.x
C 239	137	36.3	712	1	AV716842	AV716842	AV716842	AV716842	C 312	121	32.1	672	6	CD640858	CD640858	AGENCOURT
C 240	137	36.3	827	4	BG032020	602300525	BG032020	602300525	C 313	121	32.1	782	1	AI018633	AI018633	ou47h04.x
C 241	137	36.3	856	2	BF130818	601818484	BF130818	601818484	C 314	121	32.1	1078	4	BM454194	BM454194	AGENCOURT
C 242	137	36.3	918	4	BG205994	RS25429	BG205994	RS25429	C 315	120	31.8	484	1	AJ0707455	AJ0707455	AJ0707455
C 243	137	36.3	935	2	BF663243	602144361	BF663243	602144361	C 316	120	31.8	484	1	AA487743	AA487743	ab320e06.r
C 244	137	36.3	976	4	BG757286	602715271	BG757286	602715271	C 317	120	31.8	511	2	BE709305	BE709305	IL3-HT061
C 245	137	36.3	1220	5	BUI77249	AGENCOURT	BUI77249	AGENCOURT	C 318	120	31.8	606	5	BE759739	BE759739	im90a11.x
C 246	136	36.1	410	6	CA388900	co03f08.y	CA388900	co03f08.y	C 319	120	31.8	703	1	AI479008	AI479008	tm29g03.x
C 247	136	36.1	526	1	AA604363	no79g10.s	AA604363	no79g10.s	C 320	120	31.8	734	2	AW026536	AW026536	wv14f11.x
C 248	136	36.1	757	4	BG211683	RST31252	BG211683	RST31252	C 321	120	31.8	935	5	BQ673790	BQ673790	AGENCOURT
C 249	136	36.1	1020	5	BQ051750	AGENCOURT	BQ051750	AGENCOURT	C 322	120	31.8	1010	2	BE612666	BE612666	601452513
C 250	136	36.1	1041	4	BM555910	AGENCOURT	BM555910	AGENCOURT	C 323	119	31.6	601	1	AA846727	AA846727	aj99a10.s
C 251	135	35.8	438	7	D52239	HUM072A06B	D52239	HUM072A06B	C 324	119	31.6	673	5	BU738049	BU738049	UI-E-DW1
C 252	135	35.8	601	1	AA593789	nm65d01.s	AA593789	nm65d01.s	C 325	119	31.6	1029	4	BM454583	BM454583	AGENCOURT
C 253	135	35.8	617	7	CF365002	835601.MA	CF365002	835601.MA	C 326	118	31.3	405	4	BF945731	BF945731	CM1-NN021
C 254	135	35.8	643	4	BI197962	602761927	BI197962	602761927	C 327	118	31.3	559	1	AA521260	AA521260	aa75e06.s
C 255	135	35.8	763	6	C9999367	AGENCOURT	C9999367	AGENCOURT	C 328	118	31.3	770	4	BG199520	BG199520	RST185311
C 256	135	35.8	917	2	BF684044	602141379	BF684044	602141379	C 329	118	31.3	829	4	BI597323	BI597323	603251617
C 257	134	35.5	408	1	AA578724	nh23h11.s	AA578724	nh23h11.s	C 330	118	31.3	842	2	BF381815	BF381815	601816067
C 258	134	35.5	444	1	AA130255	z129c01.r	AA130255	z129c01.r	C 331	118	31.3	946	4	BG106015	BG106015	602290215
C 259	134	35.5	979	2	BF344340	602014715	BF344340	602014715	C 332	118	31.3	952	4	BG340555	BG340555	602462121
C 260	133	35.3	494	5	BK282797	BK282797	BK282797	BK282797	C 333	117	31.0	449	1	AA864947	AA864947	oh36b04.s
C 261	133	35.3	494	7	CR742450	CR742450	CR742450	CR742450	C 334	117	31.0	564	1	AI755086	AI755086	cr35c06.x
C 262	133	35.3	554	5	BQ267575	ij90a09.y	BQ267575	ij90a09.y	C 335	117	31.0	580	2	AW009156	AW009156	ws7bb05.x
C 263	133	35.3	611	2	BE257350	601108570	BE257350	601108570	C 336	117	31.0	582	7	CF768669	CF768669	CES001974
C 264	131	34.7	588	5	BU078719	im69c04.x	BU078719	im69c04.x	C 337	117	31.0	588	5	BP362057	BP362057	BP362057
C 265	131	34.7	1109	4	BP980373	602288255	BP980373	602288255	C 338	117	31.0	605	1	AA664102	AA664102	ac06a03.s
C 266	130	34.5	509	2	BE081450	QV2-BT063	BE081450	QV2-BT063	C 339	117	31.0	981	4	BG169354	BG169354	602120902
C 267	130	34.5	513	1	AA443651	z35b5b10.r	AA443651	z35b5b10.r	C 340	116	30.8	619	4	BI063996	BI063996	IL3-UT011
C 268	130	34.5	582	5	BP193654	BP193654	BP193654	BP193654	C 341	116	30.8	703	4	BG616164	BG616164	602642744
C 269	130	34.5	610	2	AW151319	KG947h08.x	AW151319	KG947h08.x	C 342	116	30.8	748	4	BG220118	BG220118	RST39890
C 270	130	34.5	854	4	BG182134	RST998.At	BG182134	RST998.At	C 343	115	30.5	398	2	BF857991	BF857991	RC5-PT019
C 271	129	34.2	403	1	AA668695	AJ668695	AA668695	AJ668695	C 344	115	30.5	493	2	AW873472	AW873472	hm01h04.x
C 272	129	34.2	603	5	BQ271252	ij90a09.x	BQ271252	ij90a09.x	C 345	115	30.5	562	4	BG686057	BG686057	602638626
C 273	129	34.2	619	4	BM857651	ij69c03.x	BM857651	ij69c03.x	C 346	115	30.5	652	6	CB437257	CB437257	684704.MA
C 274	129	34.2	654	1	AI765328	w173f10.x	AI765328	w173f10.x	C 347	114	30.2	344	6	CB135336	CB135336	K-EST0187
C 275	129	34.2	668	5	BQ002431	UI-H-EI1	BQ002431	UI-H-EI1	C 348	114	30.2	346	6	CB135453	CB135453	K-EST0187
C 276	129	34.2	671	5	BM980581	UI-CF-EN1	BM980581	UI-CF-EN1	C 349	114	30.2	534	2	BF434285	BF434285	7o95b11.x
C 277	129	34.2	673	1	AI928349	w096c03.x	AI928349	w096c03.x	C 350	114	30.2	544	2	AW236763	AW236763	xm84f08.x
C 278	129	34.2	690	7	CF135924	UI-HF-BN0	CF135924	UI-HF-BN0	C 351	114	30.2	567	1	AA846826	AA846826	aj99h03.s
C 279	129	34.2	724	7	CF135985	UI-HF-BN0	CF135985	UI-HF-BN0	C 352	114	30.2	655	2	AA467341	AA467341	he09e10.x
C 280	129	34.2	731	5	BU632784	UI-H-FE1	BU632784	UI-H-FE1	C 353	114	30.2	955	4	BG341156	BG341156	602462513
C 281	129	34.2	765	7	CF135787	UI-HF-BN0	CF135787	UI-HF-BN0	C 354	113	30.0	440	2	BE831205	BE831205	PM4-MT004
C 282	128	34.0	456	1	AI879521	au54a08.x	AI879521	au54a08.x	C 355	113	30.0	469	1	AA026942	AA026942	zk04h06.r
C 283	128	34.0	611	4	BM690806	UI-E-CX0	BM690806	UI-E-CX0	C 356	113	30.0	531	1	AI601273	AI601273	ar89b01.x
C 284	128	34.0	645	4	BM312236	ig41h09.x	BM312236	ig41h09.x	C 357	113	30.0	550	5	BP306529	BP306529	BP306529
C 285	128	34.0	1021	4	BG261332	602373094	BG261332	602373094	C 358	113	30.0	559	4	BG684675	BG684675	602635957
C 286	127	33.7	582	5	BP268725	BP268725	BP268725	BP268725	C 359	113	30.0	582	5	BP256863	BP256863	BP256863
C 287	127	33.7	587	2	BF725114	bx12d04.y	BF725114	bx12d04.y	C 360	113	30.0	632	6	CA947959	CA947959	iq19c12.x
C 288	127	33.7	695	1	AA910671	ok94a04.s	AA910671	ok94a04.s	C 361	113	30.0	815	4	BG182157	BG182157	RST1021.A
C 289	127	33.7	777	7	CO882771	BovGen.11	CO882771	BovGen.11	C 362	112	29.7	337	7	CM403770	CM403770	170006002
C 290	126	33.4	432	7	H43942	yo70f01.f1	H43942	yo70f01.f1	C 363	112	29.7	338	1	AA810339	AA810339	nx74h07.s
C 291	126	33.4	443	2	BE295596	601176557	BE295596	601176557	C 364	112	29.7	394	7	D52485	D52485	HUM079F08B
C 292	126	33.4	833	5	BU532129	AGENCOURT	BU532129	AGENCOURT	C 365	112	29.7	409	1	AA044007	AA044007	zk58e02.r
C 293	125	33.2	383	5	BP428997	BP428997	BP428997	BP428997	C 366	112	29.7	532	1	AA707260	AA707260	ag84d03.r
C 294	125	33.2	569	7	AA595249	no33b07.s	AA595249	no33b07.s	C 367	112	29.7	634	1	AA053839	AA053839	zf53c08.r
C 295	125	33.2	569	1	N31918	y721g12.bir	N31918	y721g12.bir	C 368	111	29.4	433	1	AA305861	AA305861	EST176862
C 296	125	33.2	863	4	BM011998	603636417	BM011998	603636417	C 369	111	29.4	547	2	AW250256	AW250256	2821433.5
C 297	124	32.9	938	5	BQ710910	AGENCOURT	BQ710910	AGENCOURT	C 370	111	29.4	557	1	AA622207	AA622207	no43a03.s
C 298	124	32.9	449	7	H06771	y183e01.r1	H06771	y183e01.r1	C 371	111	29.4	634	2	AW027887	AW027887	ws62e08.x
C 299	123	32.6	433	1	AA351545	EST59320	AA351545	EST59320	C 372	111	29.4	679	2	BE382430	BE382430	601297257
C 300	123	32.6	560	1	AA992575	ot97e05.s	AA992575	ot97e05.s	C 373	111	29.4	834	2	BF698561	BF698561	602130766
C 301	123	32.6	647	2	BF435610	nac33h11.	BF435610	nac33h11.	C 374	111	29.4	921	5	BQ23017		

375	110	29.2	377	2	BF919682	BF919682	RC6-NT015	448	98	26.0	931	4	BG186848	RST5825	A
376	110	29.2	721	7	H56271	H56271	YQ97604.r1	C 449	97	25.7	487	1	AA291445	ZT44009.r	
C 377	110	29.2	723	1	A1740926	A1740926	WG18d08.x	C 450	97	25.7	489	1	AI580775	TA04F05.r	
378	110	29.2	782	6	CB309143	CB309143	AGENCOCURT	C 451	97	25.7	506	1	AA456187	ZX74G06.r	
C 379	109	28.9	482	5	BX280952	BX280952		C 452	97	25.7	533	2	BF4319188	NAB6F06.r	
C 380	109	28.9	526	2	BF549514	BF549514	7b39e01.x	C 453	97	25.7	548	2	BF194965		
C 381	109	28.9	975	2	BF570206	BF570206	602185591	C 454	97	25.7	602	1	AI683620	tw52908.x	
C 382	109	28.9	978	5	BUS22118	BUS22118	AGENCOCURT	C 455	96	25.5	329	1	AA248244	CSG1720.s	
C 383	109	28.9	983	2	BF795121	BF795121	602256456	C 456	96	25.5	378	2	AAW03319	UI-HF-BK0	
C 384	109	28.9	1024	2	BB613274	BB613274	601452513	C 457	96	25.5	516	1	AA968669	OQ76405.s	
C 385	109	28.9	1035	4	BG532641	BG532641	602560368	C 458	96	25.5	603	7	CN805010	ILLUMIGEN	
C 386	108	28.6	330	5	BP432781	BP432781		C 459	95	25.5	913	4	BG212755	RST32350	
C 387	108	28.6	517	2	BF194972	BF194972	7091b11.x	C 460	95	25.2	295	6	CB107619	K-EST0146	
C 388	108	28.6	534	2	AW051330	AW051330	wy89d03.x	C 461	95	25.2	375	4	B1036674	RC6-NT015	
C 389	108	28.6	549	1	AUI60225	AUI60225		C 462	95	25.2	390	2	BF825105	RC3-HN002	
C 390	108	28.6	570	1	AA873236	AA873236	oh78e05.s	C 463	95	25.2	485	2	BE206087	BA97G12.x	
C 391	108	28.6	662	1	A1928836	A1928836	au65b11.x	C 464	95	25.2	674	6	CD366863	UI-HF-PT2	
C 392	108	28.6	700	2	BF055443	BF055443	7j80b08.x	C 465	94	24.9	478	1	AA287249	ZT20F06.r	
C 393	107	28.4	334	7	T35066	T35066	EST79711.Hu	C 466	94	24.9	480	2	BE205841	bb46H01.x	
C 394	107	28.4	421	1	AA128746	AA128746	z004b02.r	C 467	94	24.9	502	4	BM687893	UI-E-CK1	
C 395	107	28.4	440	1	AA150796	AA150796	z146b02.r	C 468	94	24.9	589	5	BUE20209	UI-H-FH1	
C 396	107	28.4	599	1	AA595432	AA595432	no34a11.s	C 469	94	24.9	680	6	CB554868	MNMP0045	
C 397	107	28.4	614	1	A1436613	A1436613	t103h01.x	C 470	94	24.9	756	2	AW073133	wy94D02.x	
C 398	107	28.4	927	2	BF575348	BF575348	602134082	C 471	93	24.7	323	1	AA493691	hh01g09.s	
C 399	107	28.4	939	4	BG292188	BG292188	602386616	C 472	93	24.7	328	2	BF086910	CW3-GN009	
C 400	106	28.1	414	2	BF918539	BF918539	CMO-NT013	C 473	93	24.7	395	4	B1036689	RC6-NT015	
C 401	106	28.1	482	7	H01360	H01360	y199c04.r1	C 474	93	24.7	411	2	BF918638	CW0-NT013	
C 402	106	28.1	581	1	AA056104	AA056104	z155E03.r	C 475	93	24.7	414	2	BE168324	QV3-HT051	
C 403	105	27.9	317	4	BM700394	BM700394		C 476	93	24.7	475	1	AI046124	TENU1210	
C 404	105	27.9	408	1	AJ7112254	AJ7112254		C 477	93	24.7	900	2	BE870482	601447050	
C 405	105	27.9	588	2	BF939453	BF939453	nac76b01.	C 478	92	24.4	409	2	AA438598	xu37a07.x	
C 406	105	27.9	531	5	BG656485	BG656485	ib37h12.x	C 479	92	24.4	464	2	BF726071	bx23f05.y	
C 407	105	27.9	511	5	BQ653339	BQ653339	AGENCOCURT	C 480	92	24.4	495	4	BM707945	UI-E-C11	
C 408	104	27.6	620	2	BG828445	BG828445	602751421	C 481	92	24.4	500	5	BUT731805	UI-E-C11	
C 409	104	27.6	645	2	AW152399	AW152399	xg64a01.x	C 482	92	24.4	558	1	AI419341		
C 410	103	27.3	463	1	AA773958	AA773958	ab57d05.r	C 483	92	24.4	613	2	BE1612458		
C 411	103	27.3	640	5	BQ429097	BQ429097	AGENCOCURT	C 484	92	24.4	778	4	BF213882		
C 412	103	27.3	671	5	BQ016234	BQ016234	UI-H-DT1	C 485	92	24.4	962	2	BG204370	601866448	
C 413	103	27.3	922	2	BE743948	BE743948	601576820	C 486	92	24.4	1133	5	BQ070688	AGENCOCURT	
C 414	102	27.1	399	1	AA053687	AA053687	z172b09.r	C 487	91	24.1	291	5	BQ187634	UI-E-EJ1	
C 415	102	27.1	454	7	H65037	H65037	YF69a12.r1	C 488	91	24.1	450	1	AA158006	z053N03.s	
C 416	102	27.1	481	4	BM539699	BM539699	hb12h03.g	C 489	91	24.1	466	2	BF092748	MK4-TN011	
C 417	102	27.1	502	1	AI126969	AI126969	q9p6d02.x	C 490	91	24.1	470	1	AA837513	oe31b11.s	
C 418	102	27.1	556	1	AA523356	AA523356	n167b10.s	C 491	91	24.1	475	2	AA861414	ak34D06.s	
C 419	102	27.1	653	4	BG759588	BG759588	602712170	C 492	91	24.1	512	1	AW019937	dF01h03.y	
C 420	102	27.1	732	1	AA923275	AA923275	om51a02.s	C 493	91	24.1	581	5	BQ212878	AGENCOCURT	
C 421	102	27.1	810	4	BG829247	BG829247	602753144	C 494	90	23.9	353	2	BF828289		
C 422	102	27.1	900	4	BG028386	BG028386	602295457	C 495	90	23.9	660	4	BM171801	imagegc	
C 423	102	27.1	944	4	BG911884	BG911884	602803475	C 496	90	23.9	463	2	BE532307	601235195	
C 424	101	26.8	405	7	L44437	L44437	HOMESTIG1.H	C 497	90	23.9	466	1	AI274874	qk61e11.x	
C 425	101	26.8	499	1	AA612651	AA612651	no42f02.s	C 498	90	23.9	567	2	AW320151	uo15a09.y	
C 426	101	26.8	728	2	BE620268	BE620268	601483387	C 499	90	23.9	582	1	AA596173	vo22d09.r	
C 427	101	26.8	873	4	BG531994	BG531994	602561020	C 500	90	23.9	659	7	CF892039	A0104B05	
C 428	100	26.5	323	2	BE766735	BE766735	IL3-NT010	C 501	90	23.9	660	4	BM972039	imagegc	
C 429	100	26.5	354	7	R83822	R83822	YD06h02.r1	C 502	90	23.9	709	2	BE911407		
C 430	100	26.5	355	7	T34543	T34543	EST70301.Hu	C 503	90	23.9	774	4	BE151414		
C 431	100	26.5	475	1	AA213581	AA213581	ZQ3B06.r	C 504	90	23.9	821	4	BE151160		
C 432	100	26.5	492	1	AI186829	AI186829	qe82h06.x	C 505	90	23.9	830	4	BE151519	603297975	
C 433	100	26.5	501	1	AI340077	AI340077	qq44b07.x	C 506	90	23.9	894	4	BE151519	603297975	
C 434	100	26.5	504	1	AA156184	AA156184	z047c01.s	C 507	90	23.9	894	4	BE151519	603297975	
C 435	100	26.5	586	2	BE589858	BE589858	1946C3.BA	C 508	90	23.9	1061	2	BE307770	601097104	
C 436	100	26.5	596	1	AA434521	AA434521	zw31d12.r	C 509	90	23.9	2348	3	BC029328	MUS MUSGU	
C 437	99	26.3	305	2	BE767780	BE767780	RC5-GN004	C 510	89	23.6	327	2	BE698538	RC0-UT002	
C 438	99	26.3	419	1	AA155818	AA155818	z047C01.r	C 511	89	23.6	483	1	AA586757	nm71C04.s	
C 439	99	26.3	811	5	EQ441544	EQ441544		C 512	89	23.6	537	2	AW290919	UI-H-BI2	
C 440	99	26.3	1126	4	BG119682	BG119682	602349304	C 513	89	23.6	601	4	BG399944	602441485	
C 441	98	26.0	476	1	AA954106	AA954106	oq65d12.s	C 514	89	23.6	612	1	AI420758	tf02h11.x	
C 442	98	26.0	476	4	BG898639	BG898639	HOA3-1-F	C 515	89	23.6	614	1	AA053911	zF52f06.r	
C 443	98	26.0	477	1	AA310730	AA310730	EST181540	C 516	89	23.6	1133	2	BF684262	602141180	
C 444	98	26.0	498	1	AA714067	AA714067	rw18g11.s	C 517	88	23.3	461	1	AA057851	z195f08.s	
C 445	98	26.0	628	2	BE220798	BE220798	hu18H03.x	C 518	88	23.3	463	2	BE326321	hw01f10.x	
C 446	98	26.0	636	1	AA205570	AA205570	zG68B08.s	C 519	88	23.3	463	4	BE1850226	imagegc	
C 447	98	26.0	829	1	AA1523625	AA1523625	tG95C02.x	C 520	88	23.3	475	5	BQ548661	1k93h12.x	

C 521 88 23.3 580 1 A1598247 tnl5d02.x
C 522 88 23.3 594 6 CB169351 KYB602702
C 523 88 23.3 757 4 BG777885 602665623
C 524 88 23.3 806 2 BF669925 602118429
C 525 87 23.1 405 4 B1036675 RC6-NT015
C 526 87 23.1 459 1 A1032951 OX06h03.s
C 527 87 23.1 497 6 CA45832 UI-H-EIO-
C 528 87 23.1 491 7 W46580 zc32809.r1
C 529 87 23.1 587 5 AA496420 ZV37C03.r
C 530 87 23.1 915 5 BU844745 AGENCOURT
C 531 86 22.8 421 1 AA157562 zc32809.s
C 532 86 22.8 424 7 T78365 YC99f11.r1
C 533 86 22.8 461 1 AA054388 ZF54f01.r
C 534 86 22.8 478 4 AA456153 Zx74a01.r
C 535 86 22.8 478 4 B1491939 df17c01.w
C 536 86 22.8 478 4 B1906154 603062603
C 537 86 22.8 479 2 AW020980 df17c01.y
C 538 86 22.8 484 2 AW403704 UI-HF-BKO
C 539 86 22.8 489 1 AA937188 ok13c10.s
C 540 86 22.8 521 1 AA417071 zui3b07.s
C 541 86 22.8 538 1 AA487524 ad20e06.s
C 542 86 22.8 630 4 BG501836 602548934
C 543 86 22.8 647 2 BF853287 MR2-ENO09
C 544 86 22.8 968 2 BF789168 601476292
C 545 85 22.5 341 1 AA209345 ZQ82e03.r
C 546 85 22.5 365 7 R75949 Y162b02.r1
C 547 85 22.5 466 1 A1306635 qn45h11.x
C 548 85 22.5 507 7 R88891 YP97b03.r1
C 549 85 22.5 549 1 AA599293 ag35c03.s
C 550 85 22.5 594 1 AU145099 AU145099
C 551 85 22.5 607 1 AA629751 ae63c01.s
C 552 85 22.5 764 1 A1800633 wgi2g10.x
C 553 85 22.5 839 4 BM014961 603640906
C 554 84 22.3 255 2 BF825099 RC3-HNO02
C 555 84 22.3 281 1 AA355875 EST64340
C 556 84 22.3 439 1 A1278881 qo42h11.x
C 557 84 22.3 447 6 CA943599 ir82d01.x
C 558 84 22.3 450 1 A1795935 wa40c11.x
C 559 84 22.3 465 5 BU069467 im22f05.x
C 560 84 22.3 572 1 AU146040 AU146040
C 561 84 22.3 630 6 CB267878 1006784 H
C 562 84 22.3 745 4 BG912921 602807320
C 563 83 22.0 325 4 BG183155 RST2025 A
C 564 83 22.0 388 7 F25987 HSPD13241 H
C 565 83 22.0 436 1 A1051917 ow38g07.s
C 566 83 22.0 446 1 A1680686 tx40b07.x
C 567 83 22.0 446 5 BU785406 in45c04.x
C 568 83 22.0 447 1 B1636109 t292h04.x
C 569 83 22.0 685 2 AW301064 xk12b11.x
C 570 82 21.8 356 7 T30826 RST23354 Hu
C 571 82 21.8 423 7 H00488 AU101887 ZK85b06.r
C 572 82 21.8 453 7 N91218 zai3f01.r1
C 573 82 21.8 459 2 AW403463 UI-HF-BKO
C 574 82 21.8 611 7 N30602 YW72b06.s1
C 575 82 21.8 647 5 AW03463 UI-HF-BKO
C 576 82 21.8 648 7 N30602 YW72b06.s1
C 577 82 21.8 650 7 A1679428 tu63f12.x
C 578 81 21.5 269 1 A1680208 ac82d11.s
C 579 81 21.5 340 2 AW993907 RC3-BNO03
C 580 81 21.5 370 7 T36202 EST98394 Hu
C 581 81 21.5 437 1 AA292432 ZT28h02.s
C 582 81 21.5 441 1 A1635372 t994c11.x
C 583 81 21.5 441 2 AW299224 X948a02.x
C 584 81 21.5 487 1 A1813543 wj83d01.x
C 585 81 21.5 578 5 BP220954 BP220954
C 586 81 21.5 659 2 B5675818 7f16f08.x
C 587 81 21.5 1083 4 BM460353 AGENCOURT
C 588 80 21.2 453 2 AW406913 UI-HF-BKO
C 589 80 21.2 459 1 A1347777 qo96c05.s
C 590 80 21.2 501 1 AA533127 nj46g02.s
C 591 80 21.2 627 4 B1250151 602995324
C 592 80 21.2 734 4 BG211729 RST31298
C 593 80 21.2 1091 2 BE894125 601438253

C 594 79 21.0 435 1 AA021376
C 595 79 21.0 453 1 A1377586
C 596 79 21.0 474 2 BE675931 TC718f07.x
C 597 79 21.0 511 1 A1355203 qt61h10.x
C 598 79 21.0 568 1 A1144511 qb73h04.x
C 599 79 21.0 902 5 BQ937545 AGENCOURT
C 600 79 21.0 937 5 BQ921119 AGENCOURT
C 601 79 21.0 1011 5 BQ63114 AGENCOURT
C 602 78 20.7 298 7 H81242 YU73d02.r1
C 603 78 20.7 339 6 CD694302 EST10825
C 604 78 20.7 385 4 B1036680 RC6-NT015
C 605 78 20.7 448 7 T61988 YB96h02.r1
C 606 78 20.7 470 2 AW062552 ILO-CT007
C 607 78 20.7 482 4 B1063842 IL3-UT011
C 608 78 20.7 504 4 B1063658 IL3-UT011
C 609 78 20.7 504 4 B1063676 IL3-UT011
C 610 78 20.7 504 4 B1063677 IL3-UT011
C 611 78 20.7 504 4 B1063980 IL3-UT011
C 612 78 20.7 505 4 B1063693 IL3-UT011
C 613 78 20.7 506 4 B1063678 IL3-UT011
C 614 78 20.7 506 4 B1063687 IL3-UT011
C 615 78 20.7 507 4 B1063663 IL3-UT011
C 616 78 20.7 507 4 B1063665 IL3-UT011
C 617 78 20.7 524 4 B1063679 IL3-UT011
C 618 78 20.7 812 9 AY412159 Pan trogl
C 619 78 20.7 853 2 BF666533 60213987
C 620 77 20.4 287 4 B1036693 RC6-NT015
C 621 77 20.4 427 1 AA961959 oq92c10.s
C 622 77 20.4 427 7 N68425 zai3e08.s1
C 623 77 20.4 499 1 AA827740 ob54h11.s
C 624 77 20.4 584 5 BP367260 BP367260
C 625 77 20.4 625 2 BF229960 PM3-CS003
C 626 77 20.4 712 4 B1153367 602918645
C 627 77 20.4 916 4 BF981165 602310440
C 628 77 20.4 1024 5 BQ071597 AGENCOURT
C 629 77 20.4 1458 4 BM473295 AGENCOURT
C 630 76 20.2 228 7 T34505 EST69511 Hu
C 631 76 20.2 231 2 AW602562 RC3-BT056
C 632 76 20.2 277 1 AA484896 ne81g10.s
C 633 76 20.2 335 7 N88322 ZK3097F Huma
C 634 76 20.2 407 1 AA146795 zo35h12.s
C 635 76 20.2 486 1 A1017489 ou29a09.x
C 636 76 20.2 942 5 BU846202 AGENCOURT
C 637 76 20.2 952 5 BQ949999 AGENCOURT
C 638 75 19.9 348 4 BG943235 ax35c01.x
C 639 75 19.9 400 1 A1140742 qa02h06.x
C 640 75 19.9 411 6 CA868145 ir78e02.y
C 641 75 19.9 417 1 A1023061 ow65d10.s
C 642 75 19.9 418 7 N41846 YW72b06.r1
C 643 75 19.9 423 1 A1002297 oq86f06.s
C 644 75 19.9 445 1 AA102742 zn75c10.s
C 645 75 19.9 452 1 AA411127 zt28g02.r
C 646 75 19.9 539 2 AW197146 xb16d03.x
C 647 75 19.9 546 1 A1914392 xb16d05.x
C 648 75 19.9 588 6 CB265551 1004456 H
C 649 75 19.9 680 4 BG661032 N335 SSH
C 650 75 19.9 683 4 BG470735 602511674
C 651 74 19.6 368 1 AJ573253 AJ573253
C 652 74 19.6 395 2 AW780047 hm96g06.x
C 653 74 19.6 414 1 AA057383 zfs9d06.s
C 654 74 19.6 451 1 A1301708 qn16h05.x
C 655 74 19.6 466 7 W21065 ZB55a09.r1
C 656 74 19.6 486 1 A1298533 qn02a11.x
C 657 74 19.6 490 1 A1609708 tf82b11.x
C 658 74 19.6 504 1 AA677163 zj56f06.s
C 659 74 19.6 526 2 BF061159 7i81g09.x
C 660 74 19.6 549 1 A1339407 qt02d03.x
C 661 74 19.6 572 5 BQ127440 i160a03.y
C 662 74 19.6 582 4 BM726598 UT-E-EJO-
C 663 74 19.6 583 1 AA401892 zt44d09.s
C 664 74 19.6 595 5 BQ127196 i157a06.y
C 665 74 19.6 701 4 B1395164 TUDPEC139
C 666 74 19.6 733 2 BF030624 601559995

667 19.6 837 1 AUI19783 AUI19783
668 19.4 283 2 BF828336 MRL-HN006
669 73 283 2 BF828372 MRL-HN006
670 73 358 6 CD678566 hp09h12.y
671 73 446 1 AA443595 zw35b10.s
672 73 488 1 R90728
673 19.4 565 1 AA455699 aa22c12.i
674 73 597 6 CA868387
675 73 776 7 CN403759
676 73 860 4 BG685185
677 19.1 399 7 H18197
678 72 413 7 N24351
679 72 424 7 R10180
680 72 436 1 AA767578
681 72 453 1 A1311374
682 72 465 1 A1311374
683 72 468 2 BF927593
684 72 475 1 AA455699
685 72 487 4 B1063801
686 72 522 6 CD465666
687 72 563 5 BU579991
688 72 583 5 BF376806
689 72 731 2 BF743763
690 72 766 4 BG110301
691 72 845 1 AA018940
692 71 848 1 AA857209
693 71 848 1 AA832379
694 71 848 2 BF832652
695 71 848 4 A1268435
696 71 848 5 BF259054
697 71 848 5 AUI47052
698 71 848 2 BF116024
699 71 848 5 BU689348
700 71 848 663 2 BE613480
701 71 848 674 6 CA448476
702 71 848 724 2 BF667981
703 71 848 745 5 BQ000493
704 71 848 800 2 BF205634
705 71 848 1064 4 BG495262
706 71 848 336 7 Z28780
707 70 474 1 AA188000
708 70 477 1 AUI59525
709 70 558 1 AUI59472
710 70 611 1 AA188001
711 70 642 1 AA573290
712 70 734 4 BG253436
713 70 1059 4 BG253436
714 69 1059 4 BG253436
715 69 1059 4 BG253436
716 69 1059 4 BG253436
717 69 1059 4 BG253436
718 69 1059 4 BG253436
719 69 1059 4 BG253436
720 69 1059 4 BG253436
721 69 1059 4 BG253436
722 68 277 2 BF866649
723 68 395 1 A1265892
724 68 435 7 W96274
725 68 493 1 A1463228
726 67 243 7 R10208
727 67 326 7 R10179
728 67 426 1 AA043972
729 67 441 7 H30847
730 67 476 4 BF63844
731 67 801 2 BE620803
732 67 834 2 BF308244
733 67 913 5 BQ221930
734 66 414 1 A1370280
735 66 437 1 AA121443
736 66 468 4 B1063827
737 66 469 2 AW859789
738 66 498 2 AW302456
739 66 517 1 A1288797

AUI19783 AUI19783
BF828336 MRL-HN006
BF828372 MRL-HN006
CD678566 hp09h12.y
AA443595 zw35b10.s
R90728 ym02a05.b1
AA455699 aa22c12.i
CA868387 ir78e02.x
CN403759 170004708
BG685185 602637072
H18197 ym47e09.r1
N24351 yf35c04.r1
R10180 yf35c04.r1
AA767578 oa91b12.s
A1311374 qo88e04.x
A1311374 qo88e04.x
BF927593 CM2-NT019
AA455699 zx89c08.i
B1063801 IL3-UT011
CD465666 LeukONI.6
BU579991 im50a11.y
BF376806 BP376806
BE743763 601577867
BG110301 602279171
AA018940 ze56a07.i
AA857209 of63d04.s
AA832379 np71h10.s
BF832652 QV3-H101
A1268435 qm03h09.x
BF259054 BP259054
AUI47052 AUI47052
BF116024 7n76e03.x
BU689348 UI-CF-ECL
BE613480 601504247
CA448476 UI-H-EIO-
BF667981 602122225
BQ000493 UI-H-DPO-
BF205634 601868404
BG495262 602542926
Z28780 HSB94D042.S
AA188000 zp67h10.i
AUI59525 tes2f07.x
AUI59472 AUI59472
AA188001 zp67h10.s
AA573290 nk98c09.s
BG253436 602368913
BG253436 602368913
A1951581 ws37a03.x
BF767779 RCS-GN004
AA299052 EST11514
AA505973 n01h04.s
BQ66739 AGENCOURT
AW843279 MR2-CN003
BE766649 IL3-NT010
A1265892 qx68a07.x
W96274 ze42e02.r1
A1463228 tj25g04.x
R10208 yf35g04.r1
R10179 yf35c03.r1
AA043972 zk58e02.s
H30847 y078e09.r1
BF63844 IL3-UT011
BE620803 601483387
BF308244 601890301
BQ221930 AGENCOURT
A1370280 qv76a01.x
AA121443 zm23g08.s
B1063827 IL3-UT011
AW859789 QV4-CT036
AW302456 xw04c02.x
A1288797 qm06g10.x

AW176627 IL4-CT007
BE855565 7910c04.x
AA191621 zp81g09.s
B1185194 UNL-P-PN-
BQ230627 AGENCOURT
BQ565115 q130h07.y
BE766760 IL3-NT010
A1952335 wx22c10.x
N25815 yx22b02.r1
R90752 ym02a05.r1
AA265239 qx54a01.x
BG716298 602676557
AA778982 ac37f07.s
BE300959 b010h11.x
AA088582 zk64b06.r
AA403398 UI-HF-BK0
AA525244 n152f05.s
R53807 y103c05.s1
H86415 y893e05.r1
AA021650 ze69d06.r
R87382 ym88f06.r1
AA134108 z129c01.s
AA18844 ze57h10.s
BE769362 PM2-FT002
AA088443 z189c07.s
CD623342 56016114H
BQ324040 CM2-CT013
BF2825103 RC3-HN002
AA10834 ze34d03.s
N23295 yx77e10.s1
CB799998 AMGNNUC:N
B1036659 RC6-NT015
H28392 y153f04.r1
EM663687 UI-E-CKO-
BF925989 MR2-NT013
B1653500 603300485
CO559445 AGENCOURT
CO403221 AGENCOURT
CO401140 AGENCOURT
CV111060 AGENCOURT
B1906096 603062484
CK476853 AGENCOURT
CK600627 AGENCOURT
CK600627 AGENCOURT
CO394917 AGENCOURT
CV117459 AGENCOURT
CO404828 AGENCOURT
BU527460 AGENCOURT
BG198262 RST17406
BQ879445 AGENCOURT
CR754276 CR754276
BF85097 RC3-HN002
AV591749 AV591749
BF577160 602135454
AW901060 CM0-NN101
AW299229 x84b02.x
AA248313 CSQ2469.s
H40555 ym87b09.s1
A1797547 w654h06.x
CD512156 AGENCOURT
AA704015 ag80b04.r
AA027118 zk04h06.s
AA001081 ze47a01.r
A1708106 A1708106
AA758596 ah58a08.s
BQ773013 UI-H-FEO-
BG183268 RST2142.A
B1048432 MP4-TN011
B1912257 603068487
AA225516 nc25b10.x
B1861443 603366672
BG422324 602448979

813	60	15.9	793	4	BG205511	RST24890	886	54	14.3	562	2	BF852812	MR3-EN009
814	60	15.9	803	1	BF43082	AU43082	C 887	54	14.3	701	1	AI568713	ch4g08.x
815	60	15.9	903	2	BF306450	601893337	888	53	14.1	349	1	AA639531	nq91c02.s
816	60	15.9	906	2	BE784177	601471391	889	53	14.1	352	2	BE539946	601060692
817	60	15.9	946	4	BG031336	602299031	890	53	14.1	353	1	AA443086	x74a01.s
818	59	15.6	195	2	BE707784	QV3-HT054	891	53	14.1	354	1	AA443122	xi74d06.s
819	59	15.6	232	4	BG218606	RST38346	C 892	53	14.1	361	2	AA493228	UI-M-BH3-
820	59	15.6	273	6	CD673801	fs04g10.Y	893	53	14.1	413	1	AA766630	oa38b09.s
821	59	15.6	327	2	BF939970	601312309	894	53	14.1	444	2	BF469374	UI-M-BH3-
822	59	15.6	362	2	BF825091	RC3-HN002	895	53	14.1	452	2	AA464684	BP230016B
823	59	15.6	388	1	AA019589	ze60c09.s	896	53	14.1	464	2	BE137044	u959a07.Y
824	59	15.6	550	6	CB554966	MMSF0031	897	53	14.1	509	1	AA050559	mj20g08.X
825	59	15.6	910	5	BQ942748	AGENCOURT	898	53	14.1	514	2	AW227144	um66e04.Y
826	59	15.6	933	5	BQ669200	AGENCOURT	899	53	14.1	516	1	AI836101	UI-M-AJ1-
827	59	15.6	953	5	BUS26745	AGENCOURT	900	53	14.1	519	2	BF456625	BF456625
828	58	15.4	275	7	R71979	y784g03.r1	901	53	14.1	519	5	EX511532	EX511532
829	58	15.4	292	7	T35540	EST86969.Hu	902	53	14.1	521	6	CD806120	UI-M-GW0-
830	58	15.4	296	7	H45224	Y003e04.r1	903	53	14.1	526	6	CA034473	CA034473
831	58	15.4	300	2	BE830506	RC6-ET008	904	53	14.1	588	2	BF041384	BP250025B
832	58	15.4	383	6	CB703771	AMGNNUC:N	905	53	14.1	600	4	BG803120	0221-16.M
833	58	15.4	395	7	W03594	za02b11.r1	906	53	14.1	620	7	CF764690	CES003367
834	58	15.4	440	7	H40679	Y050f06.s1	907	53	14.1	680	5	BQ42736	UI-M-EV0-
835	58	15.4	679	4	BG188438	RST7456.A	908	53	14.1	688	6	CD807159	UI-M-GW0-
836	58	15.4	963	4	BG164089	602341131	914	53	14.1	729	7	CF750534	UI-M-HJ0-
837	57	15.1	197	1	AA659220	nt92c11.s	910	53	14.1	741	7	CF724469	UI-M-GZ0-
838	57	15.1	247	7	N55813	J2985F.Huma	911	53	14.1	717	7	CO890616	BovGen.18
839	57	15.1	321	7	R87368	Ym88d08.r1	912	53	14.1	722	7	CN837718	AGENCOURT
840	57	15.1	409	1	AA021333	ze68b08.r	913	53	14.1	726	6	CB952709	AGENCOURT
841	57	15.1	409	2	AA0401698	UI-HF-BK0	914	53	14.1	728	5	BQ178754	UI-M-EV0-
842	57	15.1	411	7	H45216	Y003c07.r1	915	53	14.1	747	5	BQ178962	UI-M-EV0-
843	57	15.1	411	7	T15517	IB1478.Infa	916	53	14.1	747	5	BQ178962	UI-M-EV0-
844	57	15.1	416	2	BF222344	7p51f01.x	917	53	14.1	747	7	CK943550	4067471.B
845	57	15.1	420	7	H84867	Y890h07.r1	918	53	14.1	759	5	BUE14402	UI-M-EV0-
846	57	15.1	441	2	BF109033	7149d03.x	919	53	14.1	798	5	BU706227	UI-M-FR0-
847	57	15.1	454	2	AW135630	UI-B-B11-	920	53	14.1	798	7	CF950351	UI-M-HJ0-
848	57	15.1	455	7	CN403769	170006001	921	53	14.1	833	7	CO796221	AGENCOURT
849	57	15.1	457	7	N32671	Yx77e10.r1	922	53	14.1	900	5	BQ951632	AGENCOURT
850	57	15.1	501	5	B0430243	UI-HF-ENO	923	53	14.1	936	5	BQ172467	AGENCOURT
851	57	15.1	505	4	BI063845	IL3-UT011	924	53	14.1	2045	3	AK050465	Mus.muscu
852	57	15.1	538	4	BM505258	IG92e01.x	925	53	14.1	2739	3	AK079476	AK079476
853	57	15.1	576	5	BM996837	UI-H-DH0-	926	52	13.8	359	7	F36711	HSPD34599.H
854	56	14.9	323	1	AA985180	am79c06.s	927	52	13.8	380	1	AA813533	ai65g10.s
855	56	14.9	330	6	CA891650	B0167B05-	928	52	13.8	384	2	BE128724	DEPA2474
856	56	14.9	368	2	BF919657	RC6-NT015	929	52	13.8	414	7	N36758	Y734a01.s1
857	56	14.9	384	4	BI490970	df01h03.w	930	52	13.8	418	1	AA861003	aj90f10.s
858	56	14.9	384	4	BM666783	UI-B-CL1-	C 931	52	13.8	435	1	AA121968	zm25c09.s
859	56	14.9	403	1	AA018037	ze51d04.r	932	52	13.8	454	7	AA284509	zt20f06.s
860	56	14.9	432	7	CN645730	ILLUMIGEN	933	52	13.8	454	7	R87486	Ym90c07.s1
861	56	14.9	437	4	BI063825	IL3-UT011	934	52	13.8	457	1	AI360680	qx64f03.x
862	56	14.9	485	1	AA157999	zo57d09.s	C 935	52	13.8	505	4	BI063998	IL3-UT011
863	56	14.9	504	4	BI063987	IL3-UT011	936	52	13.8	545	1	AA894835	oj61f10.s
864	56	14.9	509	4	BI063979	IL3-UT011	937	52	13.8	610	2	BF243478	601879503
865	56	14.9	554	2	AW515055	xu83b04.x	938	52	13.8	901	5	BQ686351	AGENCOURT
866	56	14.9	743	2	BF797400	602257046	939	52	13.8	910	5	BQ643059	AGENCOURT
867	56	14.9	750	4	BG428886	602494873	940	52	13.8	931	5	BQ709316	AGENCOURT
868	55	14.6	262	4	BG209161	RST28675	941	51	13.5	344	7	R84956	Yc40d06.s1
869	55	14.6	350	1	AA730298	nw41c12.s	942	51	13.5	383	5	BI133769	BY133769
870	55	14.6	388	7	H85576	Y890h07.s1	C 943	51	13.5	426	1	AA146787	zo35g12.s
871	55	14.6	402	1	AI492331	ti23b03.x	944	51	13.5	431	7	R93806	Yt72a08.s1
872	55	14.6	424	2	BF197808	7p92g06.x	945	51	13.5	463	7	CF896236	A0208B12-
873	55	14.6	430	7	R85113	Yc43f02.s1	946	51	13.5	492	6	CA896306	B0198B10-
874	55	14.6	444	1	AI342973	qc027c04.x	947	51	13.5	511	7	CN674363	A0947F11-
875	55	14.6	459	7	N29011	Yx40b06.r1	948	51	13.5	541	6	CD542845	B0244B08-
876	55	14.6	460	6	CD287048	14.K2.abd	949	51	13.5	585	7	CF895975	CF895975
877	55	14.6	506	1	AA215708	xr97h07.s	C 950	51	13.5	597	7	N58511	Yv72f08.s1
878	55	14.6	693	1	AUI34091	AUI34091	951	51	13.5	600	4	BG805121	0613-68.M
879	55	14.6	1022	5	BQ059268	AGENCOURT	952	51	13.5	600	4	BI988307	3223-72.M
880	54	14.3	344	1	AI735109	Y6a02.x	953	51	13.5	600	4	BI990483	4071-72.M
881	54	14.3	440	1	AA164577	zo92d11.s	954	51	13.5	600	5	BU923128	7044-59.M
882	54	14.3	462	1	AI499883	tn97c04.x	955	51	13.5	600	6	CA527854	8053-56.M
883	54	14.3	475	1	AI801762	to95b05.x	956	51	13.5	604	1	AA882230	vx42d03.x
884	54	14.3	486	2	BF842750	QV3-HT101	957	51	13.5	604	4	BI916177	603178061
885	54	14.3	514	4	BI063978	IL3-UT011	958	51	13.5	611	5	BU787194	il55b12.Y

959	51	13.5	614	7	CF898290	A0236H09-
c 960	51	13.5	626	1	AA057586	zf62g09.i
c 961	51	13.5	653	6	CB426708	601917.MA
962	51	13.5	654	6	CB435983	616293.MA
963	51	13.5	692	2	BE877738	601486303
964	51	13.5	809	6	CB599544	AGENCOURT
965	51	13.5	844	4	BG246428	602360441
966	51	13.5	846	2	BF159549	601769045
967	51	13.5	920	5	B0529002	AGENCOURT
968	51	13.5	1110	9	AY412160	Mus muscu
969	50	13.3	253	4	BI036115	RCS-NT026
970	50	13.3	253	4	BI036116	RCS-NT026
971	50	13.3	336	4	BG200248	RS191556
c 972	50	13.3	353	1	AA558174	nc27d12.s
c 973	50	13.3	370	1	AA222844	nc27b04.s
c 974	50	13.3	379	7	R84342	Yc23e04.r1
c 975	50	13.3	420	4	BI063843	ILJ3-UT011
c 976	50	13.3	437	1	AA758948	ah77e07.s
c 977	50	13.3	441	7	W46581	zc32e09.s1
c 978	50	13.3	505	4	BI063973	ILJ3-UT011
979	50	13.3	750	4	BI855507	603382590
980	49	13.0	151	6	CB116617	X-BST0161
981	49	13.0	157	7	N56413	JU8699F.Hum
982	49	13.0	246	4	BG180306	602331150
c 983	49	13.0	357	7	N45919	Y734a01.r1
984	49	13.0	380	7	N33478	YV42c12.s1
985	49	13.0	444	2	AW512453	xu56f07.x
986	49	13.0	460	7	H39028	yp65e02.s1
987	49	13.0	486	1	AA434421	zw31d12.s
988	49	13.0	487	7	H28367	Y152f04.s1
989	49	13.0	544	7	H28143	Y078h08.s1
990	49	13.0	563	1	AA528021	nh9og04.s
991	49	13.0	600	5	B0920931	6072-17.M
992	49	13.0	601	2	B8891426	601434883
993	49	13.0	617	1	AA020986	ze65e08.s
994	49	13.0	731	2	BF241617	601878943
995	49	13.0	836	4	BI155031	602902555
996	49	13.0	913	2	B8562867	601336578
997	49	13.0	933	4	BI695196	603346642
998	49	13.0	1013	5	BQ055815	AGENCOURT
999	48	12.7	336	1	AA975283	oq36f04.s
c1000	48	12.7	352	7	H38301	yp70a04.r1

RESULT 1	614	7	CF898290	A0236H09-
LOCUS	626	1	AA057586	zf62g09.i
DEFINITION	653	6	CB426708	601917.MA
ACCESSION	654	6	CB435983	616293.MA
VERSION	692	2	BE877738	601486303
KEYWORDS	809	6	CB599544	AGENCOURT
SOURCE	844	4	BG246428	602360441
ORGANISM	846	2	BF159549	601769045
REFERENCE	920	5	B0529002	AGENCOURT
AUTHORS	1110	9	AY412160	Mus muscu
TITLE	253	4	BI036115	RCS-NT026
JOURNAL	253	4	BI036116	RCS-NT026
COMMENT	336	4	BG200248	RS191556
	353	1	AA558174	nc27d12.s
	370	1	AA222844	nc27b04.s
	379	7	R84342	Yc23e04.r1
	420	4	BI063843	ILJ3-UT011
	437	1	AA758948	ah77e07.s
	441	7	W46581	zc32e09.s1
	505	4	BI063973	ILJ3-UT011
	750	4	BI855507	603382590
	151	6	CB116617	X-BST0161
	157	7	N56413	JU8699F.Hum
	246	4	BG180306	602331150
	357	7	N45919	Y734a01.r1
	380	7	N33478	YV42c12.s1
	444	2	AW512453	xu56f07.x
	460	7	H39028	yp65e02.s1
	486	1	AA434421	zw31d12.s
	487	7	H28367	Y152f04.s1
	544	7	H28143	Y078h08.s1
	563	1	AA528021	nh9og04.s
	600	5	B0920931	6072-17.M
	601	2	B8891426	601434883
	617	1	AA020986	ze65e08.s
	731	2	BF241617	601878943
	836	4	BI155031	602902555
	913	2	B8562867	601336578
	933	4	BI695196	603346642
	1013	5	BQ055815	AGENCOURT
	336	1	AA975283	oq36f04.s
	352	7	H38301	yp70a04.r1

ALIGNMENTS	903 bp	mRNA	linear	EST 21-OCT-2002
BU956287	AGENCOURT 10613307 NIH MGC 107 Homo sapiens	cdna clone		
BU956287	IMAGE:6725846 5', mRNA sequence.			
BU956287.1	GI:24185959			
EST.				
Homo sapiens				
Homo sapiens (human)				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
1 (bases 1 to 903)				
NIH-MGC http://mgc.nci.nih.gov/ .				
National Institutes of Health, Mammalian Gene Collection (MGC)				
Unpublished (1999)				
Contact: Robert Strausberg, Ph.D.				
Email: cgabbs-r@mail.nih.gov				
Tissue Procurement: ATCC				
cdna Library Preparation: Rubin Laboratory				
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
Cloning Strategy: Agencourt Bioscience Corporation				
Cloning Distribution: MGC clone distribution information can be				
found through the I.M.A.G.E. Consortium/LLNL at:				
http://image.llnl.gov				
Plate: LLC3053 row: 1 column: 05				
High quality sequence stop: 695.				

FEATURES	Location/Qualifiers
1. .903	
/organism="Homo sapiens"	
/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone="IMAGE:6725846"	
/tissue_type="adenocarcinoma, cell line"	
/lab_host="DH10B (phage-resistant)"	
/clone_lib="NIH MGC 107"	
/note="Organ: breast; Vector: pOTB7; Site: 1: ECoRI; Site: 2: XhoI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."	
ORIGIN	
Alignment Scores:	
Pred. No.: 4.24e-247	Length: 903
Score: 261.00	Matches: 261
Percent Similarity: 100.00%	Conservative: 0
Best Local Similarity: 100.00%	Mismatches: 0
Query Match: 69.23%	Indels: 0
DB: 5	Gaps: 0
US-09-736-250-1 (1-377) x BU956287 (1-903)	
Qy 2	LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIleThr 21
Db 3	AAAGTTTCAGGGCCTTTGGAAACACAGAGATTGCTTCTCTGTGGAAAGGCAATCACT 62
Qy 22	ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 63	AGGAAACACAGATGTGGAAGTGAATGTGGGAAATGCTTCAATCAGATGTTCT 122
Qy 42	ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLysTyrGlnPheAsnLeu 61
Db 123	CCATCCAGAGAGATGAATTAATCAATGGCTGGCCAACTCAAGTAGTCAACATTCACCTT 182
Qy 62	TyrProGlnThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 183	TACCACCAAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTAGCTACCGTAAG 242
Qy 82	AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101
Db 243	GCTCATCCAAATACTTGTAGTTGTTGCAATCAGCTGTTTTTCTTAGCTGCCAAGACT 302
Qy 102	ValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
Db 303	GTTGAGGAAGATGAGAGAATTCAGTAGTACTAAGGTATTGGCAAGAGACAGTTTCTGTGGA 362
Qy 122	CysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrpAsp 141
Db 363	TGTTCCCTCATCTGAATTTTGAAGTGAAGATTAATCTGGATAGTGAATGGAT 422
Qy 142	LeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThr 161
Db 423	CTTCACACAGCCACACCATTCGATTTCTTTCATATTTCCATGTCATTCGAGTGTCAACT 482
Qy 162	ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
Db 483	AGGCCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTCTCT 542
Qy 182	ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMet 201
Db 543	ACCAAGCAACTACTTCTACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATG 602
Qy 202	LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeu 221
Db 603	CTTGCTCTGGCCATGGTTAGTCTGAAATGAGAAACTCATTTCTCTGATTTGCTTCTCTCT 662

```

Qy 222 ThrLeuGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGlu 241
Db 663 ACAATTGAACGCTTCAGAAAGCACAGATGATAGTCCCACTGATCCATTTGCGGGAG 722
Qy 242 LeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVal 261
Db 723 CTTTGGGACATACCTTTCTACTCTGAGCTCTCCCTGCTCCCTGCTGAAATTCGTTATGTC 782
Qy 262 Tyr 262
Db 783 TAC 785

RESULT 2
LOCUS BQ673252 918 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT 8349250 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6276033
5', mRNA sequence.
ACCESSION BQ673252
VERSION BQ673252.1 GI:21784086
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 918)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

FEATURES
source
1..918
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6276033"
/tissue type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 102"
/note="Organ: salivary gland; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. No.: 3 526-239 Length: 918
Score: 253.00 Matches: 253
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 67.11% Indels: 0
Gaps: 5

US-09-736-250-1 (1-377) x BQ673252 (1-918)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 108 ATGAAGTTTCCAGGCGCTTGGAAACACGAGATGTTCTTTCTCTGTTGGAAAGGCAATC 167
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40

```

```

Db 168 ACTAGGAAGCACAGATGTGAAAGTGAATGTGCGAAATGCCTTCAATCAGATGTT 227
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 228 TCTCCATCCAGAGAGATGAAGTAATTCATGCTGGCCCAACTCAAGTACCAATTCAAC 287
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 288 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTGTTCCTAGCTACCCTA 347
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 348 AGGCTCATCTCAAAATACTTGGATTGATTGCAATCAGCTGTTTTCCTAGCTGCCAAG 407
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 408 ACTGTTGAGGAAGATGAGAGAAATCCAGTAGTACTAAGGTATTGGCAGAGACAGTTTCTGT 467
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 468 GGATGTTCTCTCATCTGAAATTTTGAAGATGGAGAGAATATTCTGGATAAGTTGAATTGG 527
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 528 GATCTTCACAGCCACCATTTGGATTCTTCATATTTTCCATGTCATGTCATGTCAGTGCA 587
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 588 ACTAGGCCTCAGTTACTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 647
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 648 CTTTACCAAGCAACTACTTCACTGTATGGCTTGCACCACTCTTGTCAATTCAGAGATCC 707
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 708 ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATCTCTGATGCTTCT 767
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 768 CTTTACAATTGAACCTTTCAGAAAGCACAGATGATAGTCCCACTGATTCATTCATTCGCG 827
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 828 GAGCTTGTGGCACATCACCTTTCTACTCTGCGAGTCCTCC 866

RESULT 3
LOCUS CD358716 899 bp mRNA linear EST 29-MAY-2003
DEFINITION AGENCOURT 14284919 NIH_MGC_180 Homo sapiens cDNA clone
IMAGE:30390835 5', mRNA sequence.
ACCESSION CD358716
VERSION CD358716.1 GI:31130127
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 899)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW2460 row: c column: 10
High quality sequence stop: 708.
Location/Qualifiers
1..918
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6276033"
/tissue type="epidermoid carcinoma, cell line"
/lab host="DH10B (phage-resistant)"
/clone lib="NIH MGC 102"
/note="Organ: salivary gland; Vector: pOTB7; Site: 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed
by Ling Hong in the laboratory of Gerald M. Rubin
(University of California, Berkeley) using ZAP-cDNA
synthesis kit (Stratagene) and Superscript II RT (Life
Technologies). Note: this is a NIH_MGC Library."

```



```

Db 122 TGTTCCTTCAGTCCCAAGACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGTA 181
Qy 114 LeuAlaArgAspSerPheCysGlyCysSerSerGluLeuLeuArgMetGluArgile 133
Db 182 TTGGCAAGAGACAGTTCTCTGTGGATGTTCTCTCATCTGAAATTTTTCAGAAATGGAGAAAT 241
Qy 134 IleLeuAspLysLeuAsnTpsAspLeuHisThrAlaThrProLeuAspPheLeuHisIle 153
Db 242 ATTCTGGATAGTTGAATTTGGATCTTCACAGCCACACCATGATGATTTCTTCATATT 301
Qy 154 PheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSer 173
Db 302 TTCCATGCCATTCAGATGTCACCTAGGCTCAGTTACTTTTCAGTTTGCCCAAAATGGAGC 361
Qy 174 ProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGln 193
Db 362 CCATCTCAACATTTGGCAGTCTTACCAAGCAACTTACTTCACTGATGGCTGCAACCAA 421
Qy 194 LeuLeuGlnPheArgGlySerMetLeuAlaLeuMetValSerLeuGluMetGluLys 213
Db 422 CTTCTGCAATTCAGAGGATCCATGCTGCTCTGGCCATGGTTAGTCTGGAATGGAGAA 481
Qy 214 LeuLeuProAspTpsLeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSer 233
Db 482 CTCAATCTCGATTCGCTTCTTCAATTTGAATGACTGCTTCAGAAAGCACAGATGGATAGC 541
Qy 234 SerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSer 253
Db 542 TCCAGATTGATCCATTTGTGGGAGCTTGTGGCAGATCACCCTTCTACTCTGCAGCTTCC 601
Qy 254 LeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuValThrCysAsp 273
Db 602 CTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGACACACCTGCTGACCTGTGAC 661
Qy 274 LysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSerLysAspAsn 293
Db 662 AAAGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGAGCTTCTCCAGAGCAAC 721
Qy 294 SerLysProGluValProValArgGly 302
Db 722 AGCAAGCCAGAAAGTCCAGTCCAGAGG 748

RESULT 5
BI858571
LOCUS 603389030P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398038 5',
DEFINITION mRNA sequence.
ACCESSION BI858571
VERSION BI858571.1 GI:15999318
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 890)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DRP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM12014 row: 1 column: 07
High quality sequence stop: 855.
Location/Qualifiers
1. 890
/organism="Homo sapiens"
/mol_type="mRNA"
FEATURES
source

```

```

/db_xref="taxon:9606"
/clones="IMAGE:5398038"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_87"
/notes="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dn primed.
Average insert size 1.383 Kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN
Alignment Scores:
Pred. NO.: 3.09e-235 Length: 890
Score: 249.00 Matches: 249
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 66.05% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x BI858571 (1-890)
Qy 91 AlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArgIleProVal 110
Db 3 GCATTCAGCTGTTTTTCTTAGCTGCCAAGACTGTTGAGGAGATGAGAGAAATTCAGTA 62
Qy 111 LeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerGluLeuLeuArgMet 130
Db 63 CTAAAGGTAATGGCAAGAGACAGTTCTGTGGATGTTCTCATCTGAAATTTTGAATG 122
Qy 131 GluArgIleIleLeuAspLysLeuAsnTpsAspLeuHisThrAlaThrProLeuAspPhe 150
Db 123 GAGAGAAATTAATTCGGATAAGTTGAATGGGATCTTCACACAGCACACCATTCGATTTT 182
Qy 151 LeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPheSerLeuPro 170
Db 183 CTTCAATATTTTCCATGCCATTCAGTGTCACTAGGCTCAGTTACTTTTCAGTTTGCC 242
Qy 171 LysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHisCysMetAla 190
Db 243 AAATTTAGGCCATCTCAACATTTGGCAGTCTTACCAAGCAACTACTTCACTGATGGCC 302
Qy 191 CysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuMetValSerLeuGlu 210
Db 303 TGCAACCAACTTCTGCAATTCAGAGGATCCATGCTGCTCTGGCCATGGTTAGTCTGGA 362
Qy 211 MetGluLysLeuIleProAspTpsLeuSerLeuThrIleGluLeuLeuGlnLysAlaGln 230
Db 363 ATGGAGAAATCATCTCTGATTTGGCTTTCTTCAATTTGACTGCTTCAGAAAGCACAG 422
Qy 231 MetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisLeuSerThrLeu 250
Db 423 ATGGATAGTCTCCAGTTGATCCATTTGCGGAGCTTGTGGCAGCATCACCTTCTACTCTG 482
Qy 251 GlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThrLeuVal 270
Db 483 CAGTCTTCCCTGCTCTGAAATTCGTTTATGTCTACCGTCCCTCAAGCACACCTCTGTG 542
Qy 271 ThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAspPheSer 290
Db 543 ACCTGTGACAAAGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCAGAGATTTCTCC 602
Qy 291 LysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHisLeu 310
Db 603 AAGGACAAACAGCAAGTCCAGAGTCCAGTCCAGAGTACAGCAGCAGCTTTTACCATCATCTC 662
Qy 311 ProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluLeuMetGluVal 330
Db 663 CCAGCTCCAGTGGTGCAGAGCAGACCTCTACTAAACGCAAAAGTAGAGGAATGGAAGTG 722
Qy 331 AspAspPheTyrAspGlyIleLysArg 339
Db 723 GATGACTTCTATGATGAATCAAAACGG 749

```


17QY

/clone_lib="NIH_MGC_43"
/note="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"

ORIGIN

Alignment Scores:
Pred. No.: 3,02e-232 Length: 936
Score: 246.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.25% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BU501311 (1-936)

Qy 79 ThrVallysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPheLeuAla 98
Db 1 ACCGTAAAGGCTCATCAAAATCTGAGTTGTATGCAATCAGCTGTTTTCTTAGCT 60
Qy 99 AlalysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
Db 61 GCCAAGACTGTTGAGGAAGATGAGAGATTCCAGTACTAAAGGTATTGGCAAGAGACAGT 120
Qy 119 PheCysGlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeu 138
Db 121 TTCTGTGATGTTCTCTCATCTGAAATTTTGAATGGAGAGAAATATTCTGGATAAGTTG 180
Qy 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
Db 181 AATTGGGATCTTCACAGCCACACCATTTGATTTCTTATATTTCCATGCGCATTGCA 240
Qy 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
Db 241 GTGTCAACTAGGCGCTCAGTTACTTTTCAAGTTGGCCAAATTTGAGCCCATCTCAACATTTG 300
Qy 179 AlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArg 198
Db 301 GCAGTCCCTTACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTGAGA 360
Qy 199 GlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrp 218
Db 361 GGATCCATGCTTGCTGGCCATGTTAGTCTGGAAATGGAGAACTCATTTCTTGATTGG 420
Qy 219 LeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHis 238
Db 421 CTTTCTCTTACAATTGAATGCTTTCAGAAAGCACAGATGGATAGCTCCAGTTGATCCAT 480
Qy 239 CysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSer 258
Db 481 TGTGGGAGCTTGTGGCAGCATCCTTTCTACTCTGCAGTCTCCCTGCCCTCGAATTC 540
Qy 259 ValTrpValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArg 278
Db 541 GTTTATGTCACCGTCCCTTCAGCACACCTGTGTGACCTGTGCANAGGAGTGTTCAGA 600
Qy 279 LeuHisProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluVal 298
Db 601 TTACATCCCTCTCTGTCCAGGCCAGACTTCTCCAAGGACCAACAGCAAGCCAGAGTG 660
Qy 299 ProValArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysIleGln 318
Db 661 CCAGTCAGAGGTACAGAGCGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAG 720
Qy 319 ThrSerThrLysArgLys 324
Db 721 ACCITCTAATACGCGAG 738

RESULT 8

BU538306
LOCUS
DEFINITION BU538306 963 bp mRNA linear EST 13-SEP-2002
AGENCOURT 10181155 NIH MGC 107 Homo sapiens cDNA clone
IMAGE:6568838 5', mRNA sequence.
BU538306
VERSION BU538306.1 GI:22848747
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 963)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM2755 row: c column: 14
High quality sequence stop: 646.

FEATURES

source
1..963
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6568838"
/tissue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Alignment Scores:
Pred. No.: 3,11e-232 Length: 963
Score: 246.00 Matches: 246
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 65.25% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BU538306 (1-963)

Qy 2 LysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIleThr 21
Db 3 AAGTTTCCAGGCGCTTTGGAAACACAGATGTTCTTCTGTTGGAAAGGCAATCACT 62
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 63 AGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAATGCTTCAAAATCAGATGTTTCT 122
Qy 42 ProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeu 61
Db 123 CCATCCAGAGAGATGAAGTAATCAATGGCTGCCAAACTCAAGTACCAATTCAACCTT 182
Qy 62 TyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 183 TACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGTAGTGTTCCTAGCTACCGTAAAG 242
Qy 82 AlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThr 101

```
Db 243 GCTCATCAAAATACCTTGGATTGATTCGAATCAGCTCTTTTCTAGCTGCCAAGACT 302
Qy 102 ValGluGluAspGluuArgGluProValLeuLysValLeuAlaArgAspSerPheCysGly 121
Db 303 GTTGGAGGAAGATGAGAGAAATCCAGTACTAAGGTAATGGCAAGAGACAGATTCCTGTGGA 362
Qy 122 CysSerSerGluLeuLeuArgMetGluArgLleLeuAspLysLeuAsnTrpAsp 141
Db 363 TGTTCCTCATCTGAAATTTTGGAAATGGAGAGAAATTTCTGGATAATGGAATGGGAT 422
Qy 142 LeuHisThrAlaThrProLeuAspPheLeuHisLlePheHisAlaLleAlaValSerThr 161
Db 423 CTTACACAGGCACACCACTGGAATTTCTTCATATTTTCCATGCAATTCGCAAGTGTCACT 482
Qy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
Db 483 AGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCAATCTCAACATTTGGCAGTCTCT 542
Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSerMet 201
Db 543 ACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATG 602
Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLleProAspTrpLeuSerLeu 221
Db 603 CTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAAACTCATTCCTGATTTGGCTTTCTCTT 662
Qy 222 ThrLleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArgGly 241
Db 663 ACAATTGAACTGCTTCAGAAAGCAGATGATAGTCCCAAGTTCATTCATTTGTCGGAG 722
Qy 242 LeuValAlaHisHisLeu 247
Db 723 CTTGTGGCACATCACCTT 740
```

RESULT 9

```
BQ673277
LOCUS          920 bp      mRNA      linear      EST 15-JUL-2002
DEFINITION    AGENCOURT 8354951 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6275333
5', mRNA sequence.
```

ACCESSION

```
BQ673277
```

VERSION

```
BQ673277.1 GI:21784111
```

KEYWORDS

```
EST.
```

SOURCE

```
Homo sapiens (human)
```

ORGANISM

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
1 (bases 1 to 920)
```

```
NIH-MGC http://mgs.nci.nih.gov/.
```

```
National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
Unpublished (1999)
```

```
Contact: Robert Strausberg, Ph.D.
```

```
Email: cgaabs-remail.nih.gov
```

```
Tissue Procurement: ATCC
```

```
cDNA Library Preparation: Rubin Laboratory
```

```
cDNA Arrayed by: The I.M.A.G.E. Consortium (LML)
```

```
DNA Sequencing by: Agencourt Bioscience Corporation
```

```
Clone distribution: MGC clone distribution information can be
```

```
found through the I.M.A.G.E. Consortium/LML at:
```

```
http://image.llnl.gov
```

```
Plate: LUCM2458 row: f column: 06
```

```
High quality sequence stop: 691.
```

```
Location/Qualifiers
```

```
1. 920
```

```
/organism="Homo sapiens"
```

```
/mol_type="mRNA"
```

```
/db_xref="taxon:9606"
```

```
/clone="IMAGE:6275333"
```

```
/tissue type="epidermoid carcinoma, cell line"
```

```
/lab host="DH10B (phage-resistant)"
```

```
/clone lib="NIH_MGC_102"
```

```
/note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
```

```
Site_2: EcoRI; cDNA made by oligo-dT priming.
```

FEATURES

```
source
```

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

```
Alignment Scores:
Pred. No.:      2,82e-230      Length:      920
Score:          244.00         Matches:    244
Percent Similarity: 100.00%     Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:    64.72%         Indels:     0
DB:              5            Gaps:         0

US-09-736-250-1 (1-377) x BQ673277 (1-920)
Qy 22 ArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnValSer 41
Db 42 AGGAAGCACAGATGTGGAAGTGAATGTGGGAAATGCTTCAAATCAGAATGTTCT 101
Qy 42 ProSerGlnArgAspGluValLleGlnTrpLeuAlaLysLeuLysTrpGlnPheAsnLeu 61
Db 102 CCATCCAGAGAGATGAAGTAATTCATGGCTGGCCAACTCAAGTACCAATTCACCTT 161
Qy 62 TyrProGlnThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLys 81
Db 162 TACCCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTCAGTACCGTAAG 221
Qy 82 AlaHisProLysTrpLeuSerCysLleAlaLleSerCysPhePheLeuAlaAlaLysThr 101
Db 222 GCTCATCAAAATACTTTGAGTTGATTGCAATCAGCTGTTTTCCTAGCTGCCAAGACT 281
Qy 102 ValGluGluAspGluArgLleProValLeuLysValLeuAlaArgAspSerPheCysGly 121
Db 282 GTTGAGGAAGATGAGAGAAATTCAGTACTAAAGGTATTGGCAAGAGACAGTTTCGTGGA 341
Qy 122 CysSerSerGluLleLeuArgMetGluArgLleLleLeuAspLysLeuAsnTrpAsp 141
Db 342 TGTTCCTCANTCTGAAATTTTGAGATGAGAGAAATTAATCTGGATAGTGAATGGATG 401
Qy 142 LeuHisThrAlaThrProLeuAspPheLeuHisLlePheHisAlaLleAlaValSerThr 161
Db 402 CTTACACAGCCACACCATTTGGATTTTTCATATTTCCATTTCCATTTGCGATGTCACT 461
Qy 162 ArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeu 181
Db 462 AGGCCTCAGTTACTTTTCAGTTTGGCCAAATTCAGCCCATCTCAACATTTGGCAGTCT 521
Qy 182 ThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysMet 201
Db 522 ACCAAGCAACTACTTCACTGTATGGCTGCAACCAACTTTCCGATTTCCAGAGGATCCATG 581
Qy 202 LeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLleProAspTrpLeuSerLeu 221
Db 582 CTTGCTCTGGCCATGGTTAGTCTGGAATGGAGAAACTCATTCCTGATGGCTTCTCTT 641
Qy 222 ThrLleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLleHisCysArgGlu 241
Db 642 ACAATTCGAATGCTTCAGAAAGCACAGATGATGATGATGATGATGATGATGATGATG 701
Qy 242 LeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrVal 261
Db 702 CTTGTGGCACATCACCTTTCTACTCTGCACTCTTCCCTGCTCTGCAATTCGGTTATGTC 761
Qy 262 TyrArgProLeu 265
Db 762 TACCGTCCCTC 773

RESULT 10
BUI49962
LOCUS          BUI49962      862 bp      mRNA      linear      EST 03-SEP-2002
```

```

DEFINITION  AGENCOURT_8120758 Lupski_dorsal_root_ganglion Homo sapiens cDNA
clone IMAGE:6178515 5', mRNA sequence.
ACCESSION   BUI49962
VERSION     BUI49962.1  GI:22663494
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cspbs-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13558 row: d column: 04
High quality sequence stop: 736.
FEATURES             source
    Location/Qualifiers
        1..862
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6178515"
            /sex="male"
            /tissue_type="dorsal root ganglia"
            /dev_stage="adult, 36 yr"
            /lab_host="DH10B"
            /clone_lib="Lupski dorsal root ganglion"
            /note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
            NotI; Site_2: SalI; cDNA made by oligo-dr priming.
            Directionally cloned using the following adaptors:
            5'-TCGACCCACGGCTCCG-3' and
            5'-GACATGTTCTAGATCGGCGGCCCT(15)-3'. Size selected >
            1 kb for average insert length 1.7 kb. This is a primary
            library, non-amplified. Library constructed by Life
            Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
            College of Medicine) and is available through Life
            Technologies."
ORIGIN
Alignment Scores:
Pred. No.:      2,578-229      Length:      862
Score:          243.00      Matches:      256
Percent Similarity: 99.61%      Conservative: 0
Best Local Similarity: 99.61%      Mismatches: 0
Query Match:     64.46%      Indels:      1
DB:              5          Gaps:          0

US-09-736-250-1 (1-377) x BUI49962 (1-862)

Qy      1  MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaVal 20
Db      18  ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGTTCTTCCTGTTGGAAAGGCATC 77
Qy      21  ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db      78  ACTAGGGAAGCACACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAATCAGAATGTT 137
Qy      41  SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyGlnPheAsn 60
Db      138  TCTCCATCCACAGAGATGAGTAATTCATGTGGTGGCCAAACTCAAGTACCAATTCAC 197
Qy      61  LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db      198  CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTACCTACCGTA 257

```

```

Qy      81  LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db      258  AAGGCTCATCAAAATACATTGAGTTGTAATGCAATCAGCTGTTTTTCTTCTAGCTGCCAAG 317
Qy      101  ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db      318  ACTGTTGAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGACAGAGATTTCTGT 377
Qy      121  GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db      378  GGATGTTCTCTCATCTGAAATTTTGAAGATGGAGAGAAATTTCTGGATAAGATTGAAATGG 437
Qy      141  AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db      438  GATCTTCACACAGCCACCATTTGATTTCTTCATATTTTTCATGCAATTCAGTGTGCA 497
Qy      161  ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db      498  ACTAGGCTCAGTTACTTTTCAGTTTGCCTCCAAATGAGCCCATCTCAACATTTGCGAGTC 557
Qy      181  LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db      558  CTTACCAAGCAACTACTTCTGATGGCTTGCACCACTTCTGCAATTCAGAGGATCC 617
Qy      201  MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db      618  ATGCTTGCTCTGGCCATGGTTAGTCTGGAATGAGAAACTCATCTCTGATGGCTTCT 677
Qy      221  LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db      678  CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCCCACTGATTCATTCATGTCGG 737
Qy      241  -GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeu 256
Db      738  GGAGCTTGTGGCACAATCACCTTTCTACTCTGCACTCTTCCCTGCTCTG 786

RESULT 11
BX437607
LOCUS      BX437607 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP007YP05
DEFINITION 5-PRIME, mRNA sequence.
ACCESSION  BX437607
VERSION     BX437607.2  GI:46999917
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 830)
AUTHORS     Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE       Full-length cDNA libraries and normalization
JOURNAL     Unpublished (2001)
COMMENT     On May 15, 2003 this sequence version replaced gi:30771586.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 2356.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOCAP007CH03QP1&c=2356.r.
FEATURES             source
    Location/Qualifiers
        1..830
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="CSOCAP007YP05"
            /tissue_type="THYMUS"
            /clone_lib="Homo sapiens THYMUS"

```

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Alignment Scores:

Pred. No.: 2.35e-227 Length: 830
Score: 241.00 Matches: 273
Percent Similarity: 99.27% Conservative: 0
Best Local Similarity: 99.27% Mismatches: 1
Query Match: 63.93% Indels: 2
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BX437607 (1-830)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 9 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGTCTTCTCTGTGGAAAGGCAATC 68
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 69 ACTAGGGAAGCACAGATGTGAAAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT 128
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 129 TCTCATCCAGAGAGATGAAGTAATTCATAGCTGGCCAACTCAAGTACCAATTCAC 188
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 189 CTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGTGTTCAGTACCGTA 248
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 249 AAGGCTCATCAAAATCTTGAAGTGTATTGCAATCAGCTGTTCCTAGCTGGCCAAAG 308
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgSerPheCys 120
Db 309 ACTGTGGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 368
Qy 121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTrp 140
Db 369 GGATGTCTCTCATCTGAAATTTGAGATGAGAGAAATTTCTGGATAGTTCGAATGG 428
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 429 GATCTTACAGCCACACCATGATTTCTTATATTTTCCATGCAATTCAGAGTGTCA 488
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 489 ACTAGGCTCAGTTACTTTTTCAGTTTGCCTAAATTTGAGCCCATCTCAACATTTGGCAGTC 548
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 549 CTTTACCAAGCACTACTTCACTGTATGCGCTGCAACCACTTCTGCAATTCAGAGATCC 608
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 609 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGAGAAATCAATCTCTGATGGCTTCT 668
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 669 CTTACAAATTAAGTCTTTCAGAAAGCACAGATGATAGTCCCATGTTGATTCATTTGCGG 728
Qy 241 GluLeuValAlaHisIleSerThrLeuGlnSerSerLeuProLeuAsnSerValTy 260
Db 729 GAGCK-TGTGGCAATCACCTTTCTACTCTGAGTCTTCCCTGCTCTGAAATTCGGTTA 787
Qy 260 rValTyrArgProLeuLysHisThrLeuValThrCysAspLys 274
Db 788 TGTATACCGTCCCTCAAGCACACCTTGGTGGCTGTGACCTGTGACMAA 830

RESULT 12

BUI59699
LOCUS BUI59699
DEFINITION AGENCOURT 7888352 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:6141567
S., mRNA sequence.
ACCESSION BUI59699
VERSION BUI59699.1 GI:22673609
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov.
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13461 row: p column: 16
High quality sequence stop: 681.
Location/Qualifiers
1. 853
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6141567"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_67"
/notes="Organ: eye; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Library constructed by Life Technologies."

FEATURES

source

ORIGIN

Alignment Scores:

Pred. No.: 2.13e-222 Length: 853
Score: 236.00 Matches: 269
Percent Similarity: 99.26% Conservative: 0
Best Local Similarity: 99.26% Mismatches: 1
Query Match: 62.60% Indels: 2
DB: 5 Gaps: 0

US-09-736-250-1 (1-377) x BUI59699 (1-853)

Qy 48 ValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsnLeuTyrProGluThrPheAla 67
Db 2 GTAATTAATGGTGGCCAACTCAAGTACCAATTCACCTTACCAGAAACATTTGCT 61
Qy 68 LeuAlaSerSerLeuLeuAspArgPheLeuAlaThrValLysAlaHisProLysTyrLeu 87
Db 62 CTGGCTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTAAAGGCTCATCCAAATACTTG 121
Qy 88 SerCysIleAlaIleSerCysPhePheLeuAlaAlaLysThrValGluGluAspGluArg 107
Db 122 AGTTGATTCGAATCAGCTGTTTTTCTAGCTGCCAAGACTGTTGAGGAAGATGAGAGA 181
Qy 108 IleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIle 127
Db 182 ATTCCAGTACTAAAGGTATTGGCAAGACAGACAGTTCTCTGTGGATGTTCTCATCTGAAT 241
Qy 128 LeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrPro 147
Db 242 TTGAGATGGAGAGAAATTTCTGGATAGTTCGAATGGGATCTTCACAGCCACCA 301
Qy 148 LeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPhe 167

Db 302 TTGGATTTTTCATATTTTCATGCCATTCAGAGTCACTAGGCTCAGTTACTTTTC 361
 Qy 168 SerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHis 187
 Db 362 AGTTTGCCCAATGAGCCCATCTCAACATTTGGCAGTCTTACCAAGCACTACTTCAC 421
 Qy 188 CysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetVal 207
 Db 422 TGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCCATGCTTGCTCTGGCCATGTT 481
 Qy 208 SerLeuGluMetGluLeuLeuLeuProAspTrpLeuSerLeuThrIleGluLeuLeuGln 227
 Db 482 AGTCTGGAATGGAGAACTCATCTCCTGATTGGCTTTCTCTACAAATGAACTGCTTCAG 541
 Qy 228 LysAlaGlnMetAspSerSerGlnLeuLeuHisCysArgGluLeuValAlaHisLeu 247
 Db 542 AAAGCACAGATGGATAGTCCAGTTGATCCATGTCGGAGCTTGTGGCACATCACCTT 601
 Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTyValTyArgProLeuLysHis 267
 Db 602 TCTACTCTGCACTCTCCCTGCTGCAATTCGCTTTATGTCTACCGTCCCTCAAGCAC 661
 Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerVal-ProGlyPr 287
 Db 662 ACCCTGGTGACTGTGCAAGAGTGTTCAGATTACATCCCTCTCTGNG-TCCAGGCC 720
 Qy 287 oAspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTy 307
 Db 721 AGACTTCTCCAGGACACACAGCCAGAGAGTGCACGTACAGGTACAGAGCTTTTA 780
 Qy 307 RHISLeuProAlaAlaSerGlyCysLys 317
 Db 781 CCATCATCTCCAGCTGCGAGTGGTGCAAA 811

RESULT 13

BG205510 764 bp mRNA linear EST 21-APR-2001
 LOCUS RST24889 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.

DEFINITION BG205510
 ACCESSION BG205510.1 GI:13727148
 VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 764)

AUTHORS Harrington, J. J., Sherf, B., Rundlett, S., Jackson, P. D., Perry, R.,

Cain, S., Leventhal, C., Thornton, M., Ramchandran, R.,

Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Booser, S.,

Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K.,

Offenbacher, J., Danzig, J. and Ducar, M.

Creation of genome-wide protein expression libraries using random

activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)

JOURNAL 21227151

MEDLINE 11329013

PUBMED Contact: Scott J. Cain

COMMENT Athersys, Inc.

3201 Carnegie Ave, Cleveland, OH 44115, USA

Tel: 216 431 9900

Fax: 216 361 9596

Email: scai@atersys.com

High quality sequence stop: 551.

Location/Qualifiers

1..764

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/cell_line="HT1080"

/clone_lib="Athersys RAGE Library"

/note="See 'Creation of Genome-wide Protein Expression

Libraries using Random Activation of Gene Expression',

source

RESULT 14

BG189523

LOCUS

DEFINITION

RST8568 Athersys RAGE Library Homo sapiens cdna, mRNA sequence.

ACCESSION BG189523

VERSION BG189523.1

GI:13711210

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Alignment Scores:

Pred. No.: 1.86e-221 Length: 764
 Score: 235.00 Matches: 235
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 62.33% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-1 (1-377) x BG205510 (1-764)

Qy 39 AsnValSerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyGln 58
 Db 3 ANTGTTCCTCATCCCGAGAGAGATGAAGTAATTCAATGGCTGGCCAAACTCAAGTACCA 62
 Qy 59 PheAsnLeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAla 78
 Db 63 TTCAACCTTTACCAGAAACATTTGCTCTGGTAGCAGTCTTTTGGATAGGTTTTAGCT 122
 Qy 79 ThrValLysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAla 98
 Db 123 ACCGTAAAGGCTCATCCAAATATCTTGTAGTTGTAATTCGAATCAGCTGTTTTCTTCTAGCT 182
 Qy 99 AlalysThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSer 118
 Db 183 GCCAAGACTGTTGAGGAAGATGAGAGATTCAGTGTCTTAAGGTATTGGCAAGAGACAGT 242
 Qy 119 PheCysGlyCysSerSerSerGluIleLeuArgMetGluArgIleLeuLeuAspLysLeu 138
 Db 243 TTCTGTGGATGTTCTCATCTGAAATTTTGAAGATGAGAGAAATTTCTGGATAAGTTG 302
 Qy 139 AsnTrpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAla 158
 Db 303 AATTGGGATCTTCACAGCCACACCAATGGATTTCTTCATATTTTCCATGTCATGCA 362
 Qy 159 ValSerThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeu 178
 Db 363 GTGTCAACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTGAGCCCATCTCACATTTG 422
 Qy 179 AlaValLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArg 198
 Db 423 GCAGTCTCTTACCAAGCAACTACTTCTGATGCGCTGCAACCAACTTCTGCAATTCAGA 482
 Qy 199 GlySerMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrp 218
 Db 483 GGATCCCATGCTTGTCTGGCCATGGTTAGTCTGGAAATGGAGAAACTCATTTCTGATTGG 542
 Qy 219 LeuSerLeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHis 238
 Db 543 CTTTCTCTTACATTTGAATGCTTTCAGAAAGCACAGATGGATAGCTCCAGTTCCAT 602
 Qy 239 CysArgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSer 258
 Db 603 TGTGGGAGCTTGTGGCACATCACCTTTCTACTCTGAGTCTTCCCTGCCTCTGAAATTC 662
 Qy 259 ValTyValTyArgProLeuLysHisThrLeuValThrCysAsp 273
 Db 663 GTTTATGCTACCGTCCCTCAAGCACACCCCTGGTGTGAC 707


```
Qy 108 IleProValLeuLysValLeuAlaArgAspSerPheCysGlyCysSerSerSerGluIle 127
Db 7 ATTCAGTACTAAAGGATATGCGAAGACACAGTTTCTGTGGATGTTCTCATCTGAAAT 66
Qy 128 LeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeuHisThrAlaThrPro 147
Db 67 TTGAGATGGAGAGAATTAATCTCGATAAGTTGAATTGGGATCTTCACACAGCCACCA 126
Qy 148 LeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArgProGlnLeuLeuPhe 167
Db 127 TTGGATTTCTTCATATTTCCATGCCATTGCAGTGTCAACTAGGCCTCAGTTACTTTTC 186
Qy 168 SerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThrLysGlnLeuLeuHis 187
Db 187 AGTTTGCCCAAAATGAGCCCATCTCAACATTTGGCAGTCTTACCAAGCAACTACTTCAC 246
Qy 188 CysMetAlaCysAenGlnLeuLeuGlnPheArgGlySerMetLeuAlaLeuAlaMetVal 207
Db 247 TGTATGGCCTGCAACCAACTTCTGCAATTGGCAGTCCATGCTGTGCTCTGGCCATGGTT 306
Qy 208 SerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThrIleGluLeuLeuGln 227
Db 307 AGTCTGGAATGGAGAACTCATTCCTGATTGGCTTCTTACAAATTGAACCTGCTCAG 366
Qy 228 LysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeu 247
Db 367 AAAGCACAGATGGATAGTCCAGTTGATCCATTGTGCGAGCTTGTGGCACATCACCTT 426
Qy 248 SerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHis 267
Db 427 TCTACTCTGCAGTCTTCCCTGCCCTGTGAATTCGGTTATGTCTACCGTCCCTCAAGCAC 486
Qy 268 ThrLeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyPro 287
Db 487 ACCCTGGTGACTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGTCCAGGCCCA 546
Qy 288 AspPheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyr 307
Db 547 GACTTCTCCAAGGACAAACAGCAAGCCAGAGTGCAGTCCAGGTACAGCAGCCTTTTAC 606
Qy 308 HisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGlu 327
Db 607 CATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGAA 666
Qy 328 MetGluValAspPheTyrAspGlyIleLysArgLeuTyrAsn 342
Db 667 ATGGAAGTGGATGACTTCTATGATGGAATCAACGGCTCTATAT 711
```

Search completed: February 11, 2005, 12:21:04
Job time : 6017.84 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:56:46 ; Search time 7689.45 Seconds
(without alignments)
2375.673 Million cell updates/sec

Title: US-09-736-250-1

Perfect score: 377

Sequence: 1 MKFPGPLENQLSLLEKAI.....LSRQEGHASPPLPQPVSVVM 377

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9408497

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODSL=frame+p2n.model -DEV=xlh
-O=/cgn2.1/usPTO.apool/US09736250/runat_07022005.154942.20650/app.query.fasta_1.718
-DB=GenEmbl -QWMT=fastap -SUPPLX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1.1 3890 @runat_07022005.154942.20650 -NCPU=6 -ICPU=3
-NO.MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	377	100.0	1133	6	AR145734 Sequence
2	377	100.0	1260	6	AR087353 Sequence
3	377	100.0	1260	6	QR812312 Sequence
4	377	100.0	1260	6	AR281918 Sequence

5	377	100.0	1260	6	AR380354 Sequence
6	377	100.0	1260	9	HUMCYI
7	377	100.0	1384	9	AF135162 Homo sapi
8	377	100.0	1817	9	BC000420 Homo sapi
9	377	100.0	1889	6	CQ468129 Sequence
10	377	100.0	1889	9	BC004975 Homo sapi
11	266	70.6	2755	6	CQ414515 Sequence
12	240	63.7	1131	9	CR541783 Homo sapi
13	230	61.0	690	6	CQ721727 Sequence
14	149	39.5	29867	9	AY207372 Homo sapi
15	149	39.5	35191	9	AF111196 Homo sapi
16	149	39.5	178916	2	AP002874 Homo sapi
17	149	39.5	179443	2	AC079051 Homo sapi
18	144	38.2	444	6	AX886044 Sequence
19	144	38.2	444	6	BD025654 Sequence
20	133	36.9	444	6	CQ671106 Sequence
21	133	35.3	490	6	CQ685286 Sequence
22	129	34.2	804	6	BD079737 Cancer-as
23	126	33.4	601	11	BV180201 sqnm10841
24	123	32.6	2146	6	CQ414223 Sequence
25	118	31.3	389	6	CQ661908 Sequence
26	112	29.7	369	6	CQ688465 Sequence
27	99	26.3	601	11	BV167473 sqnm5620
28	90	23.9	536	6	AX780652 Sequence
29	90	23.9	1535	10	AF005886 Mus muscu
30	90	23.9	2348	10	BC003290 Mus muscu
31	88	23.3	1493	6	BD194541 Human nuc
32	88	23.3	1493	6	AX015395 Sequence
33	84	22.3	409	6	AX779269 Sequence
34	77	20.4	350	6	CQ675890 Sequence
35	75	19.9	486	6	CQ410226 Sequence
36	65	17.2	447	6	AX198885 Sequence
37	65	17.2	447	6	AX209412 Sequence
38	62	16.4	889	6	CQ468128 Sequence
39	50	13.3	200850	2	AC101881 Mus muscu
40	50	13.3	202228	2	AC124646 Mus muscu
41	49	13.0	426	6	CQ397543 Sequence
42	49	13.0	426	6	CQ403842 Sequence
43	47	12.5	590	11	G51451 SHGC-80948
44	46	12.2	113811	10	AF228739S2
45	46	12.2	193811	2	AC134827 Mus muscu
46	46	12.2	241543	2	AC099472 Rattus no
47	46	12.2	260517	2	AC111318 Rattus no
48	46	12.2	270068	2	AC113213 Rattus no
49	43	11.4	145795	2	AC022548 Homo sapi
50	43	11.4	146586	9	AC104771 Homo sapi
51	41	10.9	288	6	CQ712652 Sequence
52	40	10.6	477	6	CQ398303 Sequence
53	40	10.6	477	6	CQ404590 Sequence
54	40	10.6	516	6	CQ410974 Sequence
55	38	10.1	136	6	A74835 Sequence 52
56	38	10.1	136	6	A77814 Sequence 52
57	37	9.8	444	6	AX397198 Sequence
58	36	9.5	179333	2	AC117658 Mus muscu
59	34	9.0	304	6	AX914031 Sequence
60	34	9.0	304	6	BD049564 Sequence
61	34	9.0	308	6	CQ696855 Sequence
62	29	7.7	1553	5	BC075116 Xenopus t
63	29	7.7	1658	5	BC061670 Xenopus l
64	25	6.6	368	11	G53823 SHGC-85345
65	24	6.4	244	6	CQ713942 Sequence
66	22	5.8	183	6	A74629 Sequence 31
67	22	5.8	183	6	A77608 Sequence 31
68	21	5.6	818	5	BX930648 Gallus ga
69	20	5.3	200	6	CQ660642 Sequence
70	19	5.0	60	6	CQ543223 Sequence
71	15	4.0	251	6	CQ689968 Sequence
72	14	3.7	65	6	CQ558861 Sequence
73	13	3.4	135	6	A74630 Sequence 31
74	13	3.4	135	6	A77609 Sequence 31
75	13	3.4	790	5	BX930233 Gallus ga
76	13	3.4	1850	5	BX950469 Gallus ga
77	13	3.4	2166	5	BC044400 Danio rer

78	13	3.4	2339	5	BC068369	BC068369	Danio rer	151	9	2.4	228736	2	AC097228	AC097228	Pan trogl
79	13	3.4	15161	10	AF228739	Mus muscu	152	9	2.4	229252	2	AC096043	AC096043	Rattus no	
80	12	3.2	183	6	CQ704042	Sequence	153	9	2.4	231580	2	AC136817	AC136817	Rattus no	
81	10	2.7	227524	2	AC126180	Rattus no	c 154	9	2.4	236974	2	AC095207	AC095207	Rattus no	
82	10	2.7	23219	2	AC136572	Rattus no	155	9	2.4	240797	2	AC098388	AC098388	Rattus no	
83	9	2.4	756	8	AY050319	Arabidops	156	9	2.4	244637	2	AC109053	AC109053	Rattus no	
84	9	2.4	1608	8	AF139807	Arabidops	c 157	9	2.4	247119	2	AC126868	AC126868	Rattus no	
85	9	2.4	1643	6	AR237858	Sequence	c 158	9	2.4	249490	2	AC126561	AC126561	Rattus no	
86	9	2.4	2215	8	AY340621	Aspergill	c 159	9	2.4	252988	2	AC121550	AC121550	Mus muscu	
87	9	2.4	2023	10	AF207742	Mus muscu	160	9	2.4	257451	2	AC098508	AC098508	Rattus no	
88	9	2.4	6265	6	AR237859	Sequence	161	9	2.4	259629	2	AC119553	AC119553	Rattus no	
89	9	2.4	7006	14	AF296094	Porcine t	c 162	9	2.4	275688	2	AC111722	AC111722	Rattus no	
90	9	2.4	7008	14	AF296100	Porcine t	163	9	2.4	279908	2	AC151281	AC151281	Mus muscu	
91	9	2.4	7018	14	AF296117	Porcine t	164	9	2.4	296820	10	AF312033	AF312033	Mus muscu	
92	9	2.4	7019	14	AF296109	Porcine t	c 165	9	2.4	300312	2	AC111822	AC111822	Rattus no	
93	9	2.4	18544	2	AC020199	Drosophil	166	9	2.4	301136	3	AE003591	AE003591	Drosophil	
94	9	2.4	24389	6	CQ612392	Sequence	c 167	9	2.4	335551	2	AC115496	AC115496	Rattus no	
95	9	2.4	37144	1	MICB2492	Myobacteri	168	9	2.4	348950	1	MLEPRTN7	MLEPRTN7	Mycobacte	
96	9	2.4	74613	8	AB005230	Arabidops	c 169	8	2.1	236	6	ATH521114	ATH521114	Arabidops	
97	9	2.4	83178	2	AC117537	Magnaport	170	8	2.1	277	6	AR244739	AR244739	Sequence	
98	9	2.4	98546	2	AC149146	Xenopus t	c 171	8	2.1	279	6	AX916767	AX916767	Sequence	
99	9	2.4	99708	2	AC149531	Xenopus t	c 172	8	2.1	279	6	BD052300	BD052300	Sequence	
100	9	2.4	101981	9	AC003001	Homo sapi	c 173	8	2.1	282	8	AY233739	AY233739	Clavispor	
101	9	2.4	104002	9	HS388N15	Continuation (3 of	174	8	2.1	324	11	G60347	G60347	SHGC-150259	
102	9	2.4	110000	2	AC130075	Human DNA	175	8	2.1	324	11	HS065YD5	HS065YD5	SHGC-150259	
103	9	2.4	114279	2	AC083907	Homo sapi	176	8	2.1	367	11	BV105444	BV105444	H.sapiens (
104	9	2.4	130260	2	AC083907	Mus muscu	177	8	2.1	377	11	BV128386	BV128386	PZA00411	
105	9	2.4	138761	2	CR790366	Danio rer	178	8	2.1	382	6	AR521433	AR521433	Sequence	
106	9	2.4	142189	2	AC148072	Dasytus n	179	8	2.1	400	6	AR355411	AR355411	Sequence	
107	9	2.4	142948	9	AC147025	Pan trogl	180	8	2.1	400	6	AR536967	AR536967	Sequence	
108	9	2.4	146813	2	BX927104	Danio rer	181	8	2.1	400	11	BV128405	BV128405	PZA00411	
109	9	2.4	149461	2	AC019282	Homo sapi	182	8	2.1	403	11	BV128385	BV128385	PZA00411	
110	9	2.4	157410	2	AC021341	Homo sapi	183	8	2.1	407	11	BV128397	BV128397	PZA00411	
111	9	2.4	157657	9	AL353742	Human DNA	184	8	2.1	408	11	BV128395	BV128395	PZA00411	
112	9	2.4	160972	2	AC011673	Homo sapi	185	8	2.1	411	11	BV128398	BV128398	PZA00411	
113	9	2.4	163382	6	CQ869778	Sequence	186	8	2.1	412	11	BV128382	BV128382	PZA00411	
114	9	2.4	164183	2	AC079233	Homo sapi	c 187	8	2.1	413	8	AY656922	AY656922	Unculture	
115	9	2.4	164434	2	AC009841	Drosophil	188	8	2.1	418	11	BV128389	BV128389	PZA00411	
116	9	2.4	164457	8	AC138580	Medicago	189	8	2.1	421	11	BV128383	BV128383	PZA00411	
117	9	2.4	167519	9	AC013727	Homo sapi	190	8	2.1	421	11	BV128404	BV128404	PZA00411	
118	9	2.4	168037	2	AC150211	Otolemur	191	8	2.1	422	11	BV128387	BV128387	PZA00411	
119	9	2.4	168176	2	AC121101	Mus muscu	192	8	2.1	424	11	BV128396	BV128396	PZA00411	
120	9	2.4	168414	2	AC106815	Homo sapi	193	8	2.1	424	11	BV128408	BV128408	PZA00411	
121	9	2.4	169118	2	AC073313	Homo sapi	194	8	2.1	424	11	BV128410	BV128410	PZA00411	
122	9	2.4	169405	9	AC092800	Homo sapi	195	8	2.1	428	11	BV128390	BV128390	PZA00411	
123	9	2.4	170552	2	AC139659	Rattus no	196	8	2.1	428	11	BV128406	BV128406	PZA00411	
124	9	2.4	171790	2	AC011106	Homo sapi	197	8	2.1	434	11	BV128411	BV128411	PZA00411	
125	9	2.4	174588	9	AC011841	Homo sapi	c 198	8	2.1	435	6	AX779282	AX779282	Sequence	
126	9	2.4	175645	9	AC073114	Homo sapi	199	8	2.1	435	11	BV128409	BV128409	PZA00411	
127	9	2.4	176446	9	AC142327	Pan trogl	200	8	2.1	437	11	BV128392	BV128392	PZA00411	
128	9	2.4	177855	9	AC013718	Homo sapi	201	8	2.1	438	11	BV128384	BV128384	PZA00411	
129	9	2.4	178965	3	AC010117	Drosophil	202	8	2.1	438	11	BV128399	BV128399	PZA00411	
130	9	2.4	182896	2	AC011043	Homo sapi	203	8	2.1	441	11	BV128398	BV128398	PZA00411	
131	9	2.4	184795	2	AC150640	Bos tauru	204	8	2.1	441	11	BV128394	BV128394	PZA00411	
132	9	2.4	184829	2	AC133506	Mus muscu	205	8	2.1	450	11	G37490	G37490	SHGC-57864	
133	9	2.4	186059	10	AC130826	Mus muscu	c 206	8	2.1	463	1	AY261408	AY261408	Unculture	
134	9	2.4	188901	2	AC132886	Mus muscu	c 207	8	2.1	493	8	AV190539	AV190539	Clavispor	
135	9	2.4	192510	10	AC121999	Mus muscu	c 208	8	2.1	494	8	AY190541	AY190541	Clavispor	
136	9	2.4	192919	10	AL732464	Mouse DNA	c 209	8	2.1	495	8	AJ786246	AJ786246	Clavispor	
137	9	2.4	198468	9	AC098477	Homo sapi	c 210	8	2.1	511	11	G73397	G73397	ATM, exon3 R	
138	9	2.4	198649	8	AY534123	Aegilops	c 211	8	2.1	512	6	AR503348	AR503348	Sequence	
139	9	2.4	200033	9	HS021973	Homo sapi	212	8	2.1	512	6	AR518630	AR518630	Sequence	
140	9	2.4	200997	2	AC141220	Rattus no	c 213	8	2.1	517	8	CLU44817	CLU44817	Clavispora	
141	9	2.4	202914	2	AC078939	Homo sapi	214	8	2.1	558	11	G63060	G63060	SHGC-140653	
142	9	2.4	203100	9	AC145965	Pan trogl	215	8	2.1	559	11	BV054827	BV054827	S212P6038	
143	9	2.4	208840	2	CR318658	Danio rer	c 216	8	2.1	605	11	G85721	G85721	S209P6387RG	
144	9	2.4	209611	5	BX001058	Zebrafish	c 217	8	2.1	612	8	AY497690	AY497690	Clavispor	
145	9	2.4	209888	2	AC146462	Saimiri s	218	8	2.1	624	5	CR389084	CR389084	Gallus ga	
146	9	2.4	210148	10	AL928791	Mouse DNA	c 219	8	2.1	656	11	PM6C4B	PM6C4B	AL684917 Penicilli	
147	9	2.4	210136	2	AC128830	Rattus no	c 220	8	2.1	664	11	PM10G5B	PM10G5B	AL684055 Penicilli	
148	9	2.4	213776	2	AC126092	Rattus no	c 221	8	2.1	675	9	HS0328112	HS0328112	Homo sapi	
149	9	2.4	217080	10	AC105019	Mus muscu	c 222	8	2.1	681	11	PM6F10B	PM6F10B	Penicilli	
150	9	2.4	218631	2	AC109532	Rattus no	c 223	8	2.1	737	9	HSRGL14	HSRGL14	Homo sapi	

224	8	2.1	740	5	D14314	D14314 Gallus gall	297	8	2.1	1967	8	S81897	S81897 OsNramp1-Nr
225	8	2.1	773	8	AF362992	AF362992 Fucus ves	298	8	2.1	1987	8	R1CNRAMP	L41217 Oryza sativ
c 226	8	2.1	852	6	BD147371	BD147371 Primer fo	c 299	8	2.1	1989	6	CQ599940	CQ599940 Sequence
c 227	8	2.1	852	6	AX867309	AX867309 Sequence	c 300	8	2.1	1992	6	AX319765	AX319765 Sequence
228	8	2.1	879	6	CQ735521	CQ735521 Sequence	c 301	8	2.1	2000	6	AX654926	AX654926 Sequence
229	8	2.1	912	6	AX393979	AX393979 Sequence	c 302	8	2.1	2000	6	AX656434	AX656434 Sequence
230	8	2.1	912	6	AX366951	AX366951 Sequence	c 303	8	2.1	2001	6	BD193228	BD193228 Novel fam
231	8	2.1	915	1	AF503437	AF503437 Bacillus	c 304	8	2.1	2007	6	AX621706	AX621706 Sequence
232	8	2.1	921	1	AY084076	AY084076 Bacillus	c 305	8	2.1	2021	6	AX432742	AX432742 Sequence
233	8	2.1	921	11	BV005803	BV005803 BARC0051	c 306	8	2.1	2071	6	CQ842600	CQ842600 Sequence
c 234	8	2.1	1053	6	AX550723	AX550723 Sequence	c 307	8	2.1	2071	9	AK123972	AK123972 Homo sapi
c 235	8	2.1	1053	6	AX594468	AX594468 Sequence	c 308	8	2.1	2071	9	AK123972	AK123972 Homo sapi
c 236	8	2.1	1053	6	AX818588	AX818588 Sequence	c 309	8	2.1	2083	9	AK121534	AK121534 Oryza sat
c 237	8	2.1	1053	6	AX829618	AX829618 Sequence	c 310	8	2.1	2100	9	BC043385	BC043385 Homo sapi
c 238	8	2.1	1053	8	AX557694	AX557694 Saccharom	c 311	8	2.1	2126	9	AB042550	AB042550 Oryza sat
c 239	8	2.1	1059	8	AF229410	AF229410 Brassica	c 312	8	2.1	2136	5	BC053303	BC053303 Danio rer
c 240	8	2.1	1060	8	AF229412	AF229412 Brassica	c 313	8	2.1	2161	6	AX695726	AX695726 Sequence
c 241	8	2.1	1069	8	AF229409	AF229409 Brassica	c 314	8	2.1	2161	9	S57212	S57212 hMEF2C=mvoc
c 242	8	2.1	1070	8	AF229408	AF229408 Brassica	c 315	8	2.1	2165	6	AX339095	AX339095 Sequence
243	8	2.1	1073	5	GHMG2A	X63463 G.gallus HM	c 316	8	2.1	2187	6	AX346253	AX346253 Sequence
244	8	2.1	1089	6	AX339097	AX339097 Sequence	c 317	8	2.1	2218	8	AK066495	AK066495 Oryza sat
245	8	2.1	1099	6	AX109688	AX109688 Sequence	c 318	8	2.1	2248	8	D87042	D87042 Zea mays mR
246	8	2.1	1109	5	CR388627	CR388627 Gallus ga	c 319	8	2.1	2254	8	AK061881	AK061881 Oryza sat
247	8	2.1	1119	9	HUMGGFEFA	M69023 Homo sapien	c 320	8	2.1	2287	6	CQ841613	CQ841613 Sequence
c 248	8	2.1	1125	6	AR375643	AR375643 Sequence	c 321	8	2.1	2287	9	AK123255	AK123255 Homo sapi
249	8	2.1	1127	8	AF402076	AF402076 Zygosacch	c 322	8	2.1	2341	3	D86741	D86741 Caenorhabdi
250	8	2.1	1127	8	AF402085	AF402085 Kluyverom	c 323	8	2.1	2365	5	AY256908	AY256908 Danio rer
c 251	8	2.1	1174	5	GGU24675	U24675 Gallus gall	c 324	8	2.1	2390	5	AY721043	AY721043 Gallus ga
252	8	2.1	1176	6	AX339096	AX339096 Sequence	c 325	8	2.1	2420	5	AB096039	AB096039 Gallus ga
253	8	2.1	1231	6	AR505948	AR505948 Sequence	c 326	8	2.1	2431	3	D86740	D86740 Nematode mR
c 254	8	2.1	1233	6	AR451000	AR451000 Sequence	c 327	8	2.1	2450	9	HSSEC232	X97065 H.sapiens m
c 255	8	2.1	1245	10	AY288422	AY288422 Mus muscu	c 328	8	2.1	2451	6	CQ719441	CQ719441 Sequence
c 256	8	2.1	1245	10	AY633765	AY633765 Mus muscu	c 329	8	2.1	2464	9	AK027078	AK027078 Homo sapi
c 257	8	2.1	1252	5	AY423005	AY423005 Danio rer	c 330	8	2.1	2498	9	BC042553	BC042553 Homo sapi
258	8	2.1	1267	6	AR504358	AR504358 Sequence	c 331	8	2.1	2516	8	AB034803	AB034803 Pisum sat
259	8	2.1	1267	6	AR519640	AR519640 Sequence	c 332	8	2.1	2562	11	AF356180S2	AF356181 Hordeum v
c 260	8	2.1	1315	5	CR352412	CR352412 Gallus ga	c 333	8	2.1	2589	8	ATH296275	ATH296275 Arabidops
261	8	2.1	1320	9	HSM801208	AL122064 Homo sapi	c 334	8	2.1	2602	9	BC052802	BC052802 Homo sapi
c 262	8	2.1	1332	6	CQ604506	CQ604506 Sequence	c 335	8	2.1	2622	9	BC082968	BC082968 Homo sapi
263	8	2.1	1338	6	CQ735120	CQ735120 Sequence	c 336	8	2.1	2641	9	BSM808198	BSM808198 Homo sapi
264	8	2.1	1347	5	BC067660	BC067660 Danio rer	c 337	8	2.1	2655	8	POS430697	POS430697 Pleurotus
265	8	2.1	1358	8	AK103557	AK103557 Oryza sat	c 338	8	2.1	2658	1	AF087018	AF087018 Acetobact
c 266	8	2.1	1437	1	AF297010	AF297010 Pseudomon	c 339	8	2.1	2787	10	BC057212	BC057212 Mus muscu
c 267	8	2.1	1449	6	CQ745861	CQ745861 Sequence	c 340	8	2.1	2790	6	AR322399	AR322399 Sequence
c 268	8	2.1	1505	3	AY058667	AY058667 Drosophil	c 341	8	2.1	2797	9	AK123396	AK123396 Homo sapi
c 269	8	2.1	1510	8	BT015739	BT015739 Arabidops	c 342	8	2.1	2800	6	AX832899	AX832899 Sequence
c 270	8	2.1	1527	6	AR347066	AR347066 Sequence	c 343	8	2.1	2800	9	AK094119	AK094119 Homo sapi
c 271	8	2.1	1543	3	DROALDO	D10762 Drosophila	c 344	8	2.1	2826	10	MTU23922	MTU23922 Mus muscu
272	8	2.1	1550	6	CQ413710	CQ413710 Sequence	c 345	8	2.1	2833	10	BC003469	BC003469 Mus muscu
273	8	2.1	1566	8	AK110468	AK110468 Oryza sat	c 346	8	2.1	2881	5	AJ621377	AJ621377 Tetraodon
c 274	8	2.1	1621	3	AF035229	AF035229 Leishmani	c 347	8	2.1	2882	8	AK067110	AK067110 Oryza sat
c 275	8	2.1	1650	14	AY362031	AY362031 Ovine pro	c 348	8	2.1	2986	6	AX705334	AX705334 Sequence
c 276	8	2.1	1654	6	CQ585105	CQ585105 Sequence	c 349	8	2.1	3027	9	AB005590	AB005590 Homo sapi
c 277	8	2.1	1662	1	BSF010057	AJ010057 Burkholde	c 350	8	2.1	3076	8	ENU07031	ENU07031 Emericella
c 278	8	2.1	1699	6	BD156074	BD156074 Primer fo	c 351	8	2.1	3079	8	D89010	D89010 Aspergillus
c 279	8	2.1	1699	6	AX876334	AX876334 Sequence	c 352	8	2.1	3249	10	AF123388	AF123388 Mus muscu
c 280	8	2.1	1700	9	AK001249	AK001249 Homo sapi	c 353	8	2.1	3253	8	AB087620	AB087620 Aspergill
c 281	8	2.1	1705	10	RN113G2	X03914 Rattus norv	c 354	8	2.1	3272	8	AK110021	AK110021 Oryza sat
282	8	2.1	1711	6	AR258007	AR258007 Sequence	c 355	8	2.1	3275	6	CQ491966	CQ491966 Sequence
283	8	2.1	1711	6	AR282901	AR282901 Sequence	c 356	8	2.1	3394	6	CQ604505	CQ604505 Sequence
284	8	2.1	1711	6	AK401358	AK401358 Sequence	c 357	8	2.1	3407	9	AB022434	AB022434 Homo sapi
c 285	8	2.1	1715	6	BD136399	BD136399 95 human	c 358	8	2.1	3426	5	AJ719795	AJ719795 Gallus ga
c 286	8	2.1	1719	6	AX653531	AX653531 Sequence	c 359	8	2.1	3432	3	AR322398	AR322398 Sequence
c 287	8	2.1	1771	6	AX780664	AX780664 Sequence	c 360	8	2.1	3458	3	AY118518	AY118518 Drosophil
288	8	2.1	1776	3	U35251	U35251 Onchocerca	c 361	8	2.1	3486	6	CQ806568	CQ806568 Sequence
289	8	2.1	1790	9	AR055020	AR055020 Homo sapi	c 362	8	2.1	3486	6	AX598680	AX598680 Sequence
c 290	8	2.1	1828	6	AX056411	AX056411 Sequence	c 363	8	2.1	3486	6	AX795676	AX795676 Sequence
c 291	8	2.1	1857	8	D84408	D84408 Maize mRNA	c 364	8	2.1	3486	6	AX822125	AX822125 Sequence
292	8	2.1	1890	3	CEU35250	U35250 Caenorhabdi	c 365	8	2.1	3486	6	AX825765	AX825765 Sequence
293	8	2.1	1901	3	AY061150	AY061150 Drosophil	c 366	8	2.1	3560	10	AF016180	AF016180 Rattus no
c 294	8	2.1	1905	3	AX427440S3	AX427442 Leishmani	c 367	8	2.1	3568	6	AR148500	AR148500 Sequence
295	8	2.1	1907	6	BD260776	BD260776 50 human	c 368	8	2.1	3568	6	E26053	E26053 Human P27K1
296	8	2.1	1917	5	CR386254	CR386254 Gallus ga	c 369	8	2.1	3568	6	AR258001	AR258001 Sequence

370	8	2.1	3568	6	AR282895	Sequence	443	8	2.1	12342	9	AL592544	AL592544 Human DNA
371	8	2.1	3568	6	AR401352	Sequence	c 444	8	2.1	12759	1	AB011518	Leptospi
372	8	2.1	3568	6	BD012114	Vitamin D	c 445	8	2.1	14559	1	AJ608775	Homo sapi
373	8	2.1	3571	9	AB003688	Homo sapi	c 446	8	2.1	14634	9	AJ608774	Homo sapi
374	8	2.1	3578	6	BD193189	Novel fam	c 447	8	2.1	14945	1	AE008240	Agrobacte
375	8	2.1	3597	5	BC081135	Xenopus l	c 448	8	2.1	17000	6	AE560893	Sequence
376	8	2.1	3688	14	AB064600	TT Virus	c 449	8	2.1	17000	6	AX685138	Sequence
377	8	2.1	3706	6	CQ587633	Sequence	c 450	8	2.1	17626	3	CEY43CSA	Caenorhab
378	8	2.1	3706	9	AF339153	Homo sapi	c 451	8	2.1	17731	8	SC9877	Scervisia
379	8	2.1	3730	9	AF339152	Homo sapi	c 452	8	2.1	17934	6	AX346620	Sequence
380	8	2.1	3776	8	SCYOR113W	Sequence	c 453	8	2.1	20089	8	SC8142B	S.cerevisia
381	8	2.1	3819	6	BD160636	Primer fo	c 454	8	2.1	20741	1	AF372703	Pseudomon
382	8	2.1	3819	6	AX883967	Sequence	c 455	8	2.1	21025	2	AC136162	Rattus no
383	8	2.1	3826	9	AK024370	Homo sapi	c 456	8	2.1	21631	10	AB070523	Mus muscu
384	8	2.1	3826	9	AF339154	Homo sapi	c 457	8	2.1	22143	5	AB070522S2	Mus muscu
385	8	2.1	3875	3	DFU22357	Sequence	c 458	8	2.1	22199	8	AB028619	Arabidops
386	8	2.1	4080	1	CTU47637	Sequence	c 459	8	2.1	22923	8	AB028619	Arabidops
387	8	2.1	4216	8	SCAZF1	Sequence	c 460	8	2.1	22923	8	AB028619	Arabidops
388	8	2.1	4284	6	CQ849905	Sequence	c 461	8	2.1	23065	9	HUMATPFG	Homo sapien
389	8	2.1	4284	9	AK126972	Sequence	c 462	8	2.1	23366	1	AE002311	Chlamydia
390	8	2.1	4286	6	AR447980	Homo sapi	c 463	8	2.1	24681	2	AC149936	Strongylo
391	8	2.1	4407	5	AY072908	Gallus ga	c 464	8	2.1	27037	9	AB009666S1	Homo sapi
392	8	2.1	4641	1	AF378369	Staphyloc	c 465	8	2.1	27251	9	BX284661	Homo sapi
393	8	2.1	4750	6	AX336647	Sequence	c 466	8	2.1	30350	3	AF000194	Caenorhab
394	8	2.1	4750	9	H5U67092	Human ataxi	c 467	8	2.1	31587	2	AC149374	Phakopsor
395	8	2.1	4832	7	AF212847	Lactococc	c 468	8	2.1	32110	3	CEFA0G12	Caenorhabdi
396	8	2.1	4902	6	CQ600011	Sequence	c 469	8	2.1	32129	3	CET23F11	Caenorhabdi
397	8	2.1	5091	6	CQ580059	Sequence	c 470	8	2.1	32172	7	AF242738	Bacteriop
398	8	2.1	5091	6	CQ847812	Sequence	c 471	8	2.1	32436	1	AB101202	Acinetoba
399	8	2.1	5114	3	AY051698	Drosophil	c 472	8	2.1	32829	6	CQ870408	Sequence
400	8	2.1	5127	3	AF029395	Drosophil	c 473	8	2.1	34727	9	AL356586	Human DNA
401	8	2.1	5261	9	AB058772	Homo sapi	c 474	8	2.1	35089	2	AC149323	Phakopsor
402	8	2.1	5317	3	AB018796	Halocynth	c 475	8	2.1	35089	2	AC149323	Phakopsor
403	8	2.1	5335	5	AY648832	Danio rer	c 476	8	2.1	35121	3	CEFI0G8	Caenorhabdi
404	8	2.1	5395	10	RATDRP	L20319 Rattus norv	c 477	8	2.1	35257	2	AC149339	Phakopsor
405	8	2.1	5577	6	CQ720807	Sequence	c 478	8	2.1	35710	2	AC100510	Mus muscu
406	8	2.1	5957	10	AB098163	Mus muscu	c 479	8	2.1	36000	3	DMC11F6	Drosophil
407	8	2.1	6043	8	YGACDC25A	M94160 Candida alb	c 480	8	2.1	36075	3	AF025468	Caenorhab
408	8	2.1	6201	6	CQ590528	Sequence	c 481	8	2.1	36116	2	AC149332	Phakopsor
409	8	2.1	6216	9	AB007936	Homo sapi	c 482	8	2.1	36808	2	CEH36F17	Caenorhabdi
410	8	2.1	6343	10	MMHOK35	X63507 M.musculus	c 483	8	2.1	36972	6	AX059504	Sequence
411	8	2.1	6669	6	AR453029	Sequence	c 484	8	2.1	37059	6	AX059523	Sequence
412	8	2.1	6669	6	AX281141	Sequence	c 485	8	2.1	37247	9	AP000545	Homo sapi
413	8	2.1	6669	6	AX345095	Sequence	c 486	8	2.1	37350	9	AC126392	Homo sapi
414	8	2.1	6669	6	AX356372	Sequence	c 487	8	2.1	37445	3	U51998	U51998 Caenorhabdi
415	8	2.1	6858	3	AF243382	Drosophil	c 488	8	2.1	37938	5	AF110982	Gallus ga
416	8	2.1	6883	7	INKE	X02139 Bacterioph	c 489	8	2.1	38941	2	AC149346	Phakopsor
417	8	2.1	6941	9	HS118D241	ALI62331 Novel hum	c 490	8	2.1	39000	9	HSN86D4	Human DNA s
418	8	2.1	7286	1	AY077638	AY077638 Moraxella	c 491	8	2.1	39011	2	AC036140	Homo sapi
419	8	2.1	8066	7	AF212846	AF212846 Lactococc	c 492	8	2.1	39490	3	LMFL2954	Leishmani
420	8	2.1	8285	6	AR217828	Sequence	c 493	8	2.1	39651	2	AC014131	Drosophil
421	8	2.1	8541	6	AX787071	Sequence	c 494	8	2.1	39827	8	SC8142A	S.cerevisia
422	8	2.1	8541	6	CQ580058	Sequence	c 495	8	2.1	40181	9	AL645699	Human DNA
423	8	2.1	8552	1	AF212844	Lactococc	c 496	8	2.1	42416	9	AC005551	Homo sapi
424	8	2.1	8850	8	AB026637	Arabidops	c 497	8	2.1	44028	2	AC107035	Pan trogl
425	8	2.1	9224	3	DNALD	X60064 D.melanogas	c 498	8	2.1	44059	9	AL669815	Human DNA
426	8	2.1	9299	6	AX346626	Sequence	c 499	8	2.1	46120	9	AL691473	Human DNA
427	8	2.1	9352	6	AX345005	Sequence	c 500	8	2.1	48265	9	AC000388	Genomic s
428	8	2.1	9905	6	CQ612461	Sequence	c 501	8	2.1	49507	2	AC129982	Mus muscu
429	8	2.1	9922	7	AF208055	AF208055 Bacteriop	c 502	8	2.1	49587	3	DMBH48C10	Drosophil
430	8	2.1	10038	14	AF414119	AF414119 Pineapple	c 503	8	2.1	50984	8	SCXVORFS	S.cerevisia
431	8	2.1	10224	1	AX112722	AY112722 Bifidobac	c 504	8	2.1	51253	9	BX005132	Human DNA
432	8	2.1	10274	6	CQ579254	Sequence	c 505	8	2.1	52498	2	AC104583	Homo sapi
433	8	2.1	10393	1	AE011957	AE011957 Xanthomon	c 506	8	2.1	54016	5	AL845303	Zebrafish
434	8	2.1	10853	1	AE005749	Caulobact	c 507	8	2.1	54762	2	AC130294	Homo sapi
435	8	2.1	10920	6	AX406005	Sequence	c 508	8	2.1	55996	6	AX695632	Sequence
436	8	2.1	10942	6	CQ613889	Sequence	c 509	8	2.1	56943	9	AL391063	Human DNA
437	8	2.1	10969	9	AB007922	Homo sapi	c 510	8	2.1	57199	2	AC135985	Homo sapi
438	8	2.1	11043	1	AE007739	Clostridi	c 511	8	2.1	57839	2	AC106021	Homo sapi
439	8	2.1	11164	1	AE009374	Agrobacte	c 512	8	2.1	57930	9	AL445705	Human DNA
440	8	2.1	11259	1	AE014666	Bifidobac	c 513	8	2.1	58063	2	AP005496	Continuatio
441	8	2.1	11827	6	AX709316	Sequence	c 514	8	2.1	58071	5	AC147818	Xenopus t
442	8	2.1	12099	6	CQ594818	Sequence	c 515	8	2.1	58949	2	BX649482	Continuatio (4 of

516	8	2.1	5369	2	AC115765	AC115765 Mus muscu	C 589	8	2.1	88736	9	AC010420	AC010420 Homo sapi
517	8	2.1	5920	2	AC014068	AC014068 Drosophila	C 590	8	2.1	88848	8	T24H24	AF075598 Arabidops
518	8	2.1	59720	10	AL929107	AL929107 Mouse DNA	C 591	8	2.1	89134	2	AP004162	AP004162 Oryza sat
519	8	2.1	59888	2	AC011588	AC011588 Homo sapi	C 592	8	2.1	89652	5	BX324196	BX324196 Zebrafish
520	8	2.1	60014	2	AC131267	AC131267 Homo sapi	C 593	8	2.1	89677	9	AC026704	AC026704 Homo sapi
521	8	2.1	60573	2	AC018267	AC018267 Drosophila	C 594	8	2.1	90551	10	AL928543	AL928543 Mouse DNA
522	8	2.1	60661	2	AC120009	AC120009 Mus muscu	C 595	8	2.1	90601	9	AC087308	AC087308 Homo sapi
523	8	2.1	61712	10	AL929227	AL929227 Mouse DNA	C 596	8	2.1	91433	3	AC087074	AC087074 Caenorhab
524	8	2.1	61923	9	AC108139	AC108139 Homo sapi	C 597	8	2.1	91506	9	AL354761	AL354761 Human DNA
525	8	2.1	62067	2	AC120018	AC120018 Mus muscu	C 598	8	2.1	92118	9	AC074384	AC074384 Homo sapi
526	8	2.1	62209	8	NB011C21	BX294022 Neurospor	C 599	8	2.1	92154	5	BX248320	BX248320 Zebrafish
527	8	2.1	62536	9	AC005692	AC005692 Homo sapi	C 600	8	2.1	92675	8	AP006402	AP006402 Lotus cor
528	8	2.1	62768	2	AC017293	AC017293 Drosophila	C 601	8	2.1	93724	8	AC007592	AC007592 Genomic s
529	8	2.1	63726	9	AC002071	AC002071 Human PAC	C 602	8	2.1	94000	9	AP000562	AP000562 Homo sapi
530	8	2.1	63748	8	AP000604	AP000604 Arabidops	C 603	8	2.1	94696	6	AX695713	AX695713 Macaca mu
531	8	2.1	63788	2	AC136707	AC136707 Mus muscu	C 604	8	2.1	96592	6	AX695713	AX695713 Sequence
532	8	2.1	64358	9	AL162714	AL162714 Human DNA	C 605	8	2.1	98209	9	HS26079	HS26079 Human DNA
533	8	2.1	65196	3	AC004274	AC004274 Homo sapi	C 606	8	2.1	98232	9	AC012271	AC012271 Homo sapi
534	8	2.1	65321	2	AC068736	AC068736 Homo sapi	C 607	8	2.1	98532	8	AP006120	AP006120 Lotus cor
535	8	2.1	65961	2	AC016523	AC016523 Drosophila	C 608	8	2.1	98864	9	HS460D19	HS460D19 Human DNA
536	8	2.1	66786	2	AC126363	AC126363 Homo sapi	C 609	8	2.1	99241	9	AC079030	AC079030 Homo sapi
537	8	2.1	66975	9	AL135791	AL135791 Human DNA	C 610	8	2.1	99497	9	HS293L6	HS293L6 Human DNA
538	8	2.1	67338	2	AC106001	AC106001 Homo sapi	C 611	8	2.1	100000	9	AP000201	AP000201 Homo sapi
539	8	2.1	67380	2	AC110019	AC110019 Homo sapi	C 612	8	2.1	100102	10	AL954135	AL954135 Mouse DNA
540	8	2.1	67855	2	AC135340	AC135340 Homo sapi	C 613	8	2.1	100678	8	ATT18D12	ATT18D12 Arabidops
541	8	2.1	67840	2	AC135337	AC135337 Homo sapi	C 614	8	2.1	101230	9	HSBA517H2	HSBA517H2 Human DNA
542	8	2.1	68113	2	AC104972	AC104972 Homo sapi	C 615	8	2.1	101728	9	HS1090E8	HS1090E8 Human DNA
543	8	2.1	69213	2	AC135351	AC135351 Homo sapi	C 616	8	2.1	102138	5	BX510351	BX510351 Zebrafish
544	8	2.1	69303	9	AL357496	AL357496 Human DNA	C 617	8	2.1	102205	2	AC141074	AC141074 Homo sapi
545	8	2.1	69687	2	AC146558	AC146558 Medicago	C 618	8	2.1	103129	2	AC136286	AC136286 Medicago
546	8	2.1	69947	9	AL512285	AL512285 Human DNA	C 619	8	2.1	103260	10	AL713995	AL713995 Mouse DNA
547	8	2.1	70855	2	AC101491	AC101491 Mus muscu	C 620	8	2.1	104269	9	AC016596	AC016596 Homo sapi
548	8	2.1	70855	2	AC101491	AC101491 Mus muscu	C 621	8	2.1	104762	2	AC108086	AC108086 Homo sapi
549	8	2.1	71561	2	AL928982	Continuation (7 of	C 622	8	2.1	104889	2	AC141292	AC141292 Homo sapi
550	8	2.1	72101	2	AC015560	AC015560 Mus muscu	C 623	8	2.1	105410	9	AC118650	AC118650 Homo sapi
551	8	2.1	72566	9	AC011360	AC011360 Homo sapi	C 624	8	2.1	105692	2	AP003953	AP003953 Oryza sat
552	8	2.1	72591	2	AC080137	AC080137 Homo sapi	C 625	8	2.1	105866	2	AC021602	AC021602 Homo sapi
553	8	2.1	72955	2	AC108651	Continuation (4 of	C 626	8	2.1	105960	9	HS209A6	HS209A6 Human DNA
554	8	2.1	73009	8	AC007069	AC007069 Arabidops	C 627	8	2.1	105962	9	AP000439	AP000439 Homo sapi
555	8	2.1	73024	10	AL589874	AL589874 Mouse DNA	C 628	8	2.1	106115	2	AC114879	AC114879 Rattus no
556	8	2.1	73513	2	AC024520	AC024520 Homo sapi	C 629	8	2.1	106449	9	AC096949	AC096949 Homo sapi
557	8	2.1	73610	9	AL359735	AL359735 Human DNA	C 630	8	2.1	106716	8	AC008413	AC008413 Arabidops
558	8	2.1	73921	9	AB024024	AB024024 Arabidops	C 631	8	2.1	107135	9	HS145B12	HS145B12 Human DNA
559	8	2.1	73947	9	AL445248	AL445248 Human DNA	C 632	8	2.1	107318	9	AC105226	AC105226 Homo sapi
560	8	2.1	74037	9	HS1071N3	AL031728 Human DNA	C 633	8	2.1	107898	9	AF124731	AF124731 Homo sapi
561	8	2.1	74045	9	BX284671	BX284671 Human DNA	C 634	8	2.1	108022	9	AC008857	AC008857 Homo sapi
562	8	2.1	74429	9	AV523969	AV523969 Homo sapi	C 635	8	2.1	108531	2	AC145164	AC145164 Medicago
563	8	2.1	75192	2	AC009215	AC009215 Drosophila	C 636	8	2.1	108644	2	AC135320	AC135320 Medicago
564	8	2.1	75741	2	AC101412	AC101412 Mus muscu	C 637	8	2.1	108834	3	AC130389	AC130389 Drosophila
565	8	2.1	75995	2	AC017134	AC017134 Drosophila	C 638	8	2.1	109149	2	AP000681	AP000681 Homo sapi
566	8	2.1	77547	2	AC135256	AC135256 Rattus no	C 639	8	2.1	109431	8	AC035249	AC035249 Arabidops
567	8	2.1	77830	10	AL672057	AL672057 Mouse DNA	C 640	8	2.1	109485	9	AC008395	AC008395 Homo sapi
568	8	2.1	78154	9	AC002466	AC002466 Homo sapi	C 641	8	2.1	110000	1	AE017180	AE017180 Rattus no
569	8	2.1	80508	2	AC136085	AC136085 Rattus no	C 642	8	2.1	110000	1	AE017225	AE017225 Oryza sat
570	8	2.1	80577	2	AC150144	AC150144 Gallus ga	C 643	8	2.1	110000	1	AE017261	AE017261 Oryza sat
571	8	2.1	80920	9	AC002036	AC002036 Homo sapi	C 644	8	2.1	110000	1	AE017333	AE017333 Oryza sat
572	8	2.1	81522	3	AC004298	AC004298 Drosophila	C 645	8	2.1	110000	1	AE017334	AE017334 Oryza sat
573	8	2.1	81531	2	AP003529	AP003529 Oryza sat	C 646	8	2.1	110000	1	AE017355	AE017355 Oryza sat
574	8	2.1	82400	10	AC090495	AC090495 Genomic B	C 647	8	2.1	110000	1	AP006618	AP006618 Oryza sat
575	8	2.1	83039	9	AL137074	AL137074 Human DNA	C 648	8	2.1	110000	1	BS571856	BS571856 Oryza sat
576	8	2.1	83139	2	AC100630	AC100630 Mus muscu	C 649	8	2.1	110000	1	BS571857	BS571857 Oryza sat
577	8	2.1	83544	8	AB025615	AB025615 Arabidops	C 650	8	2.1	110000	1	BS571966	BS571966 Oryza sat
578	8	2.1	84387	10	AL929455	AL929455 Mouse DNA	C 651	8	2.1	110000	1	CP000001	CP000001 Oryza sat
579	8	2.1	84972	9	AL365499	AL365499 Human DNA	C 652	8	2.1	110000	1	CP000001	CP000001 Oryza sat
580	8	2.1	85463	2	AC004483	AC004483 Arabidops	C 653	8	2.1	110000	1	CP000001	CP000001 Oryza sat
581	8	2.1	86315	2	AC044789	AC044789 Homo sapi	C 654	8	2.1	110000	1	CP000011	CP000011 Oryza sat
582	8	2.1	86519	9	AP001860	AP001860 Homo sapi	C 655	8	2.1	110000	1	CP000011	CP000011 Oryza sat
583	8	2.1	86554	9	AT22477	AL021768 Arabidops	C 656	8	2.1	110000	1	CR543861	CR543861 Oryza sat
584	8	2.1	87323	2	CR762433	CR762433 Homo sapi	C 657	8	2.1	110000	2	AC091343	AC091343 Oryza sat
585	8	2.1	88186	2	AC138810	AC138810 Homo sapi	C 658	8	2.1	110000	2	AC091361	AC091361 Oryza sat
586	8	2.1	88215	9	AC006963	AC006963 Homo sapi	C 659	8	2.1	110000	2	AC094578	AC094578 Rattus no
587	8	2.1	88277	2	AC015811	AC015811 Homo sapi	C 660	8	2.1	110000	2	AC094578	AC094578 Rattus no
588	8	2.1	88356	8	AB011479	AB011479 Arabidops	C 661	8	2.1	110000	2	AC095084	AC095084 Rattus no

662	8	2.1	110000	2	AC095863_01	Continuation (2 of	c 735	8	2.1	118327	9	HSJ48613	AL050331 Human DNA
663	8	2.1	110000	2	AC095948_1	Continuation (2 of	736	8	2.1	118671	9	AL590710	Human DNA
c 664	8	2.1	110000	2	AC096204_2	Continuation (3 of	c 737	8	2.1	119211	6	AR408761	Sequence
665	8	2.1	110000	2	AC096323_2	Continuation (3 of	c 738	8	2.1	119211	6	AX067465	Sequence
c 666	8	2.1	110000	2	AC102983_0	Continuation (3 of	739	8	2.1	120249	2	AF000858	Homo sapi
c 667	8	2.1	110000	2	AC107134_0	Continuation (2 of	c 740	8	2.1	120365	9	HSBC17B	Human chr
c 668	8	2.1	110000	2	AC107134_1	Continuation (4 of	741	8	2.1	120571	9	CNS01DT3	Human chr
669	8	2.1	110000	2	AC109055_3	Continuation (2 of	c 742	8	2.1	120832	9	AP001068	Homo sapi
c 670	8	2.1	110000	2	AC109413_1	Continuation (2 of	c 743	8	2.1	121025	9	AC129912	Homo sapi
671	8	2.1	110000	2	AC109525_0	Continuation (2 of	744	8	2.1	121439	9	AC10236	Homo sapi
c 672	8	2.1	110000	2	AC111622_2	Continuation (3 of	c 745	8	2.1	121960	2	AC151662	Dasyus n
673	8	2.1	110000	2	AC120698_0	Continuation (3 of	c 746	8	2.1	122449	8	AP006666	Lotus cor
674	8	2.1	110000	2	AC121713_2	Continuation (3 of	c 747	8	2.1	122839	9	AL161898	Human DNA
675	8	2.1	110000	2	AC125589_2	Continuation (3 of	748	8	2.1	123079	2	CR376840	Danio rer
c 676	8	2.1	110000	2	AC132160_1	Continuation (2 of	c 749	8	2.1	123083	8	AP005652	Oryza sat
c 677	8	2.1	110000	2	AC147965_2	Continuation (3 of	c 750	8	2.1	123294	10	AL928633	Mouse DNA
678	8	2.1	110000	2	AC151715_1	Continuation (2 of	751	8	2.1	123297	2	AC130300	Homo sapi
679	8	2.1	110000	2	AC151828_1	Continuation (2 of	752	8	2.1	123547	2	AC015857	Homo sapi
680	8	2.1	110000	2	AC151844_1	Continuation (2 of	c 753	8	2.1	123835	10	MM303011	Mus muscu
c 681	8	2.1	110000	2	AC151846_1	Continuation (2 of	754	8	2.1	124028	2	AC027108	Homo sapi
c 682	8	2.1	110000	2	AL390202_05	Continuation (6 of	c 755	8	2.1	124162	2	AC141121	Rattus no
683	8	2.1	110000	2	AL954350_0	Continuation (6 of	c 756	8	2.1	124394	8	AC144645	Medicago
684	8	2.1	110000	2	AL954350_2	Continuation (3 of	c 757	8	2.1	124645	9	HUAC004638	Homo sapi
685	8	2.1	110000	2	AL954350_3	Continuation (4 of	c 758	8	2.1	124998	9	AC026397	Homo sapi
686	8	2.1	110000	2	AL954350_4	Continuation (5 of	759	8	2.1	125360	9	AC117406	Homo sapi
c 687	8	2.1	110000	2	AP006499_07	Continuation (8 of	760	8	2.1	125946	2	AC026390	Homo sapi
c 688	8	2.1	110000	2	LMFLCHR31_04	Continuation (5 of	c 761	8	2.1	126344	9	AP000097	Homo sapi
c 689	8	2.1	110000	8	CR382129_13	Continuation (14 o	762	8	2.1	126451	5	BX284622	Zebrafish
690	8	2.1	110000	8	CR382130_21	Continuation (22 o	c 763	8	2.1	126781	2	AC016375	Homo sapi
c 691	8	2.1	110000	8	CR382131_21	Continuation (22 o	c 764	8	2.1	127003	8	CNS08C9C	Oryza sat
c 692	8	2.1	110000	8	CR382133_01	Continuation (2 of	c 765	8	2.1	127295	9	AP002346	Homo sapi
693	8	2.1	110000	8	CR382137_04	Continuation (5 of	c 766	8	2.1	128270	9	HS444C7	Human DNA
c 694	8	2.1	110000	8	CR382137_11	Continuation (12 o	c 767	8	2.1	128526	2	AC091027	Homo sapi
c 695	8	2.1	110000	8	AB016816_1	Continuation (2 of	c 768	8	2.1	128877	2	AC026399	Homo sapi
c 696	8	2.1	110000	8	AB016816_2	Continuation (3 of	c 769	8	2.1	129098	9	HS46H23	Human DNA s
c 697	8	2.1	110000	8	AB016816_04	Continuation (5 of	c 770	8	2.1	129240	9	AC083826	Homo sapi
c 698	8	2.1	110000	14	AY318871_1	Continuation (2 of	c 771	8	2.1	129528	8	SCI30KXBV	X94335 S.cerevisia
699	8	2.1	110121	9	AL590989	AL590989 Human DNA	772	8	2.1	129642	3	AGAA38610	AY438610 Anopheles
c 700	8	2.1	110511	2	AC150442	AC150442 Medicago	773	8	2.1	130433	8	OSJN00066	AC004592 Homo sapi
c 701	8	2.1	110572	9	AC147741	AC147741 Medicago	774	8	2.1	130513	2	AC004592	Homo sapi
c 702	8	2.1	111370	9	AC067815	AC067815 Homo sapi	775	8	2.1	131613	2	AC026793	Homo sapi
c 703	8	2.1	111426	2	AC141693	AC141693 Apis mell	c 776	8	2.1	132262	9	AC084795	Homo sapi
c 704	8	2.1	111704	2	AC146847	AC146847 Ornithorh	c 777	8	2.1	132344	8	AY360388	Oryza sat
705	8	2.1	111723	2	AC020935	AC020935 Homo sapi	c 778	8	2.1	132354	2	AC017130	Drosophila
c 706	8	2.1	111777	2	AP004089	AP004089 Oryza sat	779	8	2.1	132558	2	AC141130	Rattus no
707	8	2.1	112032	2	AC145221	AC145221 Medicago	c 780	8	2.1	132724	2	AC068713	Homo sapi
c 708	8	2.1	112084	9	AC104648	AC104648 Homo sapi	781	8	2.1	132727	2	AL356914	Homo sapi
c 709	8	2.1	112135	2	CR589926	CR589926 Homo sapi	c 782	8	2.1	133042	9	AC011354	Homo sapi
c 710	8	2.1	112239	9	AC008648	AC008648 Homo sapi	c 783	8	2.1	133163	5	BX649562	Zebrafish
c 711	8	2.1	112648	9	AL356603	AL356603 Human DNA	c 784	8	2.1	133373	8	AC105734	Oryza sat
c 712	8	2.1	114144	9	AL3566240	AL3566240 Human DNA	785	8	2.1	133861	2	AC118830	Rattus no
713	8	2.1	114181	2	AC110875	AC110875 Gallus ga	c 786	8	2.1	134124	9	AL160266	Human DNA
714	8	2.1	114325	10	BX546441	BX546441 Mouse DNA	c 787	8	2.1	134362	2	AC084853	Homo sapi
715	8	2.1	114409	9	AL161742	AL161742 Human DNA	c 788	8	2.1	134413	9	AC011334	Homo sapi
716	8	2.1	115103	5	BX294163	BX294163 Zebrafish	c 789	8	2.1	134837	5	BX510372	Zebrafish
c 717	8	2.1	115227	2	AC146362	AC146362 Canis fam	790	8	2.1	134973	9	AP000818	Homo sapi
c 718	8	2.1	115402	2	AC027283	AC027283 Homo sapi	c 791	8	2.1	135224	2	AC022373	Homo sapi
719	8	2.1	115478	9	HS7576H24	AL049634 Human DNA	c 792	8	2.1	135473	10	AC102705	Mus muscu
720	8	2.1	115602	9	HS1118D24	AL031276 Human DNA	793	8	2.1	135640	9	AC036178	Homo sapi
c 721	8	2.1	115612	9	AY220758	AY220758 Homo sapi	c 794	8	2.1	135698	2	AL365218	Homo sapi
c 722	8	2.1	115780	6	CQ869701	CQ869701 Sequence	c 795	8	2.1	135843	2	AC148433	Sorex ara
723	8	2.1	115915	9	AC105922	AC105922 Homo sapi	c 796	8	2.1	136158	2	AC141363	Felis cat
c 724	8	2.1	116184	2	AC146854	AC146854 Medicago	c 797	8	2.1	136228	2	AC067916	Homo sapi
725	8	2.1	116855	9	AL365523	AL365523 Human DNA	c 798	8	2.1	136232	2	AC024006	Homo sapi
c 726	8	2.1	116919	10	BX294005	BX294005 Mouse DNA	c 799	8	2.1	136393	2	AC151700	Gallus ga
727	8	2.1	117004	2	AC108090	AC108090 Homo sapi	800	8	2.1	136968	9	AL390788	Human DNA
c 728	8	2.1	117124	2	AC129920	AC129920 Homo sapi	801	8	2.1	137296	2	AC074162	Mus muscu
c 729	8	2.1	117301	2	AC150088	AC150088 Gallus ga	802	8	2.1	137343	9	AP000946	Homo sapi
c 730	8	2.1	117329	8	AC148177	AC148177 Medicago	c 803	8	2.1	137366	9	AC079029	Oryza sat
731	8	2.1	117520	9	AP005624	AP005624 Homo sapi	c 804	8	2.1	137490	9	HSJ543J13	Human DNA
c 732	8	2.1	117710	9	AC106743	AC106743 Homo sapi	805	8	2.1	137493	10	AL732581	Mouse DNA
733	8	2.1	118131	9	AC074132	AC074132 Homo sapi	c 806	8	2.1	137509	5	BX323884	Zebrafish
734	8	2.1	118174	2	AC138014	AC138014 Medicago	c 807	8	2.1	137817	9	AC003091	Homo sapi

808	8	2.1	137991	10	AL627073	881	8	2.1	145844	9	AC004931	AC004931 Homo sapi
c 810	8	2.1	138033	2	AP002339 Homo sapi	882	8	2.1	145885	9	AC139427	AC139427 Homo sapi
c 811	8	2.1	138062	9	AL161938 Human DNA	883	8	2.1	146191	1	D50453	D50453 Bacillus su
812	8	2.1	138155	5	AC151564 Dasyapus n	c 884	8	2.1	146350	9	HS225L15	HS225L15 Homo sapi
813	8	2.1	138176	5	AC145791 Xenopus t	c 885	8	2.1	146362	2	BX294174	BX294174 Mus muscu
c 814	8	2.1	138203	10	AC110221 Mus muscu	c 886	8	2.1	146679	2	AC115713	AC115713 Mus muscu
814	8	2.1	138329	2	AC093226 Homo sapi	887	8	2.1	146783	2	AC131590	AC131590 Homo sapi
c 815	8	2.1	138434	2	AC150120 Gallus ga	c 888	8	2.1	146851	2	AC027697	AC027697 Homo sapi
816	8	2.1	138563	3	AC140575 Wacaca mu	c 889	8	2.1	147118	9	AC007513	AC007513 Homo sapi
c 817	8	2.1	138582	10	AL844864 Mouse DNA	c 890	8	2.1	147166	10	AC132272	AC132272 Mus muscu
c 818	8	2.1	138688	9	AC118553 Homo sapi	c 891	8	2.1	147179	5	CR384061	CR384061 Zebrafish
c 819	8	2.1	138688	8	AP005246 Homo sapi	c 892	8	2.1	147179	5	CR384061	CR384061 Zebrafish
c 820	8	2.1	138926	9	AC090426 Homo sapi	c 893	8	2.1	147387	5	AL954326	AL954326 Zebrafish
c 821	8	2.1	139217	8	AP006481 Oryza sat	c 894	8	2.1	147456	5	BX950856	BX950856 Zebrafish
822	8	2.1	139226	8	OSJUN00274	c 895	8	2.1	147585	10	AC126457	AC126457 Mus muscu
c 823	8	2.1	139267	2	AC135174 Homo sapi	c 896	8	2.1	147640	5	BX323035	BX323035 Zebrafish
c 824	8	2.1	139287	2	AC012837 Drosophil	c 897	8	2.1	147664	4	AC144403	AC144403 Felis cat
c 825	8	2.1	139480	9	HUAC002331	c 898	8	2.1	147836	8	AP003983	AP003983 Oryza sat
c 826	8	2.1	139591	2	CR388227 Danio rer	c 899	8	2.1	147859	2	AC015692	AC015692 Homo sapi
c 827	8	2.1	139868	8	AP004161 Oryza sat	c 900	8	2.1	147952	9	AC008712	AC008712 Homo sapi
c 828	8	2.1	139917	2	AC141246 Homo sapi	c 901	8	2.1	147999	2	AL161635	AL161635 Homo sapi
c 829	8	2.1	140596	2	RN75P15	c 902	8	2.1	148263	9	AC091988	AC091988 Homo sapi
c 830	8	2.1	140686	2	AC137773 Homo sapi	c 903	8	2.1	148275	5	BX005016	BX005016 Zebrafish
c 831	8	2.1	140714	2	RN374E16	c 904	8	2.1	148487	2	AC011583	AC011583 Homo sapi
c 832	8	2.1	140769	8	AP003508 Homo sapi	c 905	8	2.1	148540	9	HS212P9	HS212P9 Human DNA
c 833	8	2.1	140917	10	AL929380 Mouse DNA	c 906	8	2.1	148588	2	AC073827	AC073827 Mus muscu
c 834	8	2.1	141154	9	AC026442 Homo sapi	c 907	8	2.1	148693	2	AC137789	AC137789 Homo sapi
c 835	8	2.1	141319	8	AP004457 Oryza sat	c 908	8	2.1	148732	10	BX813330	BX813330 Mouse DNA
c 836	8	2.1	141447	9	AC016204 Homo sapi	c 909	8	2.1	148737	9	AC026702	AC026702 Homo sapi
c 837	8	2.1	141868	9	AC109338 Homo sapi	c 910	8	2.1	148835	2	AC128002	AC128002 Rattus no
c 838	8	2.1	141881	4	AC087421 Felis cat	c 911	8	2.1	148897	9	AL139034	AL139034 Human DNA
c 839	8	2.1	141894	9	AC093211 Homo sapi	c 912	8	2.1	148897	9	AL139034	AL139034 Human DNA
c 840	8	2.1	141895	9	AL356269 Human DNA	c 913	8	2.1	148976	2	AC130201	AC130201 Mus muscu
c 841	8	2.1	141944	9	AC122108 Homo sapi	c 914	8	2.1	149030	9	AC005375	AC005375 Homo sapi
842	8	2.1	142018	9	HS1033H22	c 915	8	2.1	149037	9	AC138511	AC138511 Homo sapi
843	8	2.1	142056	2	AC150441 Medicago	c 916	8	2.1	149287	2	AC079017	AC079017 Homo sapi
c 844	8	2.1	142056	9	AC101491 Homo sapi	c 917	8	2.1	149746	2	AC068534	AC068534 Homo sapi
c 845	8	2.1	142182	8	AP004399 Oryza sat	c 918	8	2.1	150136	9	BS000056	BS000056 Pan trogl
c 846	8	2.1	142182	2	AL162492 Homo sapi	c 919	8	2.1	150224	9	HSJ1059L7	HSJ1059L7 Human DNA
847	8	2.1	142235	2	AP005973 Oryza sat	c 920	8	2.1	150300	2	AC145019	AC145019 Felis cat
c 848	8	2.1	142350	5	BX664625 Zebrafish	c 921	8	2.1	150339	2	AC141750	AC141750 Apis mell
c 849	8	2.1	142420	2	AC102709 Mus muscu	c 922	8	2.1	150442	2	AC022782	AC022782 Mus muscu
c 850	8	2.1	142555	9	AL139214 Human DNA	c 923	8	2.1	150485	8	AC069491	AC069491 Oryza sat
c 851	8	2.1	142715	9	AC008387 Homo sapi	c 924	8	2.1	150489	2	AC069491	AC069491 Homo sapi
852	8	2.1	142726	9	AC104836 Homo sapi	c 925	8	2.1	150530	2	AC151658	AC151658 Dasyapus n
c 853	8	2.1	142728	9	HSJ792G4	c 926	8	2.1	150638	2	AC129994	AC129994 Rattus no
854	8	2.1	142764	2	AC026119 Homo sapi	c 927	8	2.1	150872	2	AC148037	AC148037 Rattus no
c 855	8	2.1	142776	2	AP005109 Oryza sat	c 928	8	2.1	150996	2	AC118264	AC118264 Mus muscu
c 856	8	2.1	143160	2	AP004796 Oryza sat	c 929	8	2.1	151327	2	AC135487	AC135487 Rattus no
c 857	8	2.1	143180	2	AC120596 Rattus no	c 930	8	2.1	151414	2	AC115523	AC115523 Rattus no
c 858	8	2.1	143280	10	AL845285 Mouse DNA	c 931	8	2.1	151505	2	AC021875	AC021875 Homo sapi
c 859	8	2.1	143444	9	AC007541 Homo sapi	c 932	8	2.1	151783	4	AC150593	AC150593 Bos tauru
c 860	8	2.1	143509	2	AC068683 Homo sapi	c 933	8	2.1	151813	2	AC026737	AC026737 Homo sapi
c 861	8	2.1	143575	2	AC092370 Homo sapi	c 934	8	2.1	151930	2	AC151171	AC151171 Bos tauru
c 862	8	2.1	143712	8	AP004995 Oryza sat	c 935	8	2.1	152005	9	AC100834	AC100834 Homo sapi
863	8	2.1	143715	9	AL589947 Human DNA	c 936	8	2.1	152186	2	AC084284	AC084284 Homo sapi
864	8	2.1	143988	2	AC129500 Homo sapi	c 937	8	2.1	152186	2	CR354581	CR354581 Danio rer
c 865	8	2.1	144084	8	CNS08CCB	c 938	8	2.1	152224	2	AC007933	AC007933 Homo sapi
c 866	8	2.1	144191	8	AC079874 Oryza sat	c 939	8	2.1	152334	9	AL356299	AL356299 Human DNA
c 867	8	2.1	144202	2	AC110179 Mus muscu	c 940	8	2.1	152350	2	AC107322	AC107322 Felis cat
c 868	8	2.1	144244	9	AC025219 Homo sapi	c 941	8	2.1	152438	9	AL139809	AL139809 Human DNA
c 869	8	2.1	144552	9	AC112723 Homo sapi	c 942	8	2.1	152620	10	AC132081	AC132081 Mus muscu
c 870	8	2.1	144644	8	AP002818 Oryza sat	c 943	8	2.1	152654	9	AC134882	AC134882 Homo sapi
c 871	8	2.1	144666	2	AL160287 Human DNA	c 944	8	2.1	152937	9	AC007157	AC007157 Homo sapi
c 872	8	2.1	144736	2	AC130299 Homo sapi	c 945	8	2.1	152952	9	AC074143	AC074143 Homo sapi
c 873	8	2.1	144741	8	AP004674 Oryza sat	c 946	8	2.1	153056	10	AL607090	AL607090 Mouse DNA
c 874	8	2.1	144792	8	AY555143 Zea may B	c 947	8	2.1	153133	9	AC091980	AC091980 Homo sapi
c 875	8	2.1	144828	9	AP001577 Homo sapi	c 948	8	2.1	153139	5	BX571971	BX571971 Zebrafish
c 876	8	2.1	145016	2	AP02418 Homo sapi	c 949	8	2.1	153320	2	AC124260	AC124260 Homo sapi
c 877	8	2.1	145066	2	AP002418 Homo sapi	c 950	8	2.1	153624	9	HS1018K9	HS1018K9 Human DNA
c 878	8	2.1	145314	8	AC146852 Medicago	c 951	8	2.1	153705	9	AL445650	AL445650 Human DNA
c 879	8	2.1	145546	2	AC120216 Mus muscu	c 952	8	2.1	153904	2	BX510650	BX510650 Homo sapi
c 880	8	2.1	145739	8	OSJUN00157	c 953	8	2.1	154228	2	AC124261	AC124261 Homo sapi

954	8	2.1 154474	8	AP006048	Oryza sat
955	8	2.1 154633	10	AC145427	Rattus no
956	8	2.1 154679	2	AC022019	Homo sapi
957	8	2.1 154704	9	AC092660	Homo sapi
958	8	2.1 154841	2	AC109793	Bos tauru
959	8	2.1 154890	3	AC008136	Drosophi
960	8	2.1 154912	2	AC141604	Homo sapi
961	8	2.1 155103	10	AL645666	Mouse DNA
962	8	2.1 155168	8	AP005948	Oryza sat
963	8	2.1 155191	2	AC149618	Papio anu
964	8	2.1 155254	2	AC129952	Mus muscu
965	8	2.1 155609	2	EX927284	Danio rer
966	8	2.1 155612	5	AL935044	Zebrafish
967	8	2.1 155666	9	AC008696	Homo sapi
968	8	2.1 155757	2	AC118548	Homo sapi
969	8	2.1 156079	5	EX088716	Zebrafish
970	8	2.1 156273	9	AC009091	Homo sapi
971	8	2.1 156292	9	CNS057D6	Human chr
972	8	2.1 156300	9	AC005919	Homo sapi
973	8	2.1 156408	2	AL772286	Homo sapi
974	8	2.1 156479	2	AC101833	Mus muscu
975	8	2.1 156504	2	AC148250	Otolemur
976	8	2.1 156592	9	AC093523	Homo sapi
977	8	2.1 156741	2	AC131312	Homo sapi
978	8	2.1 156795	2	AC135389	Rattus no
979	8	2.1 156830	2	AC027693	Homo sapi
980	8	2.1 156981	2	CR847511	Danio rer
981	8	2.1 157118	9	AC069286	Homo sapi
982	8	2.1 157145	2	AC146323	Pan trogl
983	8	2.1 157201	8	AP003048	Oryza sat
984	8	2.1 157405	2	CR790377	Danio rer
985	8	2.1 157493	2	AC111071	Mus muscu
986	8	2.1 157493	5	AC044836	Homo sapi
987	8	2.1 157502	5	AC144486	Gasterost
988	8	2.1 157509	2	AC141988	Rattus no
989	8	2.1 157574	9	AL592293	Human DNA
990	8	2.1 157606	2	AC069172	Homo sapi
991	8	2.1 157851	2	AC020509	Drosophi
992	8	2.1 157857	2	AC072032	Homo sapi
993	8	2.1 157892	9	AC008115	Homo sapi
994	8	2.1 157929	10	AC124407	Mus muscu
995	8	2.1 157974	8	AP003755	Oryza sat
996	8	2.1 158241	2	AC021804	Homo sapi
997	8	2.1 158365	2	AC150811	Callithri
998	8	2.1 158408	2	EX927402	Danio rer
999	8	2.1 158676	2	AC133921	Homo sapi
1000	8	2.1 158766	2	AC015851	Homo sapi

RESULT 1	AR145734	AR145734	linear	PAT 08-AUG-2001
LOCUS	Sequence 2	from patent US 6218115.	1133 bp	DNA
DEFINITION	Sequence 2	from patent US 6218115.		
ACCESSION	AR145734			
VERSION	AR145734.1	GI:15108923		
KEYWORDS	Unknown.			
SOURCE	Unknown.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1133)			
AUTHORS	Nakamura,T.			
TITLE	Human cyclin I and genes encoding same			
JOURNAL	Patent: US 6218115-A 2 17-APR-2001;			
FEATURES	Location/Qualifiers			
source	1..1133			
	/organism="unknown"			
	/mol_type="unassigned DNA"			
ORIGIN				
Alignment Scores:				
Pred. No.:	0			1133

Score:	377.00	Matches:	377
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-736-250-1 (1-377) x AR145734 (1-1133)	
Qy	1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db	1 ATGAGTTTCAGGGCCCTTTGGAAACACAGAGATTGCTCTTCCTGTTGGAAAAGGCAATC 60
Qy	21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db	61 ACTAGGGAAGCACAGATGTTGGAAAGTGAATGTCGGAAAATGCCTTCAATCAGAAATGTT 120
Qy	41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysLysTrpGlnPheAsn 60
Db	121 TCTCCATCCAGAGAGATGAAGTAATTAATTCATGGCTGGCCAACTCAAGTAGTACCAATTCAC 180
Qy	61 LeuTrpProGluThrPheAlaLeuAlaSerSerLeuLeuLeuAspArgPheLeuAlaThrVal 80
Db	181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGATTGTTTACCTAGCTACCGTA 240
Qy	81 LysAlaHisProLysTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db	241 AAGGCTCATCAAAATCTTTGAGTTGTTGCAATCAGCTGTTTTCCTAGCTGCCAAG 300
Qy	101 ThrValGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db	301 ACTGTTGAGGAAGATGAGAAATTCAGTACTAAGGTATTGGCAAGACAGATTCTGT 360
Qy	121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db	361 GGATGTTCTCACTGAATTTTGAGATGGAGAGATTATTCTGGATTAAGTTGAATTGG 420
Qy	141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db	421 GATCTTCACAGCCACACACCATGGAATTTCTTCATATTTTCCATGTCATTCAGAGTCA 480
Qy	161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db	481 ACTAGGCTCAGTTACTTTTCAGTTGTCCTCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy	181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db	541 CTACCAAGCAACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGATCC 600
Qy	201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db	601 ATGCTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATTTCTGATTGCTTTCT 660
Qy	221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db	661 CTTACAATTGAATGCTTCAGAAAGCACAGATGATAGTCCCGATGATCCATTTGTCGG 720
Qy	241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTrp 260
Db	721 GAGCTTGGCACATCATCTTTTCTACTCTGAGCTCTTCCCTGCTCTGAAATTCGTTAT 780
Qy	261 ValTrpArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db	781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy	281 ProSerSerValProGlyProAspPheSerLysAsnAsnSerLysProGluValProVal 300
Db	841 CCCTTCCTCTGTCCAGGCCCCAGACTTCTCCAGGACCAACAGCAGCCAGAGTCCAGTC 900
Qy	301 ArgGlyThrAlaAlaPheTrpHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db	901 AGAGGTACAGACGCTTTTACCATCATCTCCAGCTCCAGTGGTGGTCCAGACACCTCT 960
Qy	321 ThrLysArgLysValGluGluMetGluValAspAspPheTrpAspGlyIleLysArgLeu 340

```

Db      961 ACTAAACCAAGTAGAGAAATGGAAGTGATGACCTTCTATGATGGAAATCAAAACGGCTC 1020
Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1021 TATAATGAAGATAATGCTCTCAGAAAATGCGGTTCTGTGTGGCACTGATTATCAAGA 1080
Qy      361 GlnGluGlyHisAlaSerProCysProGluProLeuGlnProValSerValMet 377
Db      1081 CAAGAGGACATGCTTCCCTTTGTCACCTTTGCAGCGCTGTTCTGTGCATG 1131

RESULT 2
AR087353 LOCUS 1260 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS Yang, M., Mandabalan, K. and Schultz, V. Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES
    Location/Qualifiers
        1..1260
            /organism="unknown"
            /mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR087353 (1-1260)

Qy      1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluValAlaIle 20
Db      1 ATGAAGTTTCAGGGCCCTTGGAAACCCAGAGATTGCTTTCCCTGTTGGAAAGCCAAATC 60

Qy      21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db      61 ACTAGGGAAGCACAGATGCGAAGTGAATGTGCGGAAATGCCCTTCAAAATCAGAAATGTT 120

Qy      41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db      121 TCTCCATCCAGAGAGATGAAGTAATTCATATGGCTGGCCAAACTCAAGTACCAATTTCAAC 180

Qy      61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db      181 CTTTACCAGAAACATTTGCTGTGGCTAGCAGTCTTTTGGATAGTTTTTACGTACCGTA 240

Qy      81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db      241 AAGGCTCATCCAAATACTTGGTTGTTATTCATTCATCAGCTGTTTTCCTAGCTGCCAAG 300

Qy      101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db      301 ACTGTGTGGAAGATGAGAGAAATTCAGTACTAAAGGTATTGGCAAGAGACAGATTCTGT 360

Qy      121 GlyCysSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db      361 GGATGTTCTCATCTGAAATTTTGAATGAGAGAAATTTCTGGATAGTTGAATGG 420

Qy      141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db      421 GATCTTCACAGCCACACCATGGATTTTCTTCATATTTTCCATATTCATTCAGCTGCA 480

```

```

Qy      161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db      481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATTTAGCCCATCTCAACATTTTGGCAGTC 540

Qy      181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db      541 CTTACCAAGCACTACTTCTACTGTATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 600

Qy      201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db      601 ATGCTTCTCTGGCCATGGTTAGTCTGAAATGAGAAACTCATTTCTGATGGCTTTCT 660

Qy      221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db      661 CTTACAATTAACATGCTTTCAGAAAGACAGATGATAGTCCCAAGTATCATTTGTCGG 720

Qy      241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db      721 GAGCTTGTGGCACAATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTAT 780

Qy      261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db      781 GTCTACCGTCCCTCAAGCACACCTGTCACCTGTGCAAAAGAGTGTTCAGATTACAT 840

Qy      281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db      841 CCTCTCTCTGTCCAGGCCCCAGACTTCTCCAAGGACCAACAGCAAGCCAGAGTCCAGTC 900

Qy      301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db      901 AGAGTTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960

Qy      321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db      961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAAACGGCTC 1020

Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1021 TATAATGAAGATAATGCTCTCAGAAAATGCGGTTCTGTGTGGCACTGATTATCAAGA 1080

Qy      361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db      1081 CAAGAGGACATGCTTCCCTTTGTCACCTTTGCAGCGCTGTTCTGTGCATG 1131

RESULT 3
LOCUS CQ812312 1260 bp DNA linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CQ812312
VERSION CQ812312.1 GI:47601932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Wittig, R., Poustka, A., Mollenhauer, J. and Schadendorf, D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 64 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
(DE)
FEATURES
    Location/Qualifiers
        1..1260
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
            misc_feature 1..1260
                /note="D50310"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377

```

```
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ812312 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACCGAGATTGCTTCTTCTGGTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATCGGAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrPheAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTCTGAGTTGTTATGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATTTCTGGATAGTCTTTAGCTACCGTA 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGACACACCATCTGAGTTTCTTCAATTTTCCATGCTGCAATGCTGCTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTCTTCTGAGTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACAGAGCACTACTTCTACTGTATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTGTAGTCTGGAATGGAGAAACTCATCTCTGATTTGGCTTTCT 660

Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLysHisCysArg 240
Db 661 CTTCAATTTGAATGACTCTTCAGAAAGCAGAGTGGATGCTCCAGTTGATTCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTTGGGCATCATCTTCTACTCTGAGTCTTCCCTGCTCTGATTTCCGTTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCTCCAGGCCAGACTTCTCCAAAGGACACAGCAAGCCAGAGTGGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLeuArgLeu 340
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTTGTCTTCTGTGTCATG 1131

961 ACTAAACGCAAGTAGAGGAAATGGAAGTGGATGATCATTCTATGATGGAATCAACGGCTC 1020
341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
1021 TATAATGAAGATAATGCTCAGAAATGTGGTCTGTGTGTGGCTGATTTATCAAGA 1080
361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTTGTCTTCTGTGTCATG 1131

RESULT 4
AR281918 1260 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang M., Nandabalan K. and Schulz V.P.
TITLE HsReq1 and hSReq2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES Location/Qualifiers
source 1..1260
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores: Length: 1260
Pred. No.: 0 Matches: 377
Score: 377.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-736-250-1 (1-377) x AR281918 (1-1260)

Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACCGAGATTGCTTCTTCTGGTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCCTTCAATCAGATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTyrPheAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180

Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGTCTTTAGCTACCGTA 240

Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTCTGAGTTGTTATGCAATCAGCTGTTTCTTCTAGCTGCCAAG 300

Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTGTAGGAAGATGAGAGAAATCCAGTACTAAAGGTATTTGGCAAGACAGATTTCTGT 360

Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 361 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATTTCTGGATAGTCTTTAGCTACCGTA 420

Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGACACACCATCTGAGTTTCTTCAATTTTCCATGCTGCAATGCTGCTCA 480

Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTCTTCTGAGTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540

Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACAGAGCACTACTTCTACTGTATGCTGCAACCACTTCTGCAATTCAGAGGATCC 600

Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 601 ATGCTTGTCTGGCCATGGTGTAGTCTGGAATGGAGAAACTCATCTCTGATTTGGCTTTCT 660

Qy 221 LeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuLysHisCysArg 240
Db 661 CTTCAATTTGAATGACTCTTCAGAAAGCAGAGTGGATGCTCCAGTTGATTCATTTGTCGG 720

Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTTGGGCATCATCTTCTACTCTGAGTCTTCCCTGCTCTGATTTCCGTTTAT 780

Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGACAAAGGAGTCTTCAGATTACAT 840

Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTCTGCTCCAGGCCAGACTTCTCCAAAGGACACAGCAAGCCAGAGTGGCAGTC 900

Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGGCAGCAGACCTCT 960

Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyLysLeuArgLeu 340
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTTGCAGCTTGTCTTCTGTGTCATG 1131
```

```
Db 481 ACTAGGCTCAGTACTTTTCAGTTTGCCAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCACTGTATGCGCTGCAACCAACTTCTGCAATTCAGAGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTGTAGCTGGAAATGGAGAAACTCAITTCCTGATTTGGCTTCT 660
Qy 221 LeuThrLysGlnLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 661 CTTACAAATGAACTCTTCAGAACACAGATGGATAGCTCCAGTTGATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 721 GAGCTTGTGGCACATCACTTTCTACTCTGCAGTCTTCCCTGCCTCGATTCGGTTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 781 GTCTACCGTCCCTCAACACACACCTGTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGCCAGGCCAGACTTCTCCAGGACAAACAGCAAGCCAGAGTGGCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuSerGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspAspPheTyrAspGlyLysLysArgLys 340
Db 961 ACTAAACCAAGATAGAGAAATGGAAGTGGATGACTTCTATGATGGAAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
Db 1021 TATATGAGATAATGTCTCAGAAATGTGGTCTGTGTGGCAGCTGTTTGTGTATG 1080

RESULT 5
AR380354
LOCUS AR380354 1260 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION AR380354.1 GI:40087988
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1260)
AUTHORS Cocks,B.G., Stuart,S.G. and Seilhamer,J.J.
TITLE Compositions for the detection of blood cell and immunological response gene expression
JOURNAL Patent: US 6607879-A 899 19-AUG=2003;-
FEATURES
source Location/Qualifiers
1..1260
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x AR380354 (1-1260)
```

```
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaLys 20
Db 1 ATGAAGTTTCCAGGGCCTTTGGAAAACACAGAGATTGTCTTCTCTGTGGAAAAGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGCGGAAAATGCGCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 121 TCTCCATCCACAGAGATGAAGTAATTCATGGCTGGCCAAACTCAAGTACCAATTCAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCCAGAAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGTACCCTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaLysSerCysPhePheLeuAlaLys 100
Db 241 AAGGCTCATCCAAATATCTTGAGTTGTATTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAGATGAGAGNAATCCAGTACTAAAGGTATTGGCAAGACAGATTTCTGT 360
Qy 121 GlyCysSerSerGluLysLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTTCTCATCTGAAATTTTGAAGATGGAGAGAATATTCTGGATAAGTTGAATGG 420
Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaLysValSer 160
Db 421 GATCTTCACACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATGGCAGTGCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
Db 541 CTTACCAAGCAACTACTTCTGATGCGCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATGGTGTAGTCTGGAATGAGAAACTCATTCCTGATTTGGCTTCT 660
Qy 221 LeuThrLysGlnLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 661 GTCTACCGTCCCTCAAGCACACCTGGTGGTACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 841 CCTCTCTGTGTCAGGCCAGACTTCTTCAAGGACAAACAGCAAGCCAGAGTGGCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaLeuAspGlyCysLysGlnThrSer 320
Db 901 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCACCTCT 960
Qy 321 ThrLysArgLysValGluMetGluValAspAspPheTyrAspGlyLysLysArgLys 340
Db 961 ACTAAACCAAGATAGAGAAATGGAAGTGGATGACTTCTATGATGGAAATCAAAACGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLysSerArg 360
Db 1021 TATATGAGATAATGTCTCAGAAATGTGGTCTGTGTGGCAGCTGTTTGTATCAAGA 1080
```

```
Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
|||||
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGGCAGCTGTTCTGTGTCATG 1131

RESULT 6
HUMCYI
LOCUS Human mRNA for cyclin I, complete cds. PRI 10-FEB-1999
ACCESSION D50310.1 GI:1183161
VERSION cyclin I.
KEYWORDS Homo sapiens
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Nakamura, T., Sanokawa, R., Sasaki, Y.F., Ayusawa, D., Oishi, M. and
Mori, N.
TITLE Cyclin I: a new cyclin encoded by a gene isolated from human brain
JOURNAL Exp. Cell Res. 221 (2), 534-542 (1995)
MEDLINE 96086276
PUBMED 7493655
REFERENCE 2 (bases 1 to 1260)
AUTHORS Nakamura, T.
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1260)
AUTHORS Nakamura, T.
JOURNAL Direct Submission
TITLE Submitted (11-APR-1995) Takeshi Nakamura, Sumitomo Electric
JOURNAL Industries, Biomedical R&D Department; 1, Taya-cho, Sakae-ku,
Yokohama, Kanagawa 244, Japan (E-mail:tnakamr@pele.sumiden.co.jp,
Tel:045-853-7275, Fax:045-853-3528)
FEATURES
source
1..1260
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="FC6"
/tissue_type="Brain"
1..1133
/codon_start=1
/product="cyclin I"
/protein_id="BAA08849.1"
/db_xref="GI:1183162"
/translation="MKPPGPLENORLSFLLEKAITREAOQMKVNVKRNKPSNQVSPSQ
RDEVOMLAKLYOFNLYPETFALASSILDRFLATVKAHPKYLSCIALSCFFLAQKV
EDERI PVKVLARDSCFCSSSEILRNERIILDKLNDLHTATPLPLHIFHAIYS
TRPQLFLPKLSPSHAVLUTKQLLHCMAQNLQFQKSLMALAMVSEMEKLIPIW
LSLTELLOKQMSQLIHRELVHHLSTLQSSLPLNSVYVYRPLKHTLVTCDKGV
FRLHPSSVPGDFGSKNSKPEVPVVGTAAYFHLHPAASGCKQSTKTKRVERMEVDDEF
DGIKRLYNEDNVSENVSGVCGTDLSRQEGHASPCPPLQPVSM"
```

```
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1260
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
```

US-09-736-250-1 (1-377) x HUMCYI (1-1260)

```
Qy 1 MetLysPheProGlyProLeuGlnAsnGlnArgLeuSerPheLeuLeuGluLysAlaTle 20
|||||
Db 1 ATGAAGTTTCAGGGCCCTTGGAAACACAGAGATTGTCTTTCCTGTTGGAAAGGCAATC 60

Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
|||||
Db 61 ACTAGGGAAGCACACATGTGGAAGTGAATGTGCGGAAATAGCCTTCAATCAGAAATGTT 120

Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyGlnPheAsn 60
|||||
```

```
Db 121 TCTCCATCCAGAGAGATGAAGTAATTAATGGCTGGCCAAACCTCAAGTACCATAATCAAC 180
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
|||||
Db 181 CTTTACCAGAGAAACATTTGCTCTGGCTAGCAGCTTTTGGATAGGTTTTAGCTACCGTA 240
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaLysSerCysPhePheLeuAlaLys 100
|||||
Db 241 AAGGCTCATCCAAATACCTTGAGTTGTATTGCAATCAGCTGTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
|||||
Db 301 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAGGTTATGGCAAGAGACAGTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140
|||||
Db 361 GGATGTTCTCATCTGAAATTTTGAGATGGAGAGAAATATTCTGGATAGTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
|||||
Db 421 GATCTTCACACAGCCACACCATTTGATTTCTTCATATTTCCATGTCATTCAGTGTCA 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
|||||
Db 481 ACTAGGCTCAGTTACTTTTCAGTTTCGCCAAATTTGAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLys 200
|||||
Db 541 CTTACCAAGCACTACTCTTCTGATGGCTGCAACCACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
|||||
Db 601 ATGCTGCTCTGGCCATGTTAGTCTGGAATGAGAAACTCATTTCTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
|||||
Db 661 CTTACAATTAACCTGCTTCAGAAAGCACAGATGATAGTCCCTGAGTGTATCCATTTGTCGG 720
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
|||||
Db 721 GAGCTTGTGGCACATCACCTTTCTACTCTGCAGTCTTCCCTGCTCTGAATTCGTTAT 780
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
|||||
Db 781 GTCTACCGTCCCTCAAGCACACCTGCTGACCTGTGCAAAAGGAGTGTTCAGATTACAT 840
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
|||||
Db 841 CCTCTCTGTGCCAGGCCACAGACTTCTCCAAGGACACAGCAAGCCAGAAAGTCCAGTC 900
Qy 301 ArgGlyThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
|||||
Db 901 AGAGGTACAGCAGCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 960
Qy 321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
|||||
Db 961 ACTAAACGCAAAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAATCAAGCGGCTC 1020
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
|||||
Db 1021 TATAATGAAGATAATGTCTCAGAAATATGGGGTCTGTGTGTGGCAGCTGATTTATCAAGA 1080
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
|||||
Db 1081 CAAGAGGACATGCTTCCCTTGTCCACCTTGGCAGCTGTTCTGTGTCATG 1131

RESULT 7
AF135162
LOCUS Homo sapiens cyclin I (CYC1) mRNA, complete cds. PRI 17-MAR-2000
DEFINITION AF135162
ACCESSION AF135162
VERSION AF135162.1 GI:7259481
KEYWORDS
```

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1384)
AUTHORS Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and Qiang, B.Q.
TITLE Isolating a new cDNA coding for human cyclin protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1384)
AUTHORS Chen, J.H., Luo, W.Q., Zhou, Y., Zhou, H.J., Huang, X.W., Yuan, J.G. and Qiang, B.Q.
TITLE Direct Submission
JOURNAL Submitted (16-MAR-1999) Dept. of Biochemistry, ins. of Basic Med. Science, 5 Dong Dan 3 Tiao, Beijing 100005, P.R. China
FEATURES
source
1..1384
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
1..1384
200..1333
/gene="CYC1"
/gene="CYC1"
/codon_start=1
/product="Cyclin I"
/protein_id="AAF43786.1"
/db_xref="GI:7259482"
/translation="MKFPGPLENORLSPLLEKAITREAAQMKVNVKRNPSNONVSPSQ
REDRIQVLKLYLNDSPFCSSSEILRMERILDLKLDWLTATPLDPLHIFHAIVS
TRPQLFSLPKLSQHLAVLTQKLLHMACNQLOFGSLMALAVSLEMEKLIPOW
LSLTLELQKAMDSSQLHCRELVHHLSTLQSSPLNSVYVRPLKHLVTCDDGV
FLRHPSPVGGDFDKNSKPEVPVGTAAFYHLPLAASGCKOTSTKRVEMEDDFY
DGIKRLYNEDNVSENVSGVCGTDLRSQEGHASPCLPQPSVM"
ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1384
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-1 (1-377) x AFI35162 (1-1384)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluValLeu 20
Db 200 ATGAAGTTTCAGGGCCCTTGAAACCAGAGATTGCTTTCTCCTGTTGGAAAGGCAATC 259
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 260 ACTAGGGAAGCACAGATGGAAGAGTGAATGTGGGAAATGCCTTCAATCAGAAATGTT 319
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpGlnPheAsn 60
Db 320 TCTCCATCCAGAGAGATGAAGTAACTCAATGGCTGGCCAAACTCAAGTACCAATTCAC 379
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 380 CTTTACCAGAAACATTGCTGTGCTAGCAGTCTTTGGATAGATTTTGTAGTACCCTA 439
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 440 AAGGCTCATCAAAATACTTGATGTTGATTCGAATCAGCTGTTTTCTTAGTGGCAAG 499
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 500 ACTGTTGAGGAAGATGAGAGAAATTCAGTACTAAGAGTATTGGCAAGAGACAGATTCTGT 559
Qy 121 GlyCysSerSerSerGluLeuArgMetGluArgIleLeuLeuAspLysLeuAsnTrp 140

Db 560 GGATGTTCTCTCATCTGAAATTTTTCAGAAATGAGAGAAATATTCTGGATAAGTGAATTGG 619
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 620 GATCTTCACACAGCCACACACCATTCGATTTTCTCATATTTTCCATGCGCATGCGTCA 679
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 680 ACTAGGCTCAGTTACTTTTTCAGTTTCCCAAAATGAGCCCATCTCAACATTTGGCAGTC 739
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 740 CTTACCAAGCACTACTCTCTGATGCGCTGCAACCACTTCTGCAATTCAGAGGATCC 799
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuLeuIleProAspTrpLeuSer 220
Db 800 ATGCTTGTCTGGCCATGGTTAGTCTGAAATGAGAAACTCAITTCCTGATTGGCTTCT 859
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuLeuHisCysArg 240
Db 860 CTTACAAATTGAATGCTTCAGAAAGCAGATGGATAGTCCCACTGATTCATTTGTCGG 919
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 920 GAGCTTGTGGCAGCATCACTTTCTCTGAGCTCTTCCCTGCTCTGAATTCGGTTAT 979
Qy 261 ValTyrArgProLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 980 GTCTACCGTCCCTCAAGCACACCTGTGACCTGTGACAAAGGAGTGTTCAGATTACAT 1039
Qy 281 ProSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1040 CCCTCTCTGTGCCAGCCCACTTCTCCAAAGACCAACAGCAAGCCCAAGATGCCAGTC 1099
Qy 301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db 1100 AGAGTACAGAGAGCTTTTACCATCATCTCCAGCTGCCAGTGGTGGCAAGACCTCT 1159
Qy 321 ThrLysArgLysValGluGluMetGluValAspPheTyrAspGlyIleLysArgLeu 340
Db 1160 ACTAAACGCAAGATAGAGGAATGGAATGCAATGATGATGATGGAATCAACAGGCTC 1219
Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db 1220 TATAATGAAGATAATGTCTCAGAAATGTGGTGTCTGTGTGGCAGCTGTTTATCAAGA 1279
Qy 361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db 1280 CAAGAGGAGCATGCTTCCCTTGTCCACCTTGGAGCTGTTTCTGTCTATG 1330
RESULT 8
BC000420 1817 bp mRNA linear PRI 30-JUN-2004
LOCUS Homo sapiens cyclin I, mRNA (CDNA clone MGC:8665 IMAGE:2964432),
DEFINITION complete cds.
ACCESSION BC000420
VERSION BC000420.2 GI:38197480
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1817)
AUTHORS Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Buterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.,
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
12477932
2 (bases 1 to 1817)
Strausberg, R.
Direct Submission
Submitted (15-NOV-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
On Nov 6, 2003 this sequence version replaced gi:12653302.
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@hgrl.nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granter, S., Guan, X., Gupta, J., Haghigini, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripp, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAL plate: 1 Row: 0 Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 17738314.

FEATURES

source

Location/Qualifiers
1..1817
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MGC:8665 IMAGE:2964432"
/tissue_type="Muscle, rhabdomyosarcoma"
/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
/note="Vector: pOTS7"

gene

1..1817
/gene="CCNI"
/note="synonyms: CYC1, CYI"
/db_xref="LocusID:10983"
544..1677
/gene="CCNI"

CDS

/product="cyclin I"
/protein_id="AAH00420.1"
/db_xref="GI:12653303"
/translation="MKFPGPLENQRSLFLEKAITREQMKNVVRKMPNSQNSVPSQ
RDEVTQWLAKYQFNLYPTEPALASLLDRFLATVKAHPKYLSCIALSCFFLAQTV
BEDRI PVLKVLARSFCGSSSEILRMERITLDKLNWLTATPLDFLHIFAIYAVS
TEPQLLSLPSPSLAVLTQKLLHGMACNQLQPRGMLALAMVLEMEKLI PDW
LSLTLELQKQMSDLSLHCELVHHLSTLQSLPLNSVYVYRPLKHTLVTCDKGV
FKLPPSVFPGDFSKDNKSPFVPRGTAPAFHPLPAASGCKQTSTKRVEMEDVDFY
DGIKRLYNEDNVSENVSGVCGTDLRQEGHASPCPPLOPVSVM"

ORIGIN

Alignment Scores:
Pred. No.: 0 Length: 1817
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-1 (1-377) x BC000420 (1-1817)
Qy 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuGluLysAlaIle 20
Db 544 ATGAGTTCAGGGCCCTTTGGAAACACAGAGATTGCTTCTCTGTTGGAAAGGCAATC 603
Qy 21 ThrArgGluAlaGlnMetTyrLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 604 ACTAGGGAAGCACAGATGTGGAAGTGAATGTGGGAAAAATGCCCTTCAGAAATGTT 663
Qy 41 SerProSerGlnArgAspGluValIleGlnTyrLeuAlaLysLeuLysTyrGlnPheAsn 60
Db 664 TCTCCATCCAGAGAGATGAATTAATTCATGGCTGCCAAACTCAAGTACCAATTCAAC 723
Qy 61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 724 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTAGCTACCGTA 783
Qy 81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 784 AAGCTCATCCAAATACTTGAGTTGTTATTCATCAATCAGCTGTTTTCCTAGCTGCCAAG 843
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 844 ACTGTTGAGGAGATGAGAGATTCAGTACTAAGGTATTTGGCAAGACAGACAGTTCTGT 903
Qy 121 GlyCysSerSerGluIleLeuArgMetGluArgIleLeuAspLysLeuAsnTyr 140
Db 904 GGATGTTCTCATCTGAAATTTTGGAAATGAGAGAAATATTCTGGATAAGTTGAAATGG 963
Qy 141 AspleuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 964 GATCTTCACAGACACCAATTCAGATTGATTTCTTCATATTTTCCAATGCAATTCAGTGTCA 1023
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 1024 ACTAGGCTCAGTTACTTTTCAGTTTGCCTCCCAATAGCCCATCTCAACATTCGCGATC 1083
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgLysSer 200
Db 1084 CTTACCAAGCAACTACTTCACTGTATGCGCTGCACCAACTCTCTGCAATTCAGAGGATCC 1143
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTyrLeuSer 220
Db 1144 ATGCTTGTCTGCGCATGGTTAGTCTGGAAATGAGAAACTCATCTCTGATGCTTCTCT 1203
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db 1204 CTTACATTTGACTGCTTCAGAAAGACAGATGATAGTCTCCAGTTGATCCATTTGTCGG 1263
Qy 241 GluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db 1264 GAGCTGTGGCACATCACTTTCTACTCTGAGTCTTCCCTCCCTCTGAAATTCGGTTTAT 1323
Qy 261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db 1324 GTCTACCGTCCCTCAAGCACACCTCGTGTGACCTGTGCAAGGAGGTTCAGATTACAT 1383
Qy 281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db 1384 CCCTCTCTGTCGCCAGGCCAGAGCTTCTCCAAAGACAAACAGACCAAGAGAGTGCAGTC 1443
Qy 301 ArgGlyThrAlaAlaPheTyrHisIleuProAlaAlaSerGlyCysLysGlnThrSer 320


```

Db      1444 AGAGGTACAGAGCCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
Qy      321 ThrLysArgLysValGluMetGluValAspPheTyrAspGlyLeuLysArgLeu 340
Db      1504 ACTAAACGCAAGTAGAGAAATGGAAGTGGATGACTTCTATGATGGAATCAACCGGCTC 1563
Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1564 TATAATGAAGATTAATGTCTCAGAAATGTGGTCTCTGTGTGGCACTGATTTATCAAGA 1623
Qy      361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db      1624 CAAGAGGAGACATGCTTCCCTTGTCCACCTTTCGACCTGTTCTGTCTATG 1674

RESULT 9
LOCUS   CQ468129          1889 bp      DNA      linear      PAT 30-JAN-2004
DEFINITION Sequence 10907 from Patent WO0192581.
ACCESSION CQ468129
VERSION   CQ468129.1 GI:41433748
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Algate,P.A., Harlocker,S.L. and Jones,R.
TITLE      Compositions and methods for the therapy and diagnosis of
          ovariancancer
JOURNAL   Patent: WO 0192581-A 10907 06-DEC-2001
FEATURES
source    1..1889
          Location/Qualifiers
          /organism="Homo sapiens"
          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 0 Length: 1889
Score: 377.00 Matches: 377
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ468129 (1-1889)

Qy      1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db      544 ATGAAGTTTCCAGGGCCCTTGGAAACCCAGAGATTGTCTTCTCTGTTGGAAAGGCAATC 603
Qy      21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
Db      604 ACTAGGAGACACAGATGGAAAGTGAATGTGGCGGAAATGCCCTTCAAAATCAGAAATGTT 663
Qy      41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyrGlnPheAsn 60
Db      664 TCTCCATCCAGAGATGAGTAAATTCATGTGCTGGCCAAACTCAAGTACCAATTCAC 723
Qy      61 LeuTyrProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db      724 CTTTACCCAGAAACATTTGCTGTGGCTAGCAGCTCTTTGGATGAGTCTTTAGCTACCGTA 783
Qy      81 LysAlaHisProLysTyrLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
Db      784 AAGGCTCATCCAAATACATTGAGTTGATTTGCAATCAGCTGTTTTCTAGCTGCCAAG 843
Qy      101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db      844 ACTGTTGAGGAGATGAGAAATTCAGTACTAAAGGATTATGGCAAGAGACAGATTTCTGT 903

```

```

Qy      121 GlyCysSerSerSerGluIleLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db      904 GGATGTTTCTCATCTGAAATTTTGAATGAGAGAAATATTCTGGATTAAGTTGAATGG 963
Qy      141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db      964 GATCTTACACAGCACACCATTTGGATTTCTTATATTTTCCATGCCATTCAGTGTCA 1023
Qy      161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db      1024 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATGAGCCCATCTCAACATTTGGCAGTC 1083
Qy      181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db      1084 CTTACCAAGCAACTACTTCACTGTATGGCTTGCACCAACCAACTTCTGCAATTCAGAGGATCC 1143
Qy      201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db      1144 ATGCTTGTCTGGCCATGTTAGTCTGGAAATGGAGAAACTCATCTCTGATTTGGCTTCT 1203
Qy      221 LeuThrIleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArg 240
Db      1204 CTTACAAATTGAATGCTTTCAGAAAGCACAGATGATAGTCTCCAGTTCATCCATTTGTCGG 1263
Qy      241 GluLeuValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyr 260
Db      1264 GAGCTTGTGGCACATCACTTTTACTCTGCAGTCTTCCCTGCTCTCGAATTCGATTTAT 1323
Qy      261 ValTyrArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHis 280
Db      1324 GTCTACCGTCCCTCAAGCACACCTGTGGTACCTGTGACAAAGGAGTGTTCAGATTACAT 1383
Qy      281 ProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProVal 300
Db      1384 CCTCTCTGTCTCCAGGCCAGACTTCTTCCAAAGCACAAACAGACAGCAAGTGCAGTTC 1443
Qy      301 ArgGlyThrAlaAlaPheTyrHisLeuProAlaAlaSerGlyCysLysGlnThrSer 320
Db      1444 AGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCT 1503
Qy      321 ThrLysArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLysArgLeu 340
Db      1504 ACTAAACGCAAGTAGAGAAATGGAAGTGAATGATCTTCTATGATGGAATCAACGGCTC 1563
Qy      341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
Db      1564 TATAATGAAGATAATGTCTCAGAAATGTGGTCTGTGTGTGGCAGTGAATTTATCAAGA 1623
Qy      361 GlnGluGlyHisAlaSerProCysProLeuGlnProValSerValMet 377
Db      1624 CAAGAGGAGACATGCTTCCCTTGTCCACCTTTCGACCTGTTCTGTCTATG 1674

RESULT 10
LOCUS   BC004975          1889 bp      mRNA      linear      PRI 29-JUN-2004
DEFINITION Homo sapiens cyclin I, mRNA (cdna clone MGC:3795 IMAGE:2957878),
          complete cds.
ACCESSION BC004975
VERSION   BC004975.1 GI:13436391
KEYWORDS  MGC.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
          Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
          Altschul,S.F., Collins,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
          Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
          Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
          Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
          Scheetz,T.E., Brownstein,M.J., Uudin,T.B., Loquellano,N.A., Peters,G.J.,
          Carninci,P., Prange,C., Rana,S.S., Loquellano,N.A., Peters,G.J.,

```


Qy 321 ThrLysArgLysValGluMetGluValAspAspPheTyrAspGlyLeuValArgLeu 340
 Db 1504 ACTAAACCAAGTAGAGGAAATGGAAGTGGATGCTTCTATGATGGAAATCAAAACGGCTC 1563

Qy 341 TyrAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArg 360
 Db 1564 TATATGAGATATGCTTCAGAAATGTTGGTCTCTGTGTGGCACTGATTTATCAAGA 1623

Qy 361 GlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
 Db 1624 CAAGAGGGACATGCTTCCCTTGTCCACCTTTGACAGCGTGTCTCTGTCTCATG 1674

RESULT 11
 LOCUS CQ414515 2755 bp DNA linear PAT 23-JAN-2004
 DEFINITION Sequence 21586 from Patent WO0170979.
 ACCESSION CQ414515
 VERSION CQ414515.1 GI:41322296
 KEYWORDS
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1
 Lee, J. and Lillie, J.
 Genes, compositions, kits, and method for identification,
 assessment, prevention, and therapy of ovarian cancer
 Patent: WO 0170979-A 21586 29/SEP=2001;
 Millennium Pharmaceuticals, Inc. (US)

FEATURES
 source
 1..2755
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN
 Alignment Scores:
 Pred. No.: 2.98e-281 Length: 2755
 Score: 266.00 Matches: 266
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 70.56% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ414515 (1-2755)

Qy 103 GluGluAspGluAtgIleProValLeuLysValLeuAlaArgAspSerPheCysGlyCys 122
 Db 1099 GAGGAGATGAGAGATTCAGTACTAAAGTATTTGGCAAGACAGATTTCTGTGGATGT 1158

Qy 123 SerSerSerGluLeuArgMetGluArgIleLeuAspLysLeuAsnTrpAspLeu 142
 Db 1159 TCCTCATCTGAAATTTTTCAGAAATGAGAGAAATTTCTGGATAAGTTGAAATGGATCTT 1218

Qy 143 HisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSerThrArg 162
 Db 1219 CACACAGCCACACCATTTGATTTCTTCATATTTTCCATGTCATTTGCACTGCACTAGG 1278

Qy 163 ProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaValLeuThr 182
 Db 1279 CCTAGTTACTTTTCAGTTTCCCAATAGCCCATCTCAACATTTGGCAGTCTCTTACC 1338

Qy 183 LysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySerMetLeu 202
 Db 1339 AAGCAACTACTTCACTGTATGGCTGCAACCAACTTCTGCAATTCAGAGGATCCATGCTT 1398

Qy 203 AlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSerLeuThr 222
 Db 1399 GCTCTGGCCATGTTAGTCTGAAATGGAGAAACTCAATCTCGATTGGCTTCTCTTACA 1458

Qy 223 IleGluLeuLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeu 242
 Db 1459 ATTGAATGCTTTCAGAAAGACAGATGGATAGTCCCACTGATTCATTCATTGCGGAGCTT 1518

Qy 243 ValAlaHisHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyr 262
 Db 1519 GTGGCACATCACCTTTCTACTCTCAGTCTTCCCTGCTCTGAAATTCGTTTATGTCTAC 1578

Qy 263 ArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuHisProSer 282
 Db 1579 CGTCCCTTCAGACACACCTGTGACCTGTGACAAAGGAGTGTTCAGATTACATCCCTCC 1638

Qy 283 SerValProGlyProAspPheSerLysAspAsnSerLysProGluValProValArgGly 302
 Db 1639 TCTGTCCAGGCCAGACTTCTCCAGGACAAACAGCAGCCAGAAAGTCCAGTCCAGAGGT 1698

Qy 303 ThrAlaAlaPheTyrHisHisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLys 322
 Db 1699 ACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAA 1758

Qy 323 ArgLysValGluGluMetGluValAspAspPheTyrAspGlyIleLeuArgLeuTyrAsn 342
 Db 1759 CGCAAGTAGAGGAAATGGAGTGGATCTTCTATGATGGAATCAAAACGGCTCTATTAAT 1818

Qy 343 GluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerArgGlnGlu 362
 Db 1819 GAAGATATGCTCTCAGAAATGTTGGTCTCTGTGTGGCACTGATTTATCAAGACAGAG 1878

Qy 363 GlyHisAlaSerProCys 368
 Db 1879 GGACATGCTTCCCTTGT 1896

RESULT 12
 LOCUS CR541783 1131 bp mRNA linear PRI 29-JUN-2004
 DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for gene CCNI, cyclin I; complete cds, without stopcodon.
 ACCESSION CR541783
 VERSION CR541783.1 GI:49456522
 KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1131)
 Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
 Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 Cloning of human full open reading frames in Gateway(TM) system
 entry vector (pDONR201)
 Unpublished
 2 (bases 1 to 1131)
 Halleck, A., Ebert, L., Mkoundinya, M., Schick, M., Eisenstein, S.,
 Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
 Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
 Direct Submission
 Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
 Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
 Germany
 COMMENT
 RZPD; RZPD0834E0730D, ORFNo 3592
 www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834E0730D RZPDLIB;
 Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
 834
 www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
 www.rzpd.de/products/orfclones/
 Contact: Inge Arlart
 RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
 Heubnerweg 6, D-14059 Berlin, Germany
 Tel: +49 30 32639 100
 Fax: +49 30 32639 111
 www.rzpd.de
 This clone is available from RZPD;
 Contact RZPD (customer.service@rzpd.de) for further information.
 Clone name at Harvard Institute of Proteomics
 (www.hip.harvard.edu): FLH131015.01L
 This CDS clone is part of a collection of human full ORF clones

jointly established and verified by the Harvard Institute of Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase(TM) reaction. Additional sequence has been added in front of the start codon: att. .AAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCAGCTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM_006835 (GI:17738314) we found AA exchange(s) at position (first base of changed triplet):
223 (arg->gly) 409 (lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES

source

Location/Qualifiers
1..1131
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834E0730D"
/clone_lib="Human Full ORF Clones Gateway (TM) - RZPD"
/lab_host="DH5Alpha"
/note="Vector: pDONR201, Site_1: attP1; Site_2: attP2"
1..1131
/gene="CCNI"
1..1131
/gene="CCNI"
/codon_start=1
/protein_id="CAG46582.1"
/translation="MKFPGLENQRLSFLLEKAITREAOQMKVNRKMPNSQNVSPSQ
RDEIOWIAKUYQNLFPETPALASSLDGLFATVKAHPKYLSCIAISCFPLAAKT
BEDERIPVLKARDSPGCSSEILRMERILDLRLNWLHTATPLDPLHIFHAIAYS
TRPOLFLSLKPSQHLAVLTQKLLHMACNQLQFPGSMALAMVSLMEKILPDW
LSLTTELLQKQMDSSOLIHCKELVAHLSLQSSLPNSVVVVRPLKHTIATCDKV
FRLHPSSVGPDPFSDKNSKPEVRGTAFVHPLPAAGCGCKQTSTKRKVEHNEVDIFY
DGIKLYNEDNVSENVSGVGTDLRSQGHASFPPLQFVSM"

gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 4,776-253 Length: 1131
Score: 240.00 Matches: 375
Percent Similarity: 98.94% Conservatives: 0
Best Local Similarity: 98.94% Mismatches: 2
Query Match: 63.66% Indels: 4
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x CR541783 (1-1131)

QY 1 MetLysPheProGlyProLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
DB 1 ATGAAGTTTCCAGGGCCCTTGGAAACACAGAGATTGCTCTTCTGTTGGAAAGGCAATC 60
QY 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGluAsnVal 40
DB 61 ACTAGGAGACACAGATGTGGAAGTGAATGTGCGAAATGCCCTTCAATACAGATGTT 120
QY 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrpGlnPheAsn 60
DB 121 TCTCATCCACAGAGATGAAGTAAATCAATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
QY 61 LeuTyTrpGluThrPheAlaLeuAlaSerSerLeuLeuAspArg-PheLeuAlaThrVa 80
DB 181 CTTTACCAGAAACATTTGCTGCTGCTAGCAGTCTTTTGGATGG-GTTTTTAGTACCGT 239
QY 80 LysAlaHisProLysTyTrpLeuSerCysIleAlaIleSerCysPhePheLeuAlaLys 100
DB 240 AAAGCTCATCCAAATACTTGGTTGTATTGCAATCAGCTGTTTTTCTAGTGGCAA 299
QY 100 sThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCy 120
DB 300 GACTGTTGAGGAATGAGAGAAATCCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTG 359
QY 120 sGlyCysSerSerGluLeuLeuArgMetGluArgIleLeuLeuAspLys-LeuAsnT 140

DB 360 TGGATGTTCTCTCATCTGAAATTTTTCAGATCGAGAGATTAATCTGGATAG-GTTGAATT 418
QY 140 rpAspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaVal 160
DB 419 GGGATCTTCACACAGCCACACCATTTGGATTTCATATATTTTCATGCAATTCAGATGT 478
QY 160 erThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaV 180
DB 479 CAATAGAGCCCTCAGTTACTTTTCAGTTTGGCCAAATTTGAGCCCATCTCAACATTTGGCAG 538
QY 180 alLeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuGlnPheArgGlyS 200
DB 539 TCCATTACCAAGCAACTACTTCACTGTATGGCTGCACCAACTTCTGCAATTCAGAGAT 598
QY 200 erMetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuS 220
DB 599 CCATGCTTGTCTGCGCCATGTTAGTCTGGAATATGGAGAAACTCATCTCTGATTGGCTTT 658
QY 220 erLeuThrIleGluLeuGlnLysAlaGlnMetAspSerSerGlnLeuIleHisCysA 240
DB 659 CTCTTACAAATGAACTGCTTCAGAAACACAGATGGATAGCTCCAGTTGATCATTTGTC 718
QY 240 rgGluLeuValAlaHisLeuSerThrLeuGlnSerSerLeuProLeuAsnSerValT 260
DB 719 GGGAGCTTGTGGCACATCACCTTTCTACTCTGCACTCTTCCCTGCTCTGAATTCGGTTT 778
QY 260 yrValTyArgProLeuLysHisThrLeuValThrCysAspLysGlyValPheArgLeuH 280
DB 779 ATGTCTACCGTCCCTCAAGCACACCCCTGGTGACCTGTGCAAGAGAGTGTTCAGATTAC 838
QY 280 isProSerSerValProGlyProAspPheSerLysAspAsnSerLysProGluValProV 300
DB 839 ATCCCTCTCTGTCCAGGCCAGACTTCTCCAGGCAACAGACAGCAAGAGAGTGCAG 898
QY 300 alArgGlyThrAlaAlaPheTyHisLeuProAlaAlaSerGlyCysLysGlnThrS 320
DB 899 TCAGAGGTACAGCAGCCTTTTACCATCATCTCCAGCTGCCAGTGGGTGCAAGCAGACCT 958
QY 320 erThrLysArgLysValGluGluMetGluValAspAspPheTyArgGlyLysArgL 340
DB 959 CTACTAAACGCAAGTAGAGGAAATGGAAGTGGATGACTTCTATGATGGAAATCAAAACGC 1018
QY 340 euTyAsnGluAspAsnValSerGluAsnValGlySerValCysGlyThrAspLeuSerA 360
DB 1019 TCTATATGAGATATATGCTCAGAAATGTGGGTCTGTGTGGCAGCTGATTATCAA 1078
QY 360 rgGlnGluGlyHisAlaSerProCysProProLeuGlnProValSerValMet 377
DB 1079 GACAAGAGGACATGCTTCCCTTGTCCACCTTTGAGCCTGTTTCTGTCTCATG 1131
RESULT 13
QY21727
LOCUS
DEFINITION Sequence 7661 from Patent WO02068579.
ACCESSION QY21727
VERSION QY21727.1 GI:42282584
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE 'Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 7661 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES
Location/Qualifiers
1..690
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:

Pred. No.: 2.92e-242 Length: 690
Score: 230.00 Matches: 230
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 61.01% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-1 (1-377) x CQ721727 (1-690)

Qy 1 MetLysPheProGluPheLeuGluAsnGlnArgLeuSerPheLeuLeuGluLysAlaIle 20
Db 1 ATGAAGTTTCCAGGGCCCTTGGAAACACAGAGATTGCTTTCTCTGTTGGAAAGGCAATC 60
Qy 21 ThrArgGluAlaGlnMetTrpLysValAsnValArgLysMetProSerAsnGlnAsnVal 40
Db 61 ACTAGGGAAGCACAGATGTGGAAAGTGAATGTGGGAAATGCCTTCAATCAGATGTT 120
Qy 41 SerProSerGlnArgAspGluValIleGlnTrpLeuAlaLysLeuLysTyTrGlnPheAsn 60
Db 121 TCTCCATCCAGAGAGATGAATTCATATGGCTGGCCAAACTCAAGTACCAATTCAAC 180
Qy 61 LeuTyProGluThrPheAlaLeuAlaSerSerLeuLeuAspArgPheLeuAlaThrVal 80
Db 181 CTTTACCAGAAACATTTGCTCTGGCTAGCAGTCTTTTGGATAGGTTTTTACGTACCGTA 240
Qy 81 LysAlaHisProLysTyLeuSerCysIleAlaIleSerCysPhePheLeuAlaAlaLys 100
Db 241 AAGGCTCATCCAAATACTTGGATTGATTTGCAATCAGCTGTTTTTCTAGCTGCCAAG 300
Qy 101 ThrValGluGluAspGluArgIleProValLeuLysValLeuAlaArgAspSerPheCys 120
Db 301 ACTGTTGAGGAAGATGAGAGAATTCAGTACTAAAGGTATTGGCAAGAGACAGTTTCTGT 360
Qy 121 GlyCysSerSerSerGluLeuLeuArgMetGluArgIleIleLeuAspLysLeuAsnTrp 140
Db 361 GGATGTTCTCATCTGAAATTTTGAAGATGGAGAGAATTTATCTGGATGAATTTGAATGG 420
Qy 141 AspLeuHisThrAlaThrProLeuAspPheLeuHisIlePheHisAlaIleAlaValSer 160
Db 421 GATCTTCACAGCCACACCAATTTGATTTTCTCATATTTTCCATGCCATTCAGTGTC 480
Qy 161 ThrArgProGlnLeuLeuPheSerLeuProLysLeuSerProSerGlnHisLeuAlaVal 180
Db 481 ACTAGGCTCAGTTACTTTTTCAGTTTGGCCAAATTTAGCCCATCTCAACATTTGGCAGTC 540
Qy 181 LeuThrLysGlnLeuLeuHisCysMetAlaCysAsnGlnLeuLeuGlnPheArgGlySer 200
Db 541 CTTACCAAGCAACTACTTCTGATGTCCTGCAACCAACTTCTGCAATTCAGAGGATCC 600
Qy 201 MetLeuAlaLeuAlaMetValSerLeuGluMetGluLysLeuIleProAspTrpLeuSer 220
Db 601 ATGCTTGCTCTGGCCATCGTTAGTCTGGAATTCGAAAGAACTCATTTCTGATGGCTTCT 660
Qy 221 LeuThrIleGluLeuLeuGlnLysAlaGln 230
Db 661 CTTACAATTGAAGTCTTTCAGAAAGCACAC 690

RESULT 14

AY207372 29867 bp DNA linear PRI 05-JAN-2003
LOCUS
DEFINITION Homo sapiens cyclin I (CCNI) gene, complete cds.
ACCESSION AY207372
VERSION AY207372.1 GI:27501933
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 29867)
AUTHORS Rieder,M.J., Livingston,R.J., Daniels,M.R., Montoya,M.A.,

Chung,M.-W., Miyamoto,K.E., Nguyen,C.P., Nguyen,D.A., Poel,C.L.,
Robertson,P.D., Schackwitz,W.S., Sherwood,J.K., Witrak,L.A. and
Nickerson,D.A.
Submitted<(26-DEC-2002)>Genome Sciences, University of Washington,
1705 NE Pacific, Seattle, WA 98195, USA
To cite this work please use: NIEHS-SNPs, Environmental Genome
Project, NIEHS ES15478, Department of Genome Sciences, Seattle, WA
(URL: http://egp.gs.washington.edu).

TITLE
JOURNAL

COMMENT

FEATURES

source

1. .29867
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
256
/frequency="0.01"
/replace="a"
328
/frequency="0.01"
/replace="c"
351
/frequency="0.04"
/replace="c"
460
/frequency="0.01"
/replace="a"
494
/frequency="0.01"
/replace="a"
538
/frequency="0.13"
/replace="c"
568
/frequency="0.02"
/replace="a"
623
/frequency="0.02"
/replace="a"
646
/frequency="0.02"
/replace="a"
737
/frequency="0.01"
/replace="a"
770
/frequency="0.01"
/replace="c"
784
/frequency="0.01"
/replace="g"
832
/frequency="0.01"
/replace="g"
884 .28840
/gene="CCNI"
Join(884..1384,10453..10609,18229..18357,20541..20615,
20762..20902,21484..21714,28204..28840)
/gene="CCNI"
/product="cyclin I"
1126
/gene="CCNI"
/frequency="0.01"
/replace="t"
1178
/gene="CCNI"
/frequency="0.01"
/replace="t"
1208 .1213
/gene="CCNI"
/frequency="0.18"
/replace="a"
1269
/gene="CCNI"

Qy 329 GluValAspAspPheTyAspGlyIleLysArgLeuTyAsnGluAspAsnValSerGlu 348
 Db 28498 GAATGGATGACTTCTATGATGAATCAACGGCTCTATAATGAAGATAATGCTCTAGAA 28557
 Qy 349 AsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys 368
 Db 28558 AATGGGTTCTGTGTGGCACTGATTTATCAAGACAAGAGGGACATGCTTCCCTTGT 28617
 Qy 369 ProProLeuGlnProValSerValMet 377
 Db 28618 CCACCTTTGCAGCCTGTTCTGTCAATG 28644

RESULT 15

AC111196/c
 LOCUS AC111196 35191 bp DNA linear PRI 20-APR-2002
 DEFINITION Homo sapiens BAC clone RP11-585K17 from 4, complete sequence.

AC111196
 ACCESSION AC111196.4 GI:20069715

VERSION HTG.

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Sulston, J.E. and Waterston, R.

TITLE Toward a complete human genome sequence

JOURNAL Genome Res. 8 (11), 1097-1108 (1998)

MEDLINE 99063792

PUBMED 9847074

REFERENCE

AUTHORS Wang, C., Kozlowski, A., Spalding, L., Pearman, C. and Boyer, E.

TITLE The sequence of Homo sapiens BAC clone RP11-585K17

JOURNAL Unpublished (2001)

REFERENCE 3 (bases 1 to 35191)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (18-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 4 (bases 1 to 35191)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (03-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 5 (bases 1 to 35191)

AUTHORS Waterston, R.H.

TITLE Direct Submission

JOURNAL Submitted (08-APR-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA

REFERENCE 6 (bases 1 to 35191)

AUTHORS Waterston, R.

TITLE Direct Submission

JOURNAL Submitted (20-APR-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

On Apr 8, 2002 this sequence version replaced gi:19913343.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>

Contact: sapiens@wustl.edu

----- Summary Statistics

Center project name: H_NH0585K17

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping

clone sections once, or longer because we provide a small overlap

between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPI1-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Taten, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP11-123J14, 2000 bp overlap;
 the clone sequenced to the right is RP11-1E1, 2000 bp overlap.
 Actual end of this clone is at base position 27847 of RP11-1E1.

Polymorphisms exist between AC111196 and AC104687.

FEATURES

Location/Qualifiers

1..35191

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="4"

/map="4"

/clone="RP11-585K17"

/clone_lib="RPI1-11"

/rpt_family="(CA)n"

399..512

/rpt_family="(TA)n"

1849..2009

/rpt_family="MIR"

2359..2653

/rpt_family="Alu"

3325..3408

/rpt_family="MER103"

3468..3638

/rpt_family="MER1_type"

4238..4531

/rpt_family="Alu"

5172..5375

/rpt_family="MIR"

6003..6130

/rpt_family="MIR"

6432..6466

/rpt_family="(TG)n"

6733..6798

/rpt_family="CT-rich"

6850..6958

/rpt_family="(TA)n"

7073..7340

/rpt_family="Alu"

7489..7790

/rpt_family="Alu"

9650..9687

/rpt_family="(TG)n"

11687..11710

/rpt_family="(TTTTA)n"

14176..14470

/rpt_family="Alu"

19012..19077

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

repeat_region

QY 369 ProProLeuGlnProValSerValMet 377
Db 25344 CCACCTTTGCAGCCTGTTTCTGTCTCATG 25318

Search completed: February 11, 2005, 14:33:40
Job time : 7807.45 secs

```
/rpt_family="(TTTA)n"
19135..19445
/rpt_family="Alu"
19677..19965
/rpt_family="Alu"
20334..20613
/rpt_family="Alu"
20736..20809
/rpt_family="L2"
22646..22670
/rpt_family="(T)n"
22909..23185
/rpt_family="Alu"
26059..26084
/rpt_family="(T)n"
26206..26226
/rpt_family="AT_rich"
26492..26793
/rpt_family="Alu"
26978..27172
/rpt_family="L2"
28010..28338
/rpt_family="MER2_type"
29051..29409
/rpt_family="L1"
31198..31220
/rpt_family="AT_rich"
32557..32862
/rpt_family="Alu"
33574..33661
/rpt_family="ERV1"
33683..33986
/rpt_family="Alu"

ORIGIN
Alignment Scores:
Pred. No.: 1,058-151 Length: 35191
Score: 149.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 39.52% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-1 (1-377) x AC111196 (1-35191)

QY 229 AlaGlnMetAspSerSerGlnLeuIleHisCysArgGluLeuValAlaHisHisLeuSer 248
Db 25764 GCCCAGATGGATAGCTCCAGTTGATCCATTGTCGGAGCTTGTGGCACATCACCTTTCT 25705
QY 249 ThrLeuGlnSerSerLeuProLeuAsnSerValTyrValTyrArgProLeuLysHisThr 268
Db 25704 ACTCTGCAGTCTTCCTCCCTCTGAATTCGGTTATGTCTACCGTCCCTCAAGCACACC 25645
QY 269 LeuValThrCysAspLysGlyValPheArgLeuHisProSerSerValProGlyProAsp 288
Db 25644 CTGGTGACTGTGACAAAGGAGTGTTCAGATTACATCCCTCTCTGCCAGGCCAGAC 25585
QY 289 PheSerLysAspAsnSerLysProGluValProValArgGlyThrAlaAlaPheTyrHis 308
Db 25584 TTCTCCAAGGACACACAGCCAGTCCAGTCCAGGTACAGCAGCCCTTTTACCAT 25525
QY 309 HisLeuProAlaAlaSerGlyCysLysGlnThrSerThrLysArgLysValGluGluMet 328
Db 25524 CATCTCCAGCTGCCAGTGGGTGCAAGCAGACCTCTACTAAACGCAAGTAGAGAAATG 25465
QY 329 GluValAspAspPheTyrAspGlyIleLysArgLeuTyrAsnGluAspAsnValSerGlu 348
Db 25464 GAAGTGGATGACTTCTATGATGGATCAACGGCTCTATATGAATATATGCTCTCAGAA 25405
QY 349 AsnValGlySerValCysGlyThrAspLeuSerArgGlnGluGlyHisAlaSerProCys 368
Db 25404 AATGTGGTCTCTGTGTGGCACTGATTTATCAAGACAAGAGGACATGCTTCCCTTGT 25345
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:09 ; Search time 3.97442 Seconds
(without alignments)
1362.372 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 74
Sequence: 1 EDVSENVGVCVT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	14	AAW21966	Aaw21966 Human cyc
2	74	100.0	300	ADN01131	Adn01131 Human cel
3	74	100.0	334	AAE37938	Aae37938 Human CGD
4	74	100.0	377	AAW21965	Aaw21965 Human cyc
5	74	100.0	377	AAV52185	Aav52185 Human cyc
6	74	100.0	377	ABR39934	Abr39934 Human pro
7	74	100.0	377	ADP12615	Adp12615 Protein e
8	74	100.0	377	ABM80569	Abm80569 Tumour-as
9	44	59.5	464	ABP66192	Abp66192 Bifidobac
10	43	58.1	469	ADN23705	Adn23705 Bacterial
11	43	58.1	762	ABR61598	Abr61598 Z. mays v
12	43	58.1	764	ADN20925	Adn20925 Beta vulg
13	43	58.1	770	ABN91014	Abn91014 Herbicida
14	43	58.1	1849	ABB61023	Abb61023 Drosophil
15	42	56.8	672	ABJ25449	Abj25449 Aspergill
16	42	56.8	672	ABJ26049	Abj26049 Aspergill
17	42	56.8	720	ADE08519	Ade08519 Novel pro
18	41	55.4	345	ABB67087	Abb67087 Drosophil
19	41	55.4	544	AAR90298	Aar90298 Maize pro
20	41	55.4	544	AAW25748	Aaw25748 Maize pro
21	41	55.4	544	AAW41606	Aaw41606 Maize pro
22	41	55.4	544	AAW51256	Aaw51256 Maize pro
23	41	55.4	544	AAE08751	Aae08751 Maize pro
24	41	55.4	544	AAE14662	Aae14662 Maize pro
25	41	55.4	544	AAE10223	Aae10223 Maize pro

26	41	55.4	544	AAE13204	Aae13204 Maize pro
27	41	55.4	544	AAW21966	Aaw21966 Maize pro
28	41	55.4	544	AAE78537	Aae78537 Maize pro
29	41	55.4	544	AAE26008	Aae26008 Maize pro
30	40	54.1	135	ABB89159	Abb89159 Human pol
31	40	54.1	177	ADJ70525	Adj70525 Human hea
32	40	54.1	200	AAE80436	Aae80436 Recombina
33	40	54.1	201	AAE80918	Aae80918 Sequence
34	40	54.1	201	AAE80917	Aae80917 Sequence
35	40	54.1	201	AAE92077	Aae92077 Mouse glu
36	40	54.1	201	ADJ68233	Adj68233 Human hea
37	40	54.1	201	ADO77886	Ado77886 Glutathio
38	40	54.1	205	AAE80916	Aae80916 Sequence
39	40	54.1	293	AAE87773	Aae87773 Human T2R
40	40	54.1	293	ADR29130	Adr29130 Taste rec
41	40	54.1	300	ABU04666	Abu04666 Human exp
42	40	54.1	356	ABG07458	Abg07458 Novel hum
43	40	54.1	470	ADN47440	Adn47440 Thermococ
44	39	52.7	110	ABE15314	Abel15314 Human ner
45	39	52.7	259	ABU51611	Abu51611 Helicobac

ALIGNMENTS

RESULT 1
AAW21966
ID AAW21966 standard; protein; 14 AA.
XX

AC AAW21966;
XX
DT 02-DEC-1997 (first entry)
XX
DE Human cyclin I peptide fragment.
XX
KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX
OS Homo sapiens.
XX
FN WO9712973-A1.
PD 10-APR-1997.
XX
PF 07-OCT-1996; 96WO-JP002905.
XX
PR 05-OCT-1995; 95JP-00284663.
XX
PA (SUME) SUMITOMO ELECTRIC IND CO.
XX
FI Nakamura T;
XX
DR WPI; 1997-226217/20.
XX
PT Human cyclin I protein and related (anti:sense) DNA - used for neuron
labelling method and cancer cell detection.
XX
Claim 7; Page 30; 45pp; Japanese.
XX
This peptide is a fragment of human cyclin I which can be specifically
recognised by antibodies of the invention. The antibodies are used to
detect the presence of cyclin I. Antisense cyclin I polynucleotides are
useful for as probes and can be labelled and used for detection of
neurons by hybridisation with mRNA for cyclin I (contained in the
neurons and arising by the expression of the cyclin I gene in these
cells). The gene can be used for detection of cancer cells by detecting
the expression of the cyclin I gene in these cells.

SQ Sequence 14 AA;

Query Match 100.0%; Score 74; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCCT 14
DB 1 EDNVSENVGVCCT 14

RESULT 2
ID ADN01131 standard; protein; 300 AA.
XX ADN01131;
XX
XX
XX 01-JUL-2004 (first entry)
XX Human cell growth, differentiation, and death-associated protein #15.
XX human; cell growth; cell differentiation; cell death; CGDD;
KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
KW cirrhosis; hepatitis; polycythemia vera; psoriasis; cancer;
KW developmental disorder; Cushing's syndrome; hypothyroidism;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease;
KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
KW reproductive disorder; infertility; endometriosis; uterine fibroid.
XX Homo sapiens.
XX WO2004031364-A2.
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
XX 03-OCT-2002; 2002US-0416205P.
XX 25-OCT-2002; 2002US-0421521P.
XX 21-NOV-2002; 2002US-0428376P.
XX 23-DEC-2002; 2002US-0436258P.
XX 10-JAN-2003; 2003US-0439292P.
XX 13-FEB-2003; 2003US-0447578P.
XX
XX (INCY-) INCYTE CORP.
XX (BURR/) BURRILL J D.
XX
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
PI Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
PI Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
PI Yang YG, Gietzen KJ, Hafalia AJA;
XX
XX WPI; 2004-330172/30.
XX N-PSDB; ADN01156.
XX
XX New isolated polypeptides associated with cell growth, differentiation
PT and death, useful for diagnosing, treating or preventing e.g.
PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anaemia,
PT diabetes mellitus or infertility.
XX
XX Claim 1; SEQ ID NO 15; 213pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
CC proteins that are associated with cell growth, differentiation, and death
CC (CGDD). The DNA and protein sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of CGDD, such as: cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
CC polycythemia vera, psoriasis and cancers), developmental disorders (e.g.
CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
CC disease, Parkinson's disease and multiple sclerosis);
CC autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
CC contact dermatitis and diabetes mellitus), and reproductive disorders
CC (e.g. infertility, endometriosis and uterine fibroid). The present amino
CC acid sequence represents a human CGDD-associated protein of the
CC invention.

XX SQ Sequence 300 AA;
Query Match 100.0%; Score 74; DB 8; Length 300;
Best Local Similarity 100.0%; Pred. No. 0.00026; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0;
QY 1 EDNVSENVGVCCT 14
DB 266 EDNVSENVGVCCT 279

RESULT 3
ID AAE37938 standard; protein; 334 AA.
XX AAE37938;
XX 06-NOV-2003 (first entry)
XX Human CGDD-27 protein.
XX
XX Human: cell growth, differentiation and death protein; CGDD; leukaemia;
KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;
KW muscular disorder; myotonic dystrophy; catatonia; endocrine disorder;
KW diabetes; Grave's disease; cancer; immunological disorder; scleroderma;
KW systemic lupus erythematosus; allergy; Crohn's disease; renal disorder;
KW gastrointestinal disorder; Goodpasture's syndrome; infection; cirrhosis;
KW cardiovascular disorder; atherosclerosis; hepatic disease; transgenic;
KW transgenic animal; gene therapy; neuroprotective; relaxant; cytostatic;
KW dermatological; immunosuppressive; cerebroprotective; anticonvulsant;
KW antibacterial; antiparasitic; fungicide; virucide; uropathic; cardiant;
KW protozoacide; nootropic.
XX Homo sapiens.
XX WO2003050253-A2.
XX 19-JUN-2003.
XX
XX 04-DEC-2002; 2002WO-US039133.
XX
XX 07-DEC-2001; 2001US-0340747P.
XX 20-DEC-2001; 2001US-0342761P.
XX 15-JAN-2002; 2002US-0349705P.
XX 06-FEB-2002; 2002US-0354764P.
XX 12-FEB-2002; 2002US-0356216P.
XX (INCY-) INCYTE GENOMICS INC.
XX
XX Griffin JA, Ramkumar J, Emerling BM, Kable AE, Elliott VS;
PI Marquis JP, Baughn MR, Gorvad AE, Yue H, Lee EA, Becha SD, Tang YT;
PI Tran UK, Swarnakar A, Lee S, Ison CH, Hafalia AJA, Tran B;
PI Sprague WW, Lee SY, Khare R, Gandhi AR, Gietzen KJ, Bhatia U;
PI Burriil JD, Blake JJ, Ho A, Zheng W;
XX
XX WPI; 2003-532903/50.
XX N-PSDB; AAD57247.
XX
XX New CGDD polypeptides, useful for diagnosing, preventing, and treating
PT disorders associated with an abnormal expression or activity of CGDD,
PT e.g. neuromuscular, immunological, cardiovascular disorders, cancer
PT and/or infections.
XX
XX Claim 1; Page 250; 299pp; English.
XX
XX The present invention relates to novel cell growth, differentiation and
CC death (CGDD) proteins and polynucleotides encoding them. The sequences of
CC the invention are useful in diagnosing, preventing and treating disorders
CC associated with an abnormal expression or activity of CGDD such as
CC neurodegenerative disorders (e.g. Parkinson's disease, Alzheimer's
CC disease), muscular disorders (e.g. myotonic dystrophy, catatonia),
CC endocrine disorders (e.g. diabetes, Grave's disease), cancers (e.g.

CC leukaemia, cervical or breast cancers), immunological disorders (e.g.
 CC scleroderma, systemic lupus erythematosus, allergies), gastrointestinal
 CC disorders (e.g. Crohn's disease), renal disorders (e.g. Goodpasture's
 CC syndrome), infections (e.g. viral, bacterial, fungal, parasitic,
 CC protozoal, helminthic), cardiovascular disorders (e.g. atherosclerosis)
 CC and hepatic diseases (e.g. cirrhosis). The polynucleotides can be used to
 CC create humanised animals or transgenic animals to model human diseases.
 CC The invention is also used in gene therapy. The present sequence is human
 CC CGDD-27 protein
 XX
 XX Sequence 334 AA;

Query Match 100.0%; Score 74; DB 7; Length 334;
 Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 300 EDNVSENVGVCVT 313

RESULT 4
 AAW21965
 ID AAW21965 standard; protein; 377 AA.

XX AAW21965;
 DT 02-DEC-1997 (first entry)
 XX Human cyclin I.
 DE human; cyclin I; antisense; probe; neurone; cancer; antibody.
 XX Homo sapiens.

OS
 XX WO9712973-A1.
 PN 10-APR-1997.

XX 07-OCT-1996; 96WO-JP002905.
 XX 05-OCT-1995; 95JP-00284663.

XX (SUME) SUMITOMO ELECTRIC IND CO.
 XX Nakamura T;
 XX WPI; 1997-226217/20.

XX N-PSDB; AAT73937.
 XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
 PT labelling method and cancer cell detection.

XX Claim 1; Fig 1; 45pp; Japanese.
 XX This sequence is human cyclin I. Antisense polynucleotides are useful for
 CC as probes and can be labelled and used for detection of neurones by
 CC hybridisation with mRNA for cyclin I (contained in the neurones and
 CC arising by the expression of the cyclin I gene in these cells). The gene
 CC can be used for detection of cancer cells by detecting the expression of
 CC the cyclin I gene in these cells. Also antibodies specific for the
 CC fragments of the protein (especially AAW21966) can be used for detection
 XX

XX Sequence 377 AA;
 Query Match 100.0%; Score 74; DB 2; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 343 EDNVSENVGVCVT 356

RESULT 6

RESULT 5
 AAY52185
 ID AAY52185 standard; protein; 377 AA.

XX AAY52185;
 AC AAY52185;
 DT 09-FEB-2000 (first entry)

XX Human cyclin I amino acid sequence.
 XX Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
 KW ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
 KW atherosclerosis; tumour.

XX Homo sapiens.
 OS WO9925829-A2.
 PN 27-MAY-1999.

XX 12-NOV-1998; 98WO-US024095.
 XX 13-NOV-1997; 97US-00969106.

XX (CURA-) CURAGEN CORP.
 XX Yang M, Nandabalan K, Schulz VP;
 PI WPI; 2000-061923/05.

XX N-PSDB; AAZ37836.
 XX New complexes of the cyclin-dependent kinase 2 protein with its
 PT interacting proteins, used to treat, e.g. atherosclerosis.

XX Example; Fig 2; 90pp; English.
 XX This is the human Cyclin I amino acid sequence. Cyclin I is expressed at
 CC almost constant levels throughout the cell cycle, and is implicated in
 CC controlling cell cycle progression and transcriptional control. Cyclins
 CC form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent
 CC kinase 2, is used in the invention which relates to complexes of the CDK2
 CC protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1
 CC and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in
 CC S phase of the cell cycle, and is pivotal for G1/S transition.

XX Compositions containing a CDK2 complex, an antibody targeting the
 CC complex, and nucleotide sequences encoding CDK2 or its derivatives can be
 CC used therapeutically. The complexes and their nucleotide sequences can be
 CC used to treat diseases or disorders associated with increased or
 CC decreased levels of the complex. Screening the complex, or a derivative
 CC or a modulator of the complex for neoplastic activity by measuring the
 CC survival or proliferation of cells from a malignant cell line when in
 CC contact with the complex can be used to indicate if the the complex has
 CC anti-neoplastic activity. Screening for molecules that modulate the
 CC formation of the complexes can be used for treating or preventing
 CC atherosclerosis or atherosclerosis-associated disease by contacting cells
 CC or using a test animal, in which tumour growth or regression is measured
 CC to test whether anti-neoplastic activity is displayed. Diseases which can
 CC be treated or prevented by molecule/s which modulate the function of the
 CC complex include cancer, hyperproliferative disorders and atherosclerosis
 XX

XX Sequence 377 AA;
 Query Match 100.0%; Score 74; DB 3; Length 377;
 Best Local Similarity 100.0%; Pred. No. 0.00032; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0;

Qy 1 EDNVSENVGVCVT 14
 |||||
 Db 343 EDNVSENVGVCVT 356

```

ABR39934
ID  ABR39934 standard; protein; 377 AA.
AC  ABR39934;
XX
DT  11-AUG-2003 (first entry)
DE  Human prostate selective polypeptide Pr325.
KW  Prostate; molecular marker; cancer; cytostatic; gene therapy; human.
XX
OS  Homo sapiens.
XX  WO2003014298-A2.
XX  PN
XX  PD 20-FEB-2003.
XX
PF  02-AUG-2002; 2002WO-US024431.
XX
PR  03-AUG-2001; 2001US-0309470P.
XX  PR  30-OCT-2001; 2001US-0330747P.
XX
PA  (ORIG-) ORIGENE TECHNOLOGIES INC.
XX
PI  Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;
XX
DR  WPI; 2003-256562/25.
XX  DR  N-PSDB; ACC47339.
XX
PT  New polynucleotide, useful for preparing a composition for treating
XX  prostate disease, e.g., cancer.
XX
PS  Claim 5; Page 147-149; 212pp; English.
XX
CC  The invention relates to prostate selective polynucleotides and
XX  polypeptides. The polynucleotides are expressed in prostate and are
XX  useful as molecular markers, as drug targets, and for detecting,
XX  monitoring, preventing or treating diseases and conditions related to
XX  prostate, such as prostate cancers. The present sequence represents a
XX  prostate specific polypeptide
XX
SQ  Sequence 377 AA;

Query Match      100.0%; Score 74; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  |||||
    343 EDNVSENVGVCVGT 356

RESULT 7
ADP12615
ID  ADP12615 standard; protein; 377 AA.
XX
AC  ADP12615;
XX
DT  12-AUG-2004 (first entry)
XX
DE  Protein encoded by mRNA of the invention #225.
XX
KW  transplant rejection; immune system; rheumatoid arthritis; lupus;
XX  inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX
OS  Homo sapiens.
XX
XX  WO2004042346-A2.
XX  PN
XX  PD 21-MAY-2004.
XX
PF  24-APR-2003; 2003WO-US012946.
XX
PR  Wu TD, Zhang Z, Zhou Y;

Query Match      100.0%; Score 74; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  |||||
    343 EDNVSENVGVCVGT 356

RESULT 8
ABM80569
ID  ABM80569 standard; protein; 377 AA.
XX
AC  ABM80569;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
XX
KW  Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX  tumour; diagnosis; cell proliferative disorder; breast cancer;
XX  colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX  central nervous system cancer; bladder cancer; pancreatic cancer;
XX  cervical cancer; melanoma; leukaemia; hybridisation probe;
XX  chromosome identification; chromosome mapping; gene mapping;
XX  gene therapy; cytostatic.
XX
OS  Homo sapiens.
XX
XX  WO2004030615-A2.
XX  PN
XX  PD 15-APR-2004.
XX
PF  29-SEP-2003; 2003WO-US028547.
XX
PR  02-OCT-2002; 2002US-0414971P.
XX
PA  (GETH ) GENENTECH INC.
XX
XX  Wu TD, Zhang Z, Zhou Y;

```

```

PR  24-APR-2002; 2002US-00131831.
XX  PR  20-DEC-2002; 2002US-00325899.
XX
PA  (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX
PI  Wohlgenuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX  PI  Rosenberg S;
XX
DR  WPI; 2004-400724/37.
XX
PT  Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX  pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX  rejection, in an individual, comprises detecting the expression level of
XX  the genes.
XX
PS  Claim 65; SEQ ID NO 2624; 1762pp; English.
XX
CC  The present invention relates to diagnosing or monitoring transplant
XX  rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX  comprises detecting the expression level of one or more genes. The
XX  methods, system and kits are useful in diagnosing or monitoring
XX  transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX  islet, lung, bone marrow or stem cell transplant rejection.
XX  xenotransplant rejection or mechanical organ replacement rejection, in an
XX  individual. The method is also useful in assessing the immune status of
XX  an individual. The methods are also useful in diagnosing and monitoring
XX  diseases that involve the immune system, e.g. rheumatoid arthritis,
XX  lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX  viral, bacterial or fungal infection. The present sequence represents a
XX  protein that is encoded by the mRNA of the invention.
XX
SQ  Sequence 377 AA;

Query Match      100.0%; Score 74; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1 EDNVSENVGVCVGT 14
Db  |||||
    343 EDNVSENVGVCVGT 356

RESULT 8
ABM80569
ID  ABM80569 standard; protein; 377 AA.
XX
AC  ABM80569;
XX
DT  18-NOV-2004 (first entry)
XX
DE  Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ:1450.
XX
KW  Tumour-associated antigenic target; TAT; human; overexpression; cancer;
XX  tumour; diagnosis; cell proliferative disorder; breast cancer;
XX  colorectal cancer; lung cancer; ovarian cancer; liver cancer;
XX  central nervous system cancer; bladder cancer; pancreatic cancer;
XX  cervical cancer; melanoma; leukaemia; hybridisation probe;
XX  chromosome identification; chromosome mapping; gene mapping;
XX  gene therapy; cytostatic.
XX
OS  Homo sapiens.
XX
XX  WO2004030615-A2.
XX  PN
XX  PD 15-APR-2004.
XX
PF  29-SEP-2003; 2003WO-US028547.
XX
PR  02-OCT-2002; 2002US-0414971P.
XX
PA  (GETH ) GENENTECH INC.
XX
XX  Wu TD, Zhang Z, Zhou Y;

```


PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX
XX WPI; 2004-061375/06.
DR
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 6358; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 469 AA;
SQ
Query Match 58.1%; Score 43; DB 8; Length 469;
Best Local Similarity 58.3%; Pred. No. 91;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 3 NVSENVGSVCGT 14
| | | | | : | | | |
Db 330 NQSEIGNACGT 341

RESULT 11
ABR61598
ID ABR61598 standard; protein; 762 AA.
XX
XX ABR61598;
XX
XX 15-JAN-2004 (first entry)
XX
XX Z. mays vacuolar pyrophosphatase.
XX
XX Silk excretion; plant; transformation; transgenic; gl2; cell expansion;
XX vacuolar pyrophosphatase; enzyme.
XX
XX Zea mays.
XX
XX W02003087313-A2.
XX
XX 23-OCT-2003.
XX
XX 08-APR-2003; 2003WO-US010544.
XX
XX 08-APR-2002; 2002US-0370796P.
XX
XX

(PION-) PIONEER HI-BRED INT INC.
XX
XX Zinselmeier C, Helentjaris TG;
XX
XX WPI; 2003-845315/78.
DR N-PSDB; ACF58166.
XX
XX Enhancing silk excretion in a Zea mays plant under stress, relative to a
PT non-transformed Zea mays plant under stress by transforming the plant or
PT its ancestor with a construct comprising a silk-specific or silk-
PT preferred promoter.
XX
XX Example; Page 94-98; Opp; English.
XX
XX The invention relates to enhancing silk excretion in a Zea mays plant
CC under stress, relative to a non-transformed Zea mays plant under stress.
CC The method involves transforming the plant or its ancestor with a
CC construct comprising a silk-specific or silk-preferred promoter operably
CC linked to a polynucleotide encoding a polypeptide that increases cell
CC division. The present sequence represents a Z. mays vacuolar
CC pyrophosphatase, a polypeptide which increases the rate of cell expansion
XX
XX Sequence 762 AA;
SQ
Query Match 58.1%; Score 43; DB 7; Length 762;
Best Local Similarity 58.3%; Pred. No. 1.5e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DNVENVGSVCG 13
| | | | | : | | | |
Db 275 DNVGDNVGDIAG 286

RESULT 12
ADS20925
ID ADS20925 standard; protein; 764 AA.
XX
XX ADS20925;
XX
XX 16-DEC-2004 (first entry)
XX
XX Beta vulgaris vacuolar beta pyrophosphatase (Bvpl) protein SeqID 5.
DE
XX beta pyrophosphatase; bvp1; enzyme; transgenic; sugar beet; plant;
XX vacuolar pyrophosphatase; V-Pase; cytosolic pyrophosphatase;
XX nuclear localised pyrophosphatase; C-Pase.
XX
XX Beta vulgaris.
OS
XX WO2004083440-A1.
XX
XX 30-SEP-2004.
XX
XX 14-FEB-2004; 2004WO-EF001405.
XX
XX 20-MAR-2003; 2003DE-01013795.
XX
XX (SUED-) SUEZUCKER AG MANNHEIM/OCHSENFURT.
XX
XX Greiner S, Harms K, Kunz M, Munir M, Rausch T, Schirmer M;
XX
XX WPI; 2004-691058/67.
DR N-PSDB; ADS20924.
XX
XX Preparation of transgenic sugar beet with increased sucrose content, by
PT transformation with genes encoding both vacuolar and cytosolic/nuclear
PT pyrophosphatase.
XX
XX Claim 2; SEQ ID NO 5; 89pp; German.
XX
XX This invention relates to a novel method for preparing a transgenic sugar
CC beet plant. Specifically, it refers to the introduction into cells of at
CC least two transgenes, one encoding vacuolar pyrophosphatase (V-Pase) and

CC a second encoding a cytosolic and/or nuclear localised pyrophosphatase (C
 CC -Pase). The present invention describes producing transgenic plants with
 CC an increased sucrose content in the root, increased or prolonged meristem
 CC activity and/or reduced sucrose degradation during storage. The
 CC transgenes isolated from Beta vulgaris (B. vulgaris) are under the
 CC control of the cauliflower mosaic virus 35S promoter in separate vectors
 CC that were subsequently used to transform the sugar beet plant. This
 CC polypeptide sequence is the B. vulgaris vacuolar beta pyrophosphatase
 CC (bvpl) protein (V-Pase) of the invention.
 CC XX
 SQ Sequence 764 AA;

Query Match 58.1%; Score 43; DB 8; Length 764;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
 ||| : ||| : |
 Db 277 DNVDNVDIAG 288

RESULT 13
 ABB91014
 ID ABB91014 standard; protein; 770 AA.
 XX
 AC ABB91014;
 DT 31-MAY-2002 (first entry)
 XX
 DE Herbicidally active polypeptide SEQ ID NO 225.
 XX
 KW Herbicidal; plant; agriculture; herbicide.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200210210-A2.
 XX
 PD 07-FEB-2002.

XX 28-AUG-2001; 2001WO-EP009892.

XX 28-AUG-2001; 2001WO-EP009892.

XX (FARB) BAYER AG.

XX Tietjen K, Weidler M;

XX WPI; 2002-269010/31.

XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms.

XX Claim 5; SEQ ID NO 225; 261pp + Sequence Listing; English.

XX The invention relates to identifying target proteins (ABB90790-ABB94016)
 CC for herbicidally active compounds, comprising aligning and comparing
 CC nucleic acid or amino acid sequences from plant with nucleic acid or
 CC amino acid sequences from non-plant organisms using suitable search
 CC parameters, where plant sequences having an E-value greater by a factor
 CC of 3 than the E-value of most similar non-plant sequences are selected.
 CC The polypeptides or nucleic acids encoding them are useful for
 CC identifying modulators. The identified modulators are useful as
 CC herbicides
 CC XX
 SQ Sequence 770 AA;

Query Match 58.1%; Score 43; DB 5; Length 770;
 Best Local Similarity 58.3%; Pred. No. 1.5e+02;
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13

Db 283 DNVDNVDIAG 294
 ||| : ||| : |

RESULT 14

ABB61023

ID ABB61023 standard; protein; 1849 AA.

XX ABB61023;

AC ABB61023;

DT 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 9861.

XX Drosophila; developmental biology; cell signalling; insecticide;

XX pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US009231.

XX 23-MAR-2000; 2000US-0191637P.

XX 11-JUL-2000; 2000US-00614150.

XX (PEKE) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX WPI; 2001-656860/75.

XX N-PSDB; ABL05126.

XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signaling and cell-cell
 PT interactions.

XX Disclosure; SEQ ID NO 9861; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signaling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1849 AA;

Query Match 58.1%; Score 43; DB 4; Length 1849;

Best Local Similarity 63.6%; Pred. No. 3.8e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 NVSENVSVCVCG 13

Db 1148 NVQMNIGVCG 1158

RESULT 15

ABJ25449

ID ABJ25449 standard; protein; 672 AA.

XX ABJ25449;

XX 16-APR-2003 (first entry)

XX Aspergillus fumigatus essential gene protein #107.

XX

KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
KW cancer; contamination; biofilm; antibody; immune response.
XX Aspergillus fumigatus.

XX WO200286090-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013142.

XX 23-APR-2001; 2001US-0285697P.

XX 27-APR-2001; 2001US-0287066P.

XX 05-JUN-2001; 2001US-0295890P.

XX 09-JUL-2001; 2001US-0303899P.

XX 31-AUG-2001; 2001US-0316362P.

XX (ELIT-) ELITRA PHARM INC.

XX Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;

XX WPI; 2003-093124/08.

XX New purified or isolated nucleic acids of essential genes of Aspergillus
XX fumigatus, useful for treating or preventing infections by A. fumigatus,
XX or for treating a non-infectious disease in a subject e.g. cancer.

XX Disclosure; Page; 175pp; English.

XX The invention relates to novel purified or isolated nucleic acids of
XX essential genes of Aspergillus fumigatus. The isolated nucleic acids of
XX the invention are used to treat or prevent infections by a pathogenic
XX organism such as A. fumigatus, to treat a non-infectious disease in a
XX subject (e.g. cancer), to prevent or contain contamination of an object
XX by A. fumigatus, or to prevent or inhibit formation on a surface of a
XX biofilm comprising A. fumigatus. The polynucleotides are useful for
XX expressing recombinant protein for characterisation, screening or
XX therapeutic use, as markers for host tissues in which the pathogenic
XX organisms invade or reside, for comparing with the DNA sequence of A.
XX fumigatus to identify duplicated genes or paralogues having the same or
XX similar biochemical activity and/or function, for comparing with DNA
XX sequences of other related or distant pathogenic organisms to identify
XX potential orthologous essential or virulence genes, for selecting and
XX making oligonucleotides for attachment to a nucleic acid array for examination
XX of expression patterns, for raising anti-protein antibodies, as an
XX antigen to raise anti-DNA antibodies or to elicit another immune
XX response, and for identifying polynucleotides encoding the other protein.
XX with which binding occurs or to identify inhibitors of the binding
XX interaction. The polypeptides may be used to raise antibodies or to
XX elicit immune response, as a reagent in assays designed to quantitatively
XX determine levels of the protein in biological fluids, as a marker for
XX host tissues in which pathogenic organism invade or reside, and to
XX isolate correlative receptors or ligands in the case of virulence
XX factors. This sequence represents a protein of one of the essential genes
XX of Aspergillus fumigatus of the invention

XX Sequence 672 AA;

Query Match 56.8%; Score 42; DB 6; Length 672;
Best Local Similarity 61.5%; Pred. No. 2e+02;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCG 13

Db 41 EDSVQENYGVIG 53

Search completed: February 11, 2005, 03:03:28
Job time : 6.97442 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:00:19 ; Search time 1.18159 Seconds
(without alignments)
884.478 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	14	3	US-09-054-492B-5
2	74	100.0	377	2	US-08-969-106-6
3	74	100.0	377	3	US-09-054-492B-1
4	74	100.0	377	4	US-09-338-125-6
5	41	55.4	544	1	US-08-472-028A-8
6	41	55.4	544	2	US-08-808-931-8
7	41	55.4	544	3	US-08-808-323-8
8	41	55.4	544	3	US-09-050-603A-8
9	41	55.4	544	3	US-09-102-420B-8
10	41	55.4	544	3	US-09-071-236-8
11	41	55.4	544	3	US-09-196-268-8
12	41	55.4	544	3	US-09-015-683-8
13	41	55.4	544	3	US-09-191-998-8
14	41	55.4	544	3	US-09-497-698-8
15	41	55.4	544	4	US-09-730-525-8
16	40	54.1	122	4	US-09-538-092-912
17	40	54.1	201	4	US-09-538-092-865
18	40	54.1	226	3	US-09-045-973-8
19	39	52.7	1095	4	US-09-543-681A-6594
20	38	51.4	91	4	US-09-540-236-3719
21	38	51.4	114	4	US-09-583-110-4846
22	38	51.4	190	4	US-09-538-092-954
23	38	51.4	316	4	US-09-902-540-11232
24	37	50.0	91	4	US-09-270-767-60251
25	37	50.0	132	4	US-09-489-039A-11744
26	37	50.0	157	4	US-09-270-767-33175
27	37	50.0	157	4	US-09-270-767-48392

28	37	50.0	332	4	US-09-270-767-44788	Sequence 44788, A
29	37	50.0	346	4	US-09-170-496D-254	Sequence 254, App
30	37	50.0	346	4	US-09-170-496D-274	Sequence 274, App
31	37	50.0	358	4	US-09-809-665A-155	Sequence 155, App
32	37	50.0	380	3	US-08-468-846-2	Sequence 2, Appli
33	37	50.0	380	3	US-08-915-096A-2	Sequence 2, Appli
34	37	50.0	384	4	US-09-949-016-9661	Sequence 9661, Ap
35	37	50.0	401	2	US-08-820-521-2	Sequence 2, Appli
36	37	50.0	401	3	US-09-248-715-2	Sequence 2, Appli
37	37	50.0	401	3	US-09-248-715-2	Sequence 2, Appli
38	37	50.0	488	4	US-09-809-665A-44	Sequence 44, Appli
39	37	50.0	568	4	US-09-198-452A-1073	Sequence 1073, Ap
40	37	50.0	684	4	US-09-809-665A-109	Sequence 109, App
41	37	50.0	697	4	US-09-252-391A-27283	Sequence 27283, A
42	37	50.0	698	4	US-09-438-185A-1000	Sequence 1000, Ap
43	37	50.0	699	4	US-09-540-236-2259	Sequence 2259, Ap
44	37	50.0	705	4	US-09-328-352-8112	Sequence 8112, Ap
45	37	50.0	716	4	US-09-809-665A-171	Sequence 171, App

ALIGNMENTS

RESULT 1
US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-054-492B-5

Query Match 100.0%; Score 74; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
|||
Db 1 EDNVSENVGVCVT 14

RESULT 2


```
US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-969-106-6
Query Match 100.0%; Score 74; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 3
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B

US-08-969-106-6
Query Match 100.0%; Score 74; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 3
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B

US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-969-106-6
Query Match 100.0%; Score 74; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNVSENVGVCVT 356

RESULT 4
US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Lealie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-09-338-125-6
```

```
Query Match      100.0%; Score 74; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 EDNVSENVGVC GT 14
Db      343 EDNVSENVGVC GT 356
|||||
|||||

RESULT 5
US-08-472-028A-8
; Sequence 8, Application US/08472028A
; Patent No. 5767373
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472.028A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-028A-8

Query Match      55.4%; Score 41; DB 1; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EDNVSENVGVC 12
Db      182 EEHLSVSGSFC 193
|:::|:|:|

RESULT 6
US-08-808-931-8
; Sequence 8, Application US/08808931
; Patent No. 5939602
; GENERAL INFORMATION:
; APPLICANT: Volrath, Sandra
; APPLICANT: Johnson, Marie
; APPLICANT: Potter, Sharon
; APPLICANT: Ward, Eric
; APPLICANT: Heifetz, Peter
; TITLE OF INVENTION: DNA Molecules Encoding Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase and Inhibitor-Resistant Mutants
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 35
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5939602artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,931
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1847
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-931-8

Query Match      55.4%; Score 41; DB 2; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy      1 EDNVSENVGVC 12
Db      182 EEHLSVSGSFC 193
|:::|:|:|

RESULT 7
US-08-808-323-8
; Sequence 8, Application US/08808323
; Patent No. 6018105
; GENERAL INFORMATION:
; APPLICANT: Johnson, Marie
; APPLICANT: Volrath, Sandra
; APPLICANT: Ward, Eric
; TITLE OF INVENTION: Promoters from Plant
; TITLE OF INVENTION: Protoporphyrinogen Oxidase Genes
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6018105artis Corporation
; STREET: 520 White Plains Road, P.O. Box 2005
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/08/808,323
FILING DATE: 28-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1846
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-808-323-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDVSENVGSVC 12
Db 182 EEHLSVGSFC 193

RESULT 8
US-09-050-603A-8
Sequence 8, Application US/09050603A
Patent No. 6023012
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Potter, Sharon
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: DNA Molecules Encoding Plant
PROTOPORPHYRINOGEN OXIDASE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6023012artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,603A
FILING DATE: 30-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612

FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC 1847
TELEPHONE: (919) 541-8587
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-050-603A-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDVSENVGSVC 12
Db 182 EEHLSVGSFC 193

RESULT 9
US-09-102-420B-8
Sequence 8, Application US/09102420B
Patent No. 6084155
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
APPLICANT: Johnson, Marie
APPLICANT: Ward, Eric
APPLICANT: Heifetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
OXIDASE ("PROTOX")
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6084155artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,420B
FILING DATE: 22-JUN-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/059,164
FILING DATE: 13-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,612

;; FILING DATE: 28-FEB-1996
;; PRIOR APPLICATION NUMBER: US 60/020,003
;; FILING DATE: 21-JUN-1996
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/472,028
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weigs, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: CGC 1847/CIP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (919) 541-8587
;; TELEFAX: (919) 541-8689
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 544 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-102-420B-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVSGSFC 193

RESULT 10
US-09-071-296-8
; Sequence 8, Application US/09071296
; Patent No. 6177245
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,296
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-09-102-420B-8

US-09-071-296-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVSGSFC 193

RESULT 11
US-09-196-268-8
; Sequence 8, Application US/09196268
; Patent No. 6282837
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,268
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-09-196-268-8

Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSVSGSFC 193

RESULT 12
US-09-015-683-8
; Sequence 8, Application US/09015683
; Patent No. 6288306
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric R
; APPLICANT: Volrath, Sandra
; TITLE OF INVENTION: Manipulation of Protoporphyrinogen
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,683
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/261,198
; FILING DATE: 16-JUN-94
; ATTORNEY/AGENT INFORMATION:
; NAME: Elmer, James Scott
; REGISTRATION NUMBER: 36,129
; REFERENCE/DOCKET NUMBER: CGC 1748/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8614
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;; US-09-015-683-8

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,683
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: CGC 1748/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-015-683-8
Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSSEVGSFC 193
RESULT 13
US-09-191-998-8
Sequence 8, Application US/09191998
Patent No. 6307129
GENERAL INFORMATION:
APPLICANT: Ward, Eric R
TITLE OF INVENTION: Manipulation of Protoporphyrinogen
TITLE OF INVENTION: Oxidase Enzyme Activity in Eukaryotic Organisms
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/191,998
FILING DATE: 06-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/261,198
FILING DATE: 16-JUN-94
ATTORNEY/AGENT INFORMATION:
NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: CGC 1748/CIP.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8614
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-191-998-8
Query Match 55.4%; Score 41; DB 3; Length 544;
Best Local Similarity 58.3%; Pred. No. 1.2e+02;
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EDNVSENVGSVC 12
Db 182 EEHLSSEVGSFC 193
RESULT 14
US-09-497-698-8
Sequence 8, Application US/09497698
Patent No. 6308458
GENERAL INFORMATION:
APPLICANT: Volrath, Sandra
Johnson, Marie
Ward, Eric
Heifetz, Peter
TITLE OF INVENTION: HERBICIDE-TOLERANT PROTOPORPHYRINOGEN
OXIDASE ("PROTCX")
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6308458artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/497,698
FILING DATE: 03-Feb-2000
CLASSIFICATION: <Unknown>
30-MAR-1998
11-MAR-1998
28-FEB-1997
28-FEB-1996
28-FEB-1996
21-JUN-1996
06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/102,420
FILING DATE: <Unknown>
APPLICATION NUMBER: US 09/050,603
FILING DATE: 30-MAR-1998
APPLICATION NUMBER: US 60/126,430
FILING DATE: 11-MAR-1998
APPLICATION NUMBER: US 08/808,931
FILING DATE: 28-FEB-1997
APPLICATION NUMBER: US 60/012,705
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/013,612
FILING DATE: 28-FEB-1996
APPLICATION NUMBER: US 60/020,003
FILING DATE: 21-JUN-1996
APPLICATION NUMBER: US 08/472,028
FILING DATE: 06-JUN-1995

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1847/CIP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-497-698-8
;
; Query Match 55.4%; Score 41; DB 3; Length 544;
; Best Local Similarity 58.3%; Pred. No. 1.2e+02;
; Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 EDNVSENVGSVC 12
; |:::||:|
; Db 182 EEHLSVGSVC 193
;
; RESULT 15
; US-09-730-525-8
; Sequence 8, Application US/09730525
; Patent No. 6808904
; GENERAL INFORMATION:
; APPLICANT: Ward, Eric
; Volrath, Sandra
; Johnson, Marie
; Potter, Sharon
; TITLE OF INVENTION: Herbicide Tolerant Protox Genes
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6808904artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/730,525
; FILING DATE: 05-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/102,419
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 09/050,603
; FILING DATE: 30-MAR-1998
; APPLICATION NUMBER: US 09/038,878
; FILING DATE: 11-MAR-1998
; APPLICATION NUMBER: US 08/808,931
; FILING DATE: 28-FEB-1997
; APPLICATION NUMBER: US 60/012,705
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 60/013,612
; FILING DATE: 28-FEB-1996
; APPLICATION NUMBER: US 60/020,003
; FILING DATE: 21-JUN-1996
; APPLICATION NUMBER: US 08/472,028
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
;
; REFERENCE/DOCKET NUMBER: CGC 1847/CIP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8587
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 8:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-730-525-8
;
; Query Match 55.4%; Score 41; DB 4; Length 544;
; Best Local Similarity 58.3%; Pred. No. 1.2e+02;
; Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
;
; Qy 1 EDNVSENVGSVC 12
; |:::||:|
; Db 182 EEHLSVGSVC 193
;
; Search completed: February 11, 2005, 03:06:29
; Job time : 2.18159 secs
```

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:24 ; Search time 3.22251 Seconds
(without alignments)
1419.543 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1376875 seqs, 326749119 residues

Total number of hits satisfying chosen parameters: 1376875

Minimum DB-seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	14	US-09-736-250-5	Sequence 5, Appli
2	74	100.0	377	US-09-736-250-1	Sequence 1, Appli
3	44	59.5	109	US-10-424-599-246648	Sequence 246648, A
4	43	58.1	226	US-10-424-599-272932	Sequence 272932, A
5	43	58.1	469	US-10-369-493-6358	Sequence 6358, Ap
6	43	58.1	489	US-10-767-701-45549	Sequence 45549, A
7	43	58.1	504	US-10-767-701-46948	Sequence 46948, A
8	43	58.1	551	US-10-425-114-71458	Sequence 71458, A
9	43	58.1	762	US-10-409-701-25	Sequence 25, Appli
10	43	58.1	766	US-10-767-701-46989	Sequence 46989, A
11	43	58.1	767	US-10-424-599-198727	Sequence 198727, A
12	43	58.1	956	US-10-437-963-167398	Sequence 167398, A
13	43	58.1	966	US-10-437-963-134857	Sequence 134857, A

14	42	56.8	136	15	US-10-425-114-68537	Sequence 68537, A
15	42	56.8	208	15	US-10-425-114-68381	Sequence 68381, A
16	42	56.8	672	14	US-10-128-714-3107	Sequence 3107, Ap
17	42	56.8	672	14	US-10-128-714-8107	Sequence 8107, Ap
18	41	55.4	544	9	US-09-730-525-8	Sequence 8, Appli
19	41	55.4	544	9	US-09-730-917-8	Sequence 8, Appli
20	40	54.1	129	16	US-10-767-701-37922	Sequence 37922, A
21	40	54.1	135	15	US-10-264-237-1535	Sequence 1535, Ap
22	40	54.1	177	16	US-10-408-765A-2331	Sequence 2331, Ap
23	40	54.1	201	16	US-10-408-765A-39	Sequence 39, Appli
24	39	52.7	336	15	US-10-282-122A-58646	Sequence 58646, A
25	39	52.7	337	16	US-10-437-963-130322	Sequence 130322, A
26	39	52.7	345	9	US-09-815-242-11068	Sequence 11068, A
27	39	52.7	503	9	US-09-801-368-424	Sequence 424, App
28	39	52.7	503	15	US-10-369-493-1943	Sequence 1943, App
29	39	52.7	699	15	US-10-369-493-13011	Sequence 13011, A
30	39	52.7	729	15	US-10-282-122A-61234	Sequence 61234, A
31	39	52.7	801	14	US-10-156-761-12150	Sequence 12150, A
32	39	52.7	1037	16	US-10-437-963-170931	Sequence 170931, A
33	38	51.4	39	15	US-10-424-599-267118	Sequence 267118, A
34	38	51.4	126	16	US-10-437-963-132930	Sequence 132930, A
35	38	51.4	159	17	US-10-472-928-74	Sequence 74, Appli
36	38	51.4	309	15	US-10-424-599-238011	Sequence 238011, A
37	38	51.4	358	9	US-09-815-242-10187	Sequence 10187, A
38	38	51.4	358	15	US-10-369-493-866	Sequence 866, App
39	38	51.4	358	15	US-10-282-122A-56577	Sequence 56577, A
40	38	51.4	365	15	US-10-425-114-42890	Sequence 42890, A
41	38	51.4	371	15	US-10-424-599-207707	Sequence 207707, A
42	38	51.4	483	15	US-10-424-599-258507	Sequence 258507, A
43	38	51.4	662	16	US-10-437-963-134490	Sequence 134490, A
44	38	51.4	700	16	US-10-437-963-127893	Sequence 127893, A
45	38	51.4	709	15	US-10-282-122A-77113	Sequence 77113, A

ALIGNMENTS

RESULT 1
US-09-736-250-5
; Sequence 5, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 5
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized
US-09-736-250-5

Query Match 100.0%; Score 74; DB 12; Length 14;
Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14

Db 1 EDNVSENVGVCVT 14

RESULT 2
US-09-736-250-1
; Sequence 1, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 377
; ORGANISM: Homo sapiens
US-09-736-250-1

Query Match 100.0%; Score 74; DB 12; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDVSENVGVCVT 14
Db 343 EDVSENVGVCVT 356

RESULT 3
US-10-424-599-246648
; Sequence 246648, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 246648
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_64754C.1.pep
US-10-424-599-246648

Query Match 59.5%; Score 44; DB 15; Length 109;
Best Local Similarity 77.8%; Pred. No. 19;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENGVGVC 13
Db 79 AENVGSICG 87

RESULT 4
US-10-424-599-272932
; Sequence 272932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 272932
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(226)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_88480C.1.pep
US-10-424-599-272932

Query Match 58.1%; Score 43; DB 15; Length 226;
Best Local Similarity 58.3%; Pred. No. 60;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVC 13
Db 16 DNVDNVGDIAG 27

RESULT 5
US-10-369-493-6358
; Sequence 6358, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6358
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6358

Query Match 58.1%; Score 43; DB 15; Length 469;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NVSENVGVCVT 14
Db 330 NQSEENACGT 341

RESULT 6

US-10-767-701-45549
; Sequence 45549, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53535)B

; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 45549
; LENGTH: 489
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(489)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C8573_1.pep
US-10-767-701-45549

Query Match 58.1%; Score 43; DB 16; Length 489;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 76 DNVDNVDIAG 87

RESULT 7

US-10-767-701-46948
; Sequence 46948, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46948
; LENGTH: 504
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(504)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_282.pep
US-10-767-701-46948

Query Match 58.1%; Score 43; DB 16; Length 504;
Best Local Similarity 58.3%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 276 DNVDNVDIAG 287

RESULT 8

US-10-425-114-71458
; Sequence 71458, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 71458
; LENGTH: 551
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700101735_FLI.pep
US-10-425-114-71458

Query Match 58.1%; Score 43; DB 15; Length 551;
Best Local Similarity 58.3%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 64 DNVDNVDIAG 75

RESULT 9

US-10-409-701-25
; Sequence 25, Application US/10409701
; Publication No. US20030221224A1
; GENERAL INFORMATION:
; APPLICANT: Zinselmeier, Chris
; APPLICANT: Helentjaris, Timothy G.
; TITLE OF INVENTION: Enhanced Silk Exsersion Under Stress
; FILE REFERENCE: 1421
; CURRENT APPLICATION NUMBER: US/10/409,701
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,796
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25
; LENGTH: 762
; TYPE: PRT
; ORGANISM: Zea mays
US-10-409-701-25

Query Match 58.1%; Score 43; DB 15; Length 762;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 275 DNVDNVDIAG 286

RESULT 10

US-10-767-701-46989
; Sequence 46989, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46989
; LENGTH: 766
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_323.pep
US-10-767-701-46989

Query Match 58.1%; Score 43; DB 16; Length 766;

Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCV 13
DB 279 DNVGDNVGDIA 290

RESULT 11
US-10-424-599-198727
; Sequence 198727, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J.
; APPLICANT: Kovalic David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 198727
; LENGTH: 767
; TYPE: PRT
; ORGANISM: Glycine max
; NAME/KEY: unsure
; LOCATION: (1) (767)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21474C.1.pep
US-10-424-599-198727

Query Match 58.1%; Score 43; DB 15; Length 767;
Best Local Similarity 58.3%; Pred. No. 2.2e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCV 13
DB 281 DNVGDNVGDIA 292

RESULT 12
US-10-437-963-167398
; Sequence 167398, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 167398
; LENGTH: 956
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_66012C.1.pep
US-10-437-963-167398

Query Match 58.1%; Score 43; DB 16; Length 956;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EDNVSENVGVCV 12
DB 563 EDCISENLGSR 574

RESULT 13
US-10-437-963-134857
; Sequence 134857, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 134857
; LENGTH: 966
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_3658C.1.pep
US-10-437-963-134857

Query Match 58.1%; Score 43; DB 16; Length 966;
Best Local Similarity 58.3%; Pred. No. 2.8e+02;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCV 13
DB 481 DNVGDNVGDIA 492

RESULT 14
US-10-425-114-68537
; Sequence 68537, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68537
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMROMO17114A05_FLI.pep
US-10-425-114-68537

Query Match 56.8%; Score 42; DB 15; Length 136;
Best Local Similarity 58.3%; Pred. No. 51;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCV 13

```
Db      25 DNVGDNVGDIVG 36
      ||| :||| :|
RESULT 15
US-10-425-114-68381
; Sequence 68381, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 68381
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17138G11_FLI.pep
US-10-425-114-68381
Query Match      56.8%; Score 42; DB 15; Length 208;
Best Local Similarity 58.3%; Pred. No. 80;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy      2 DNVSENVGSVCG 13
      ||| :||| :|
Db      97 DNVGDNVGDIVG 108
```

Search completed: February 11, 2005, 03:13:13
Job time : 4.22251 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:59:54 ; Search time 1.07417 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	59.5	726	2 D72409	pyrophosphatase, p
2	43	58.1	360	2 S54173	inorganic diphosph
3	43	58.1	469	2 T33963	hypothetical prote
4	43	58.1	541	2 S61425	inorganic diphosph
5	43	58.1	761	1 JCI466	inorganic diphosph
6	43	58.1	761	2 T14563	inorganic diphosph
7	43	58.1	764	2 S61422	inorganic diphosph
8	43	58.1	764	2 S42893	inorganic diphosph
9	43	58.1	765	2 S54172	inorganic diphosph
10	43	58.1	765	2 S61423	inorganic diphosph
11	43	58.1	765	2 T14564	inorganic diphosph
12	43	58.1	765	2 T10841	inorganic diphosph
13	43	58.1	766	2 S61424	inorganic diphosph
14	43	58.1	766	2 T07801	probable inorganic
15	43	58.1	767	2 S72527	inorganic diphosph
16	43	58.1	770	1 A38230	inorganic diphosph
17	43	58.1	771	2 S72526	inorganic diphosph
18	42	56.8	390	2 C94579	probable SET-domai
19	41	55.4	270	2 C97772	diaminopimelate ep
20	41	55.4	497	2 T41467	hypothetical prote
21	41	55.4	547	2 T30269	hypothetical prote
22	41	55.4	803	2 T10060	receptor-like prot
23	40	54.1	122	2 S05317	glutathione peroxi
24	40	54.1	187	2 S32968	probable membrane
25	40	54.1	190	1 A45207	glutathione peroxi
26	40	54.1	200	1 S03723	glutathione peroxi
27	40	54.1	201	1 OPMSE	glutathione peroxi
28	40	54.1	201	1 OPRTE	glutathione peroxi
29	40	54.1	202	1 OPHUE	glutathione peroxi

30	40	54.1	205	1 OPROE	glutathione peroxi
31	40	54.1	226	2 T21380	hypothetical prote
32	40	54.1	512	2 A96695	hypothetical prote
33	40	54.1	1214	2 T21915	hypothetical prote
34	39	52.7	109	2 S64313	probable membrane
35	39	52.7	336	2 D64544	UDP-3-O-[3-hydroxy
36	39	52.7	345	2 C64082	ATP-binding protei
37	39	52.7	389	2 D64333	pyruvate synthase
38	39	52.7	503	2 S63257	probable membrane
39	39	52.7	712	2 AD2721	H+ translocating p
40	39	52.7	712	2 D87418	proton pump, proba
41	39	52.7	713	2 AE2586	polyribonucleotide
42	39	52.7	713	2 F97368	polyribonucleotide
43	39	52.7	714	2 H97502	n+ translocating p
44	39	52.7	714	2 AC3497	polyribonucleotide
45	39	52.7	775	2 AC3400	inorganic diphosph

ALIGNMENTS

RESULT 1

D72409

Pyrophosphatase, proton-translocating - Thermotoga maritima (strain MSBB)

C:Species: Thermotoga maritima

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C:Accession: D72409

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;

C.M.

Nature 399, 323-329, 1999

A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq

A:Reference number: A72200; MUID:99287316; PMID:10360571

A:Accession: D72409

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-726 <ARN>

A:Cross-references: UNIPROT:Q9S5X0; GB:AE001702; GB:AE000512; NID:g4980662; PIDN:AAD3526

A:Experimental source: strain MSB8

C:Genetics:

A:Gene: TM0174

C:Superfamily: H(+)-translocating inorganic pyrophosphatase

Query Match 59.5%; Score 44; DB 2; Length 726;

Best Local Similarity 66.7%; Pred. No. 11;

Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCVG 13

Db 228 DNVGDNVGDVAG 239

RESULT 2

S54173

Inorganic diphosphatase (EC 3.6.1.1) - common tobacco

C:Species: Nicotiana tabacum (common tobacco)

C>Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 03-Nov-2003

C:Accession: S54173

R:Lerchl, J.

submitted to the EMBL Data Library, January 1995

A:Reference number: S54169

A:Accession: S54173

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-360 <LER>

A:Cross-references: EMBL:X83729

C:Superfamily: H(+)-translocating inorganic pyrophosphatase

C:Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 360;

Best Local Similarity 59.3%; Pred. No. 7.9;

Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 279 DNVDNVGDIAG 290

RESULT 3

T33963
hypothetical protein F46E10.7 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T33963
R:Johnson, D.; Bradshaw, H.
submitted to the EMBL Data Library, February 1999
A:Description: The sequence of C. elegans cosmid F46E10.
A:Reference number: Z21446
A:Accession: T33963
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-469 <JOH>
A:Cross-references: EMBL:AF125955; PIDN:AA14717.1; GSPDB:GN00023; CESP:F46E10.7
A:Experimental source: strain Bristol N2; clone F46E10
C:Genetics:
A:Gene: CESP:F46E10.7
A:Map position: 5
A:Introns: 20/3; 141/1; 181/1; 224/3; 242/3; 263/3; 384/1; 424/1

Query Match 58.1%; Score 43; DB 2; Length 469;
Best Local Similarity 58.3%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 NVSENVSVCVCGT 14
||| :||| :
Db 330 NQSEIGNACGT 341

RESULT 4

S61425
inorganic diphosphatase (EC 3.6.1.1), H+-translocating (clone TVP17), vacuolar membrane
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S61425; S54171
R:Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A:Title: Molecular cloning, characterization and expression analysis of isoforms encoding
A:Reference number: S61422; MUID:96128024; PMID:8541508
A:Accession: S61425
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Residues: 1-541 <LER>
A:Cross-references: UNIPROT:Q43796; EMBL:X83728; NID:G790474; PIDN:CAA58699.1; PID:G7904
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
C:Superfamily: H(+)-translocating inorganic pyrophosphatase
C:Keywords: hydrolase; transmembrane protein

Query Match 58.1%; Score 43; DB 2; Length 541;
Best Local Similarity 58.3%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 54 DNVDNVGDIAG 65

RESULT 5

JC1466
inorganic diphosphatase (EC 3.6.1.1) - barley
C:Species: Hordeum vulgare (barley)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 27-Oct-2003
C:Accession: JC1466
R:Tanaka, Y.; Chiba, K.; Maeda, M.; Maeshima, M.
Biochem. Biophys. Res. Commun. 190, 1110-1114, 1993
A:Title: Molecular cloning of cDNA for vacuolar membrane proton-translocating inorganic
A:Reference number: JC1466; MUID:93176156; PMID:8382487

A:Accession: JC1466
A:Molecule type: mRNA
A:Residues: 1-761 <TAN>
A:Cross-references: DDBJ:D13472; NID:G285637; PIDN:BAA02717.1; PID:G285638
A:Experimental source: root
C:Superfamily: H(+)-translocating inorganic pyrophosphatase
C:Keywords: hydrolase; transmembrane protein
F:11-32/Domain: transmembrane #status predicted <TM1>
F:91-110/Domain: transmembrane #status predicted <TM2>
F:131-154/Domain: transmembrane #status predicted <TM3>
F:184-204/Domain: transmembrane #status predicted <TM4>
F:217-236/Domain: transmembrane #status predicted <TM5>
F:306-341/Domain: transmembrane #status predicted <TM6>
F:360-381/Domain: transmembrane #status predicted <TM7>
F:398-417/Domain: transmembrane #status predicted <TM8>
F:454-477/Domain: transmembrane #status predicted <TM9>
F:534-555/Domain: transmembrane #status predicted <TM10>
F:570-589/Domain: transmembrane #status predicted <TM11>
F:649-672/Domain: transmembrane #status predicted <TM12>

Query Match 58.1%; Score 43; DB 1; Length 761;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 274 DNVDNVGDIAG 285

RESULT 6

T14563
inorganic diphosphatase (EC 3.6.1.1) - beet
C:Species: Beta vulgaris (beet)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 27-Oct-2003
C:Accession: T14563
R:Kim, Y.; Kim, E.J.; Rea, P.A.
Plant Physiol. 106, 375-382, 1994
A:Title: Isolation and characterization of cDNAs encoding the vacuolar H(+)-pyrophosphatase
A:Reference number: Z18141; MUID:95062743; PMID:7972521
A:Accession: T14563
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-761 <KIM>
A:Cross-references: EMBL:L32791; NID:G485741; PIDN:AAA61609.1; PID:G485742
A:Experimental source: strain Detroit dark
C:Function:
A:Description: catalyzes hydrolyzation of pyrophosphate
C:Superfamily: H(+)-translocating inorganic pyrophosphatase
C:Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 761;
Best Local Similarity 58.3%; Pred. No. 17;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNSENVSVCVCG 13
||| :||| :
Db 274 DNVDNVGDIAG 285

RESULT 7

S61422
inorganic diphosphatase (EC 3.6.1.1) (clone TVP5) - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003
C:Accession: S61422
R:Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A:Title: Molecular cloning, characterization and expression analysis of isoforms encoding
A:Reference number: S61422; MUID:96128024; PMID:8541508
A:Accession: S61422
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-764 <LER>

A;Cross-references: EMBL:X77915
A;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 764;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 8
S42893
inorganic diphosphatase (EC 3.6.1.1) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 20-May-1994 #sequence_revision 10-Nov-1995 #text_change 27-Oct-2003
C;Accession: S42893
R;Lerchl, J.
submitted to the EMBL Data Library, February 1994

A;Reference number: S42893
A;Accession: S42893
A;Molecule type: mRNA
A;Residues: 1-764 <LER>
A;Cross-references: EMBL:X77915; NID:g633598; PIDN:CAA54869.1; PID:g457744
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 764;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 9
S54172
inorganic diphosphatase (EC 3.6.1.1) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change 27-Oct-2003
C;Accession: S54172
R;Lerchl, J.
submitted to the EMBL Data Library, January 1995

A;Reference number: S54169
A;Accession: S54172
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-765 <LER>
A;Cross-references: EMBL:X83730; NID:g790478; PIDN:CAA58701.1; PID:g790479
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 278 DNVDNVDIAG 289

RESULT 10
S61423
inorganic diphosphatase (EC 3.6.1.1) (clone TVP9) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003
C;Accession: S61423
R;Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A;Title: Molecular cloning, characterization and expression analysis of isoforms encoding

A;Reference number: S61422; MUID:96128024; PMID:8541508
A;Accession: S61423
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-765 <LER>
A;Cross-references: EMBL:X83730
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 278 DNVDNVDIAG 289

RESULT 11
T14564
inorganic diphosphatase (EC 3.6.1.1), vacuolar - beet
C;Species: Beta vulgaris (beet)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 27-Oct-2003
C;Accession: T14564
R;Kim, Y.; Kim, E.J.; Rea, P.A.
Plant Physiol. 106, 375-382, 1994
A;Title: Isolation and characterization of cDNAs encoding the vacuolar H(+)-pyrophosphatase
A;Reference number: Z18141; MUID:95062743; PMID:7972521
A;Accession: T14564
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-765 <KIM>
A;Cross-references: EMBL:L32792; NID:g485743; PIDN:AAA61610.1; PID:g485744
A;Experimental source: strain Detroit dark
C;Function:
A;Description: catalyzes the electrogenic translocation of H+ from the cytosol to vacuol
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 277 DNVDNVDIAG 288

RESULT 12
T10841
inorganic diphosphatase (EC 3.6.1.1) - mung bean
C;Species: Vigna radiata (mung bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10841
R;Hung, S.
submitted to the EMBL Data Library, July 1995

A;Reference number: Z17181
A;Accession: T10841
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-765 <HUN>
A;Cross-references: UNIPROT:P21616; EMBL:U11467; NID:g951322; PID:g951323
A;Experimental source: tissue type hypocotyl; clone VVP
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 765;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNNVSVCG 13
|||:||||:|
Db 279 DNVDNVDIAG 290

C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 767;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 2 DNVSENVGVCVCG 13
||| :||| :
Db 280 DNVDNVGDIAG 291

Search completed: February 11, 2005, 03:05:49
Job time : 2.07417 secs

RESULT 13
S61424
inorganic diphosphatase (EC 3.6.1.1) (clone TVP31) - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 27-Oct-2003
C;Accession: S61424
R;Lerchl, J.; Koenig, S.; Zrenner, R.; Sonnwald, U.
Plant Mol. Biol. 29, 833-840, 1995
A;Title: Molecular cloning, characterization and expression analysis of isoforms encoding
A;Reference number: S61422; MUID:96128024; PMID:8541508
A;Accession: S61424
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-766 <LER>
A;Cross-references: EMBL:X83729
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 766;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCVCG 13
||| :||| :
Db 279 DNVDNVGDIAG 290

RESULT 14
T07801
probable inorganic diphosphatase (EC 3.6.1.1) - mung bean
C;Species: Vigna radiata (mung bean)
C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 27-Oct-2003
C;Accession: T07801
R;Nakanishi, Y.; Maeshima, M.
Plant Physiol. 116, 589-597, 1998
A;Title: Molecular cloning of vacuolar H(+)-pyrophosphatase and its developmental expres
A;Reference number: 216141; MUID:98150269; PMID:9489011
A;Accession: T07801
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-766 <NAK>
A;Cross-references: EMBL:AB009077; NID:g2653445; PIDN:BAA23649.1; PID:g2653446
A;Experimental source: strain Wilczek
C;Superfamily: H(+)-translocating inorganic pyrophosphatase
C;Keywords: hydrolase

Query Match 58.1%; Score 43; DB 2; Length 766;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 DNVSENVGVCVCG 13
||| :||| :
Db 279 DNVDNVGDIAG 290

RESULT 15
S72527
inorganic diphosphatase (EC 3.6.1.1), H(+)-translocating, vacuolar membrane (clone OVP2)
C;Species: Oryza sativa (rice)
C;Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C;Accession: S72527
R;Sakakibara, Y.; Kobayashi, H.; Kasano, K.
Plant Mol. Biol. 31, 1029-1038, 1996
A;Title: Isolation and characterization of cDNAs encoding vacuolar H(+)-pyrophosphatase
A;Reference number: S72526; MUID:97000915; PMID:8843945
A;Accession: S72527
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-767 <SAK>
A;Cross-references: UNIPROT:Q8H616; EMBL:D45384; NID:g1747295; PIDN:BAA08233.1; PID:g174
A;Note: only a part of the nucleic acid sequence is shown

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 02:58:24 ; Search time 3.72379 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	377	1	CYCI_HUMAN
2	74	100.0	377	2	Q6FHH0
3	62	83.8	377	1	CYCI_MOUSE
4	62	83.8	377	2	Q8C7E2
5	62	83.8	377	2	Q99LF2
6	44	59.5	181	2	Q6UB55
7	44	59.5	196	2	Q6DUU8
8	44	59.5	464	2	Q8G446
9	44	59.5	659	2	Q67L99
10	44	59.5	671	1	HPPA_FUSNN
11	44	59.5	673	1	HPPA_CLOTE
12	44	59.5	673	2	Q7P6V4
13	44	59.5	688	2	Q6MNC1
14	44	59.5	704	1	HPPA_LEPIN
15	44	59.5	704	2	Q7Q2Q9
16	44	59.5	721	1	HPPA_PYRAE
17	44	59.5	726	1	HPPA_THEMEA
18	44	59.5	734	1	HPPA_EACTN
19	44	59.5	734	2	Q64ZB8
20	44	59.5	751	2	Q9STC7
21	44	59.5	816	2	Q9BK07
22	44	59.5	816	2	Q9BK08
23	43	58.1	227	2	Q965V9
24	43	58.1	509	2	Q41758
25	43	58.1	541	2	Q43796
26	43	58.1	666	2	Q6SEU0
27	43	58.1	666	2	Q6SGH1
28	43	58.1	667	2	Q6SHA7
29	43	58.1	676	1	HPPI_METAC
30	43	58.1	676	1	HPPI_METNA
31	43	58.1	759	2	Q946X5

RESULT 1

ID	CYCI_HUMAN	STANDARD	PRT	377 AA
AC	Q14094			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Cyclin I.			
GN	Name=CCNI;			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Forebrain cortex;			
RX	MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;			
RA	Nakamura T., Sanokawa R., Sasaki Y.F., Ayubawa D., Oishi M., Mori N.;			
RT	"Cyclin I: a new cyclin encoded by a gene isolated from human brain.";			
RL	Exp. Cell Res. 221:534-542(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,			
RA	Qiang B.Q.;			
RT	"Isolating a new cDNA coding for human cyclin protein.";			
RL	Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT ILB-207.			
RA	Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,			
RA	Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,			
RA	Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;			
RT	"NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department			
RL	of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";			
RN	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney, and Muscle;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Zellberg B., Wagner F.S., Wagner C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Haie S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,			

ALIGNMENTS

32	43	58.1	759	2	Q9M4S1
33	43	58.1	761	2	Q42650
34	43	58.1	762	1	AVP3_HORVU
35	43	58.1	762	2	Q93Y49
36	43	58.1	762	2	Q704F4
37	43	58.1	762	2	Q75U53
38	43	58.1	762	2	Q7Y070
39	43	58.1	764	1	AVP3_PHAHU
40	43	58.1	764	2	Q8LSB2
41	43	58.1	764	2	Q43801
42	43	58.1	765	2	Q42651
43	43	58.1	765	2	Q43798
44	43	58.1	766	2	Q22124
45	43	58.1	766	2	Q43797

Q9M4S1 vitis vinif
Q42650 beta vulgar
Q65572 hordeum vul
Q93Y49 chlamydomon
Q704F4 oryza sativ
Q75U53 oryza sativ
Q7Y070 triticum ae
P21616 phaseolus a
Q8LSB2 chenopodium
Q43801 nicotiana t
Q42651 beta vulgar
Q43798 nicotiana t
Q22124 phaseolus a
Q43797 nicotiana t

```
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RL and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
[5]  
RN SEQUENCE OF 1-178 FROM N.A.  
RC TISSUE=Testis;  
RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;  
RA Zhu X., Naz R.K.;  
RT "Expression of a novel isoform of cyclin I in human testis.";   
RL Biochem. Biophys. Res. Commun. 249:56-60 (1998).  
CC -1- TISSUE SPECIFICITY: Highest levels in adult heart, brain and  
CC skeletal muscle. Lower levels in adult placenta, lung, kidney and  
CC pancreas. Also high levels in fetal brain and lower levels in  
CC fetal lung, liver and kidney. Also abundant in testis and thyroid.  
CC -1- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle  
CC in lung fibroblasts.  
CC -1- SIMILARITY: Belongs to the cyclin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC  
DR EMBL; D50310; BAA08849.1; -;  
DR EMBL; AY207372; AA013492.1; -;  
DR EMBL; BC000420; AAH00420.1; -;  
DR EMBL; BC004975; AAH04975.1; -;  
DR EMBL; AF135162; AAF43786.1; -;  
DR PIR; JE0264; JE0264.  
DR Genew; HGNC:1595; CCNI.  
DR H-TnvdB; HIX0004313; -;  
DR GO; GO:007283; P:spermatogenesis; NAS.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin_like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.  
KW Cyclin; Polymorphism.  
FT VARIANT 207 207  
FT V -> I (in dbSNP:4252903).  
FT /FTID=VAR_016312.  
FT N -> D (in Ref. 5).  
FT Q -> R (in Ref. 5).  
FT R -> G (in Ref. 5).  
FT  
SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA/4698F6C CRC64;  
  
Query Match 100.0%; Score 74; DB 1; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDNVSENVGVCVT 14  
Db 343 EDNVSENVGVCVT 356  
|||||  
-----  
RESULT 2  
Q6FHHO PRELIMINARY; PRT; 377 AA.  
ID Q6FHHO  
AC Q6FHHO;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE CCNI protein (Fragment).  
GN Name=CCNI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OC NCBI_TaxID=9606;  
RN [1]
```

```
RP SEQUENCE FROM N.A.  
RA Halleck A., Ebert L., Mkomdinya M., Schick M., Eisenstein S.,  
RA Hebert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,  
RA Korn B., Zuo D., Hu Y., LaBaer J.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: Belongs to the cyclin family.  
DR EMBL; CR541783; CAG46582.1; -;  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin_like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
KW Cyclin.  
FT NON TER 377 377  
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;  
  
Query Match 100.0%; Score 74; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 EDNVSENVGVCVT 14  
Db 343 EDNVSENVGVCVT 356  
|||||  
-----  
RESULT 3  
CYCI_MOUSE STANDARD; PRT; 377 AA.  
ID CYCI_MOUSE  
AC Q9Z2Y9;  
DT 18-OCT-2001 (Rel. 40, Created)  
DT 18-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Cyclin I.  
GN Name=Ccni;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,  
RA Thorgeirsson S.S.;  
RT "Assignment of the cyclin I gene (Ccn1) to mouse chromosome 5E3.3-F1.  
RT 3 by in situ hybridization.";  
RL Cytogenet. Cell Genet. 83:242-243 (1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;  
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgeirsson S.S.;  
RT "In vivo expression and genomic organization of the mouse cyclin I  
RT gene (Ccn1).";  
RL Gene 256:59-67 (2000).  
CC -1- SIMILARITY: Belongs to the cyclin family.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC  
DR EMBL; AF005886; AAD01253.2; -;  
DR EMBL; AF228740; AAF43391.1; -;  
DR EMBL; AF228739; AAF43391.1; JOINED.  
DR MGD; MGI:1341077; Ccni.  
DR InterPro; IPR006670; Cyclin.  
DR InterPro; IPR011028; Cyclin_like.  
DR InterPro; IPR006671; Cyclin_N.  
DR Pfam; PF00134; Cyclin_N; 1.  
DR SMART; SM00385; CYCLIN; 1.  
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
```

KW Cyclin.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AE677 CRC64;
Query Match 83.8%; Score 62; DB 1; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCCT 14
Db 343 EDNGPENVGVCCT 356
RESULT 4
Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, RIKEN full-length
DE enriched library, clone:CS20001G04 product:cyclin I, full insert
DE sequence.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes."
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoaka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer."
RL Genome Res. 10:1757-1771(2000).
RN [6]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirokawa T.,
RA Hori P., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK050465; BAC34271.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42206 MW; A1B803EBE135B0E8 CRC64;
Query Match 83.8%; Score 62; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCCT 14
Db 343 EDNGPENVGVCCT 356
RESULT 5
Q99LF2 PRELIMINARY; PRT; 377 AA.
ID Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Maman A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

```
RP SEQUENCE FROM N.A.
RA STRAIN=FVB/N; TISSUE=Mammary tumor;
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the cyclin family.
RR EMBL; BC003290; AA030290.1; -.
DR MGD; MGI:1341077; Ccn1.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; Cyclin; 1.
DR Cyclin.
KW CYCLIN.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match      83.8%; Score 62; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNGPENVGVCVT 356

RESULT 6
Q6UB65
ID Q6UB65 PRELIMINARY; PRT; 181 AA.
AC Q6UB65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative H+ translocating inorganic pyrophosphatase (Fragment).
OS Hyaloperonospora parasitica.
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Peronosporaceae;
OC Hyaloperonospora.
OX NCBI_TaxID=123356;
RN SEQUENCE FROM N.A.
RC STRAIN=Maks9;
RA Bittner-Bddy P., Allen R., Rehmany A., Birch P., Beynon J.;
RT "Use of suppression subtractive hybridization to identify downy mildew
  genes expressed during infection of Arabidopsis thaliana.";
RL Mol. Plant Pathol. 0:0-0(2003).
DR EMBL; AY373944; AAQ83502.1; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 18752 MW; B2B134292CDE01D1 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 181;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSSENVGVCVT 13
Db 66 DNVDGNDVGVAG 77

RESULT 7
Q6DUU8
ID Q6DUU8 PRELIMINARY; PRT; 196 AA.
AC Q6DUU8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vacuolar-type H+-pyrophosphatase (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;

RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the cyclin family.
RR EMBL; BC003290; AA030290.1; -.
DR MGD; MGI:1341077; Ccn1.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; Cyclin; 1.
DR Cyclin.
KW CYCLIN.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match      83.8%; Score 62; DB 2; Length 377;
Best Local Similarity 85.7%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
Db 343 EDNGPENVGVCVT 356

RESULT 6
Q6UB65
ID Q6UB65 PRELIMINARY; PRT; 181 AA.
AC Q6UB65;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative H+ translocating inorganic pyrophosphatase (Fragment).
OS Hyaloperonospora parasitica.
OC Eukaryota; stramenopiles; Oomycetes; Peronosporales; Peronosporaceae;
OC Hyaloperonospora.
OX NCBI_TaxID=123356;
RN SEQUENCE FROM N.A.
RC STRAIN=Maks9;
RA Bittner-Bddy P., Allen R., Rehmany A., Birch P., Beynon J.;
RT "Use of suppression subtractive hybridization to identify downy mildew
  genes expressed during infection of Arabidopsis thaliana.";
RL Mol. Plant Pathol. 0:0-0(2003).
DR EMBL; AY373944; AAQ83502.1; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
FT NON_TER 1
FT NON_TER 181
SQ SEQUENCE 181 AA; 18752 MW; B2B134292CDE01D1 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 181;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSSENVGVCVT 13
Db 66 DNVDGNDVGVAG 77

RESULT 7
Q6DUU8
ID Q6DUU8 PRELIMINARY; PRT; 196 AA.
AC Q6DUU8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Vacuolar-type H+-pyrophosphatase (Fragment).
OS Medicago sativa (Alfalfa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
OX NCBI_TaxID=3879;
```

```
RN SEQUENCE FROM N.A.
RP Wu M.S., Wang P.Q.;
RA Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY642597; AAT65202.1; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
FT NON_TER 1
FT NON_TER 196
SQ SEQUENCE 196 AA; 20630 MW; B43885E81B02759E CRC64;

Query Match      59.5%; Score 44; DB 2; Length 196;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSSENVGVCVT 13
Db 14 DNVDGNDVGVAG 25

RESULT 8
Q8G446
ID Q8G446 PRELIMINARY; PRT; 464 AA.
AC Q8G446;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN OrderedLocustNames=BL1547;
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCC 2705;
RX MEDLINE=22294977; PubMed=12381787; DOI=10.1073/pnas.212527599;
RA Schell M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zwaehlen M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
  to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014789; AAN25339.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006043; Xant/urac/vitC.
DR Pfam; PF00860; Xan_ur_permease; 1.
KW Complete proteome.
SQ SEQUENCE 464 AA; 48723 MW; CD744DD8CA6AD556 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 464;
Best Local Similarity 38.5%; Pred. No. 51;
Matches 5; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

Qy 2 DNVSSENVGVCVT 14
Db 317 DSATSGAICGT 329

RESULT 9
Q67L99
ID Q67L99 PRELIMINARY; PRT; 659 AA.
AC Q67L99;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Inorganic H+ pyrophosphatase.
GN ORFNames=STH2562;
OS Symbiobacterium thermophilum.
OC Bacteria; Actinobacteria; Symbiobacterium.
OX NCBI_TaxID=2734;
```

```

RN  SEQUENCE FROM N.A.
RC  STRAIN=IAM14863;
RA  Ueda K., Yamashita A., Ishikawa J., Shimada M., Watsuji T.,
RA  Morimura K., Ikeda H., Hattori M., Beppu T.;
RT  "Complete genome sequence of an uncultured bacterium Symbiobacterium
RL  thermophilum.";
RL  Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AP006840; BAD41547.1; -.
DR  InterPro; IPR004131; H_PPase.
DR  Pfam; PF03030; H_PPase; 1.
DR  PIRSF; PIRSF001265; H+-PPase; 1.
DR  TIGRFAMs; TIGR01104; V_PPase; 1.
SQ  SEQUENCE 659 AA; 66602 MW; 67BB1A62D01BB1A4 CRC64;

Query Match      59.5%; Score 44; DB 2; Length 659;
Best Local Similarity 66.7%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  2 DNVSENVGSVCG 13
    ||| : ||| |
Db  199 DNVDGNDVDVAG 210

RESULT 10
HPPA_FUSNN          STANDARD;          PRT;          671 AA.
AC  Q8RHJ2;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-
DE  energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
DE  proton-translocating pyrophosphatase).
GN  Name=hppA; OrderedLocusNames=FN2030;
OS  Fusobacterium nucleatum (subsp. nucleatum).
OC  Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC  Fusobacterium.
OX  NCBI_TaxID=76856;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 25586;
RX  MEDLINE=21886394; PubMed=11889109;
RX  DOI=10.1128/JB.184.7.2005-2018.2002;
RA  Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA  Bhattacharya A., Barton A., Gardner W., Grechkin G., Zhu L.,
RA  Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA  Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA  Forsttein M., Kyrpides N.C., Overbeek R.;
RT  "Genome sequence and analysis of the oral bacterium Fusobacterium
RT  nucleatum strain ATCC 25586.";
RL  J. Bacteriol. 184:2005-2018 (2002).
CC  -!- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC  fully reversible reaction, thus being able to synthesize
CC  pyrophosphate when the proton motive force is sufficient (By
CC  similarity).
CC  -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC  -!- COFACTOR: Magnesium and potassium (By similarity).
CC  -!- SUBUNIT: Homodimer (Potential).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC  -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC  (TC 3.A.10) family. Subfamily 1.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
-----
CC  HEMBL; AB010505; AAU941115.1; -.
DR  HAMAP; MF_01129; -; 1.

```

```

DR  InterPro; IPR004131; H_PPase.
DR  Pfam; PF03030; H_PPase; 1.
DR  PIRSF; PIRSF001265; H+-PPase; 1.
DR  TIGRFAMs; TIGR01104; V_PPase; 1.
KW  Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW  Potassium; Transmembrane.
FT  TRANSMEM 4 26 Potential.
FT  TRANSMEM 60 94 Potential.
FT  TRANSMEM 126 148 Potential.
FT  TRANSMEM 161 183 Potential.
FT  TRANSMEM 225 247 Potential.
FT  TRANSMEM 254 276 Potential.
FT  TRANSMEM 291 313 Potential.
FT  TRANSMEM 315 337 Potential.
FT  TRANSMEM 361 383 Potential.
FT  TRANSMEM 390 412 Potential.
FT  TRANSMEM 450 472 Potential.
FT  TRANSMEM 493 515 Potential.
FT  TRANSMEM 560 579 Potential.
FT  TRANSMEM 581 603 Potential.
FT  TRANSMEM 646 668 Potential.
FT  SITE Determinant of potassium dependence (By
FT  similarity).
SQ  SEQUENCE 671 AA; 68989 MW; B9519DE6D3554ACB CRC64;

Query Match      59.5%; Score 44; DB 1; Length 671;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy  2 DNVSENVGSVCG 13
    ||| : ||| |
Db  213 DNVDGNDVDVAG 224

RESULT 11
HPPA_CLOTE          STANDARD;          PRT;          673 AA.
AC  Q898Q9;
DT  10-OCT-2003 (Rel. 42, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  25-OCT-2004 (Rel. 45, Last annotation update)
DE  Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-
DE  energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
DE  proton-translocating pyrophosphatase).
GN  Name=hppA; OrderedLocusNames=CTC00383;
OS  Clostridium tetani.
OC  Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC  Clostridium.
OX  NCBI_TaxID=1513;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Massachusetts / E88;
RX  MEDLINE=22457253; PubMed=12552129; DOI=10.1073/pnas.0335853100;
RA  Brueggemann H., Baeumer S., Fricke W.F., Wierzer A., Liesegang H.,
RA  Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA  Gottschalk G.;
RT  "The genome sequence of Clostridium tetani, the causative agent of
RT  tetanus disease.";
RL  Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
CC  -!- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC  fully reversible reaction, thus being able to synthesize
CC  pyrophosphate when the proton motive force is sufficient (By
CC  similarity).
CC  -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC  -!- COFACTOR: Magnesium and potassium (By similarity).
CC  -!- SUBUNIT: Homodimer (Potential).
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC  -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC  (TC 3.A.10) family. Subfamily 1.
-----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its

```

use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

```
CC CC use by non-profit institutions as long as its content is in no way
CC CC modified and this statement is not removed. Usage by and for commercial
CC CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC CC or send an email to license@isb-sib.ch).
CC -----
CC DR EMBL; AB015937; AAC035020.1; -.
CC DR HANAP; MF_01129; -. 1.
CC DR InterPro; IPR004131; H_PPase.
CC DR Pfam; PF03030; H_PPase_1
CC DR PIRSF; PIRSF001265; H+-PPase; 1.
CC DR Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW Potassium; Transmembrane.
KW TRANSMEM 4 26 Potential.
FT TRANSMEM 57 74 Potential.
FT TRANSMEM 78 100 Potential.
FT TRANSMEM 121 143 Potential.
FT TRANSMEM 153 175 Potential.
FT TRANSMEM 245 267 Potential.
FT TRANSMEM 282 304 Potential.
FT TRANSMEM 309 331 Potential.
FT TRANSMEM 360 382 Potential.
FT TRANSMEM 389 411 Potential.
FT TRANSMEM 447 469 Potential.
FT TRANSMEM 482 504 Potential.
FT TRANSMEM 554 573 Potential.
FT TRANSMEM 580 602 Potential.
FT TRANSMEM 650 672 Potential.
FT SITE 449 449 Determinant of potassium dependence (By
KW similarity); E3505682EE1OFF56 CRC64;
KW SEQUENCE 673 AA; 69282 MW; E3505682EE1OFF56 CRC64;
Query Match 59.5%; Score 44; DB 1; Length 673;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13
Db 206 DNVDNVDVAG 217
|||||
RESULT 12
Q7P6V4 PRELIMINARY; PRT; 673 AA.
ID Q7P6V4
AC Q7P6V4
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1).
GN Name=FN1867;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Karpatrial V., Ivanova N., Anderson I., Reznik G., Bhattacharyya A.,
RA Gardner W.L., Mikhailova N., Larsen N., D'Souza M., Walunas T.,
RA Haseltorn R., Overbeek R., Kyrtides N.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -! CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AABF0100026; EAA24540.1; -.
CC GO; GO:0016020; C-membrane; IEA.
CC GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.
CC GO; GO:0016787; F:hydrolase activity; IEA.
CC GO; GO:0004427; F:inorganic diphosphatase activity; IEA.
CC GO; GO:0015992; P:proton transport; IEA.
CC InterPro; IPR004131; H_PPase.
CC Pfam; PF03030; H_PPase_1.
CC PIRSF; PIRSF001265; H+-PPase; 1.
CC TIGRFAMs; TIGR01104; V_PPase; 1.

KW Hydrolase.
KW SEQUENCE 673 AA; 69259 MW; 174E87796E7DE14B CRC64;
Query Match 59.5%; Score 44; DB 2; Length 673;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13
Db 213 DNVDNVDVAG 224
|||||
RESULT 13
Q6MWC1 PRELIMINARY; PRT; 688 AA.
ID Q6MWC1
AC Q6MWC1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Vacuolar-type H+-pyrophosphatase precursor (EC 3.6.1.1).
GN Name=ppa; OrderedLocusNames=Bd1715;
OS Bdellovibrio bacteriovorus.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
OC Bdellovibrionaceae; Bdellovibrio.
OX NCBI_TaxID=959;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
RX PubMed=14752164; DOI=10.1126/science.1093027;
RA Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C.,
RA Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F.,
RA Sockett R.E., Schuster S.C.;
RT "A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
RT genomic perspective."
RL Science 303:689-692(2004).
DR EMBL; BX842650; CAB79584.1; -.
DR GO; GO:0016020; C-membrane; IEA.
DR GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. . .; IEA.
DR GO; GO:0004427; F:inorganic diphosphatase activity; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR TIGRFAMs; TIGR01104; V_PPase; 1.
KW Complete proteome.
FT SIGNAL 1 10 Potential.
KW SEQUENCE 688 AA; 69153 MW; DB14954596AAB7BC CRC64;
Query Match 59.5%; Score 44; DB 2; Length 688;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSENVGVCV 13
Db 212 DNVDNVDVAG 223
|||||
RESULT 14
HPA LEPIN STANDARD; PRT; 704 AA.
ID HPA_LEPIN
AC Q8F641;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Pyrophosphate-energized proton pump (EC 3.6.1.1) (Pyrophosphate-
DE energized inorganic pyrophosphatase) (H+-PPase) (Membrane-bound
DE proton-translocating pyrophosphatase).
GN Name=hppa; OrderedLocusNames=LAI471;
OS Leptospira interrogans.
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=173;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
```

```

RX MEDLINE=22598143; PubMed=12712204; DOI=10.1038/nature01597;
RA Ren S.-X., Fu G., Jiang X.-G., Zeng R., Miao Y.-G., Xu H.,
RA Zhang Y.-X., Xiong H., Lu G., Lu L.-F., Jiang H.-Q., Jia J., Tu Y.-F.,
RA Zhang J.-X., Gu W.-Y., Zhang Y.-Q., Cai Z., Sheng H.-H., Yin H.-F.,
RA Zhang Y., Zhu G.-F., Wan M., Huang H.-L., Qian Z., Wang S.-Y., Ma W.,
RA Yao Z.-J., Shen Y., Qiang B.-O., Xia Q.-C., Guo X.-K., Danchin A.,
RA Saint Girons I., Somerville R.L., Wen Y.-M., Shi M.-H., Chen Z.,
RA Xu J.-G., Zhao G.-P.;
RT "Unique physiological and pathogenic features of Leptospira
RT interogens revealed by whole-genome sequencing.";
RL Nature 422:888-893(2003).
CC -!- FUNCTION: Generates a proton motive force; it probably catalyzes a
CC fully reversible reaction, thus being able to synthesize
CC pyrophosphate when the proton motive force is sufficient (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Magnesium and potassium (By similarity).
CC -!- SUBUNIT: Homodimer (Potential).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the H(+)-translocating pyrophosphatase
CC (TC 3.A.10) family. Subfamily 1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE011327; ANA48670.1; -.
DR HAMAP; MF_01129; -.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR PIRSF; PIRSF001265; H+-PPase; 1.
DR TIGRFAMs; TIGR01104; V_PPase; 1.
KW Complete proteome; Hydrogen ion transport; Hydrolase; Magnesium;
KW Potassium; Transmembrane.
FT TRANSMEM 4 23 Potential.
FT TRANSMEM 64 81 Potential.
FT TRANSMEM 91 113 Potential.
FT TRANSMEM 143 165 Potential.
FT TRANSMEM 175 197 Potential.
FT TRANSMEM 276 298 Potential.
FT TRANSMEM 308 327 Potential.
FT TRANSMEM 348 370 Potential.
FT TRANSMEM 390 412 Potential.
FT TRANSMEM 419 441 Potential.
FT TRANSMEM 481 503 Potential.
FT TRANSMEM 516 538 Potential.
FT TRANSMEM 586 605 Potential.
FT TRANSMEM 612 634 Potential.
FT TRANSMEM 671 693 Potential.
FT SITE 481 481 Determinant of potassium dependence (By
FT similarity).
SQ SEQUENCE 704 AA; 73105 MW; 9369E135382D96BC CRC64;

Query Match 59.5%; Score 44; DB 1; Length 704;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNGVSGC 13
Db 232 DNVDNVDVAG 243

RESULT 15
Q72029
ID Q72029 PRELIMINARY; PRT; 704 AA.
AC Q72029;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

```

```

DE H+-translocating pyrophosphatase.
GN Name:avp; OrderedLocNames=LIIC2285;
OS Leptospira interrogans (serogroup Icterohaemorrhagiae / serovar
OS Copenhagen).
OC Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
OX NCBI_TaxID=44275;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Floeruz LI-130;
RX PubMed=15028702; DOI=10.1128/JB.186.7.2164-2172.2004;
RA Nascimento A.L.T.O., Ko A.I., Martins E.A.L., Monteiro-Vitorello C.B.,
RA Ho P.L., Haake D.A., Verjovski-Almeida S., Hartskeerl R.A.,
RA Marques M.V., Oliveira M.C., Menck C.F.M., Leite L.C.C., Carrer H.,
RA Coutinho L.J., Degraeve W.M., Dellagostin O.A., El-Dorry H.,
RA Ferro E.S., Ferro M.I.T., Furlan L.R., Gamberini M., Gigliotti E.A.,
RA Goes-Neto A., Goldman G.H., Goldman M.H.S., Harakava R.,
RA Jeronimo S.M.B., Junqueira-de-Azevedo J.L.M., Kimura E.T.,
RA Kuranae E.E., Lemos E.G.M., Lemos M.V.F., Marino C.L., Nunes L.R.,
RA de Oliveira R.C., Pereira G.G., Reis M.S., Schriefer A.,
RA Siqueira W.J., Sommer P., Tsai S.M., Simpson A.J.G., Ferro J.A.,
RA Camargo L.E.A., Kitajima J.P., Setubal J.C., Van Sluys M.A.;
RT "Comparative genomics of two Leptospira interrogans serovars reveals
RT novel insights into physiology and pathogenesis.";
RL J. Bacteriol. 186:2164-2172(2004).
DR EMBL; AE017296; AAS70856.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0009678; F:hydrogen-translocating pyrophosphatase acti. .; IEA.
DR GO; GO:0015992; P:proton transport; IEA.
DR InterPro; IPR004131; H_PPase.
DR Pfam; PF03030; H_PPase; 1.
DR PIRSF; PIRSF001265; H+-PPase; 1.
DR TIGRFAMs; TIGR01104; V_PPase; 1.
DR Complete proteome.
SQ SEQUENCE 704 AA; 73105 MW; 9369E135382D96BC CRC64;

Query Match 59.5%; Score 44; DB 2; Length 704;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DNVSNGVSGC 13
Db 232 DNVDNVDVAG 243

Search completed: February 11, 2005, 03:05:17
Job time : 5.72379 secs

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:50 ; Search time 285.586 Seconds
(without alignments)
2375.375 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154924_20406/app.query.fasta_1.718
-DB=GenEmbl -QMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOPEXT=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250 @CGN 1 1 3890 @runat_07022005_154924_20406 -NCPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	6 A74835	A74835 Sequence 52
2	74	100.0	136	6 A77814	A77814 Sequence 52
3	74	100.0	288	6 CQ712652	CQ712652 Sequence
4	74	100.0	350	6 CQ675890	CQ675890 Sequence

C	5	74	100.0	444	6	AX397198	Sequence
	6	74	100.0	447	6	AX198885	Sequence
	7	74	100.0	447	6	AX209412	Sequence
C	8	74	100.0	601	11	BV180201	sgml10841
	9	74	100.0	804	6	BD079737	Cancer-as
	10	74	100.0	1131	9	CR541783	Homo sapi
	11	74	100.0	1133	6	AR145734	Sequence
	12	74	100.0	1260	6	AR087353	Sequence
	13	74	100.0	1260	6	CQ812312	Sequence
	14	74	100.0	1260	6	AR281918	Sequence
	15	74	100.0	1260	6	AR380354	Sequence
	16	74	100.0	1260	9	HUMCVI	D50310 Human mRNA
	17	74	100.0	1384	9	AF135162	Homo sapi
	18	74	100.0	1493	6	BD194541	Human nuc
	19	74	100.0	1493	6	AX015395	Sequence
	20	74	100.0	1817	9	BC000420	Homo sapi
	21	74	100.0	1889	9	CQ468129	Sequence
	22	74	100.0	1889	9	BC004975	Homo sapi
	23	74	100.0	2146	6	CQ414223	Sequence
	24	74	100.0	2755	6	CQ414515	Sequence
	25	74	100.0	29867	9	AY207372	Homo sapi
C	26	74	100.0	35191	9	AC111196	Homo sapi
	27	74	100.0	178916	2	AP002874	Homo sapi
C	28	74	100.0	179443	2	AC079051	Homo sapi
	29	70	94.5	308	6	CQ696855	Sequence
	30	69	93.2	304	6	AX914031	Sequence
	31	69	93.2	304	6	BD049564	Sequence
C	32	65	87.8	200850	2	AC101881	Mus muscu
	33	65	87.8	202228	2	AC124646	Mus muscu
C	34	62	83.8	1535	10	AF005886	Mus muscu
	35	62	83.8	2348	10	BC003290	Mus muscu
	36	62	83.8	11793	10	AF228739S2	Mus muscu
	37	62	83.8	179333	2	AC117658	Mus muscu
	38	62	83.8	193811	10	AC134827	Mus muscu
C	39	62	83.8	241543	2	AC099472	Rattus no
	40	62	83.8	260517	2	AC111318	Rattus no
	41	62	83.8	270068	2	AC113213	Rattus no
C	42	50	67.6	3039	6	CQ583995	Sequence
	43	50	67.6	5856	6	CQ583994	Sequence
C	44	50	67.6	15921	3	AF034856	Drosophil
	45	50	67.6	58569	2	AC015033	Drosophil

ALIGNMENTS

RESULT 1	A74835	A74835	Sequence 521 from Patent WO9401548.	136 bp	DNA	linear	PAT 15-OCT-1999
LOCUS	A74835	Sequence 521 from Patent WO9401548.					
DEFINITION	A74835	Sequence 521 from Patent WO9401548.					
ACCESSION	A74835	Sequence 521 from Patent WO9401548.					
VERSION	A74835.1	GI:6064849					
KEYWORDS							
SOURCE		unidentified					
ORGANISM		unclassified.					
REFERENCE	1	(bases 1 to 136)					
AUTHORS	Sibson,D.R. and Gross,J.						
TITLE	HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW						
JOURNAL	Patent: WO 9401548-A 521 20-JAN-1994;						
FEATURES	MEDICAL RES COUNCIL (GB); SIBSON DAVID ROSS (GB)						
source	Location/Qualifiers						
	1. .136						
	/organism="unidentified"						
	/mol_type="unassigned DNA"						
	/db_xref="taxon:32644"						

ORIGIN

Alignment Scores:					
Pred. No.:	4.02e-05	Length:	136		
Score:	74.00	Matches:	14		
Percent Similarity:	100.00%	Conservative:	0		
Best Local Similarity:	100.00%	Mismatches:	0		

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ712652 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAAATGGGGTCTCTGTGTGGCACT 104

RESULT 4
LOCUS CQ675890 350 bp DNA PAT 03-FEB-2004
DEFINITION Sequence 20816 from Patent WO02070737.
ACCESSION CQ675890
VERSION CQ675890.1 GI:42180044
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Liew,C.C., Marshall,W.E. and Zhang,H.
AUTHORS Compositions and methods relating to osteoarthritis
TITLE Patent: WO 02070737-A 20816 12-SEP-2002;
JOURNAL Chondrogene Inc. (CA)
FEATURES Location/Qualifiers
source 1..350
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: Length: 350
Pred. No.: 0.000102 Matches: 14
Score: 74.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-736-250-5 (1-14) x CQ675890 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAAATGGGGTCTCTGTGTGGCACT 170

RESULT 5
LOCUS AX397198 444 bp DNA PAT 18-MAY-2002
DEFINITION Sequence 1413 from Patent WO0212328.
ACCESSION AX397198
VERSION AX397198.1 GI:21067945
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 King,G.E., Meagher,M.J., Xu,J. and Secrist,H.
AUTHORS Compositions and methods for the therapy and diagnosis of colon
TITLE Patent: WO 0212328-A 1413 14-FEB-2002;
JOURNAL cancer
FEATURES Location/Qualifiers
source 1..444
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: Length: 444
Pred. No.: 0.000129 Matches: 170
Score: 74.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x A74835 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAAATGGGGTCTCTGTGTGGCACT 65

RESULT 2
LOCUS A77814 136 bp DNA PAT 19-OCT-1999
DEFINITION Sequence 521 from Patent EP0587279.
ACCESSION A77814
VERSION A77814.1 GI:6089479
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 136)
AUTHORS Sibeon,D.R. and Hadfield,K.M.
TITLE HUMAN NUCLEIC ACID FRAGMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,
JOURNAL PLACENTA OR BONE MARROW AND THEIR USE
MEDICAL RES COUNCIL (GB)
FEATURES Location/Qualifiers
source 1..136
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

ORIGIN
Alignment Scores: Length: 136
Pred. No.: 4.02e-05 Matches: 14
Score: 74.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

US-09-736-250-5 (1-14) x A77814 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAAATGGGGTCTCTGTGTGGCACT 65

RESULT 3
LOCUS CQ712652 288 bp DNA PAT 03-FEB-2004
DEFINITION Sequence 57578 from Patent WO02070737.
ACCESSION CQ712652
VERSION CQ712652.1 GI:42273509
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Liew,C.C., Marshall,W.E. and Zhang,H.
AUTHORS Compositions and methods relating to osteoarthritis
TITLE Patent: WO 02070737-A 57578 12-SEP-2002;
JOURNAL Chondrogene Inc. (CA)
FEATURES Location/Qualifiers
source 1..288
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores: Length: 288
Pred. No.: 8.44e-05 Matches: 14
Score: 74.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 6

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX397198 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 436 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 395

RESULT 6
 AX198885
 LOCUS AX198885 447 bp DNA linear PAT 29-AUG-2001
 DEFINITION Sequence 1340 from Patent WO015153.
 ACCESSION AX198885
 VERSION AX198885.1 GI:15389211

KEYWORDS Homo sapiens (human)
 SOURCE
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Algate, P.A.
 TITLE Ovarian tumor-associated sequences
 JOURNAL Patent: WO 015153-A 1340 19-JUL-2001;
 CORIXA CORPORATION (US)

FEATURES
 source
 1..447
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 0.00013 Length: 447
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX198885 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134

RESULT 7
 AX209412
 LOCUS AX209412 447 bp DNA linear PAT 31-AUG-2001
 DEFINITION Sequence 1252 from Patent WO0157207.
 ACCESSION AX209412
 VERSION AX209412.1 GI:15423835

KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Algate, P.A. and Mannion, J.
 TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
 JOURNAL Patent: WO 0157207-A 1252 09-AUG-2001;
 CORIXA CORPORATION (US)

FEATURES
 source
 1..447
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

ORIGIN

Alignment Scores:
 Pred. No.: 0.00013 Length: 447
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX209412 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 93 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 134

RESULT 8
 BV180201/c
 LOCUS BV180201 601 bp DNA linear STS 10-JUN-2004
 DEFINITION sgml08417 Human DNA (Sequenom) Homo sapiens STS genomic, sequence tagged site.
 ACCESSION BV180201
 VERSION BV180201.1 GI:48017195
 KEYWORDS STS.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 601)
 AUTHORS Nelson, R.M., Marnellos, G., Kammerer, S., Hoyal, C.R., Shi, M.M., Cantor, C.R. and Braun, A.
 TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene Regions
 JOURNAL Genome Res. (2004) In press
 COMMENT

Contact: Andreas Braun
 Pharmaceuticals division
 Sequenom, Inc.
 3595 John Hopkins Court, San Diego, CA 92121, USA
 Tel: 18582029018
 Fax: 18582029020
 Email: abraun@sequenom.com
 Primer A: No primer sequence submitted
 Primer B: No primer sequence submitted
 STS size: 601.

FEATURES
 source
 1..601
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone_lib="Human DNA (Sequenom)"
 <1..5601

STS ORIGIN

Alignment Scores:
 Pred. No.: 0.000174 Length: 601
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x BV180201 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 327 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 286

RESULT 9
 BD079737/c

LOCUS BD079737 804 bp DNA linear
 DEFINITION Cancer-associated nucleic acids and polypeptides.
 ACCESSION BD079737
 VERSION BD079737.1 GI:22625340
 KEYWORDS JP 2001516009-A/403.

PAT 27-AUG-2002

SOURCE
ORGANISM Homo sapiens (human)

REFERENCE
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)

TITLE
JOURNAL Old, L.J., Scanlan, M.J., Stockert, E., Gure, A., Chen, Y.T., Gout, I., Ogihara, M., Obata, Y., Pfeundschnur, M., Tureci, O. and Sahin, U.
Patent: JP 2001516009-A 403 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH

COMMENT
OS Homo sapiens (human)
PN JP 2001516009-A/403
PD 25-SEP-2001
PR 15-JUL-1998 JP 2000503425
PR 17-JUL-1997 US 08/896164, 10-OCT-1997 US 60/061599 PR
10-OCT-1997 US 60/061765, 10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2, 22-JUN-1998 US 09/102322 PI LLOYD
J OLD, MATTHEW J SCANLAN, ELISABETH STOCKERT, ALI GURE, YAO PI TSENG
CHEN,
PI IVAN GOUT, MICHAEL O'HARE, YUICHI OBATA, MICHAEL PFEUNDSCHUR, PI
OZLEM TURECI,
PI UGUR SAHIN
PC
GOIN33/574, A61K38/00, A61K39/395, A61K39/395, A61K45/00, A61K48/00, PC
A61P35/00,
PC C07K14/82, C07K16/32, C12N15/09//C07K16/46, C12P21/08, A61K37/02,
PC C12N15/00
CC Cancer-associated nucleic acids and polypeptides. FH Key
Location/Qualifiers
FT source i..804
FT Location/Qualifiers
1..804
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
ORIGIN

Alignment Scores:
Pred. No.: 0.000232 Length: 804
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x BD079737 (1-804)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 301 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 260
|||||

RESULT 10
CR541783 1131 bp mRNA linear PRI 29-JUN-2004
LOCUS
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
gene CCNI, cyclin I; complete cds, without stopcodon.
ACCESSION CR541783
VERSION CR541783.1 GI:49456522
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1131)

REFERENCE
AUTHORS Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Cloning of human full open reading frames in Gateway(TM) system
entry vector (pDONR201)

TITLE
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1131)
AUTHORS Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,

TITLE
JOURNAL Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD; RZPD0834E0730D, ORFNO 3592
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834E0730D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Amlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.011
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att..AAAAA GCA GGC TCC ACC (ATG)
The last codon is followed by the 3' att site: GACCCAGCTTTT.. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_006835 (GI:17738314) we found
AA exchange(s) at position (first base of changed triplet):
22 (arg->gly) 409 (lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES
source
ORIGIN

Alignment Scores:
Pred. No.: 0.000326 Length: 1131
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x CR541783 (1-1131)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
|||||

Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mar, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD; RZPD0834E0730D, ORFNO 3592
www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=RZPD0834E0730D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB NO.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi/response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Amlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.011
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been inserted into pDONR201 via a BP Clonase(TM)
reaction. Additional sequence has been added in front of the start
codon: att..AAAAA GCA GGC TCC ACC (ATG)
The last codon is followed by the 3' att site: GACCCAGCTTTT.. att
The clone is validated by full sequence check.
Compared to the reference sequence NM_006835 (GI:17738314) we found
AA exchange(s) at position (first base of changed triplet):
22 (arg->gly) 409 (lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/.

FEATURES
source
ORIGIN

Alignment Scores:
Pred. No.: 0.000326 Length: 1131
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x CR541783 (1-1131)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 1068
|||||

```
RESULT 11
ARI45734
LOCUS ARI45734 linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6218115.
ACCESSION ARI45734
VERSION ARI45734.1 GI:15108923
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1133)
AUTHORS Nakamura,T.
TITLE Human cyclin I and genes encoding same
JOURNAL Patent: US 6218115-A 2 17-APR-2001;
FEATURES
source
1..1133
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000326 Length: 1133
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x ARI45734 (1-1133)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 12
AR087353
LOCUS AR087353 linear PAT 07-SEP-2000
DEFINITION Sequence 5 from patent US 5986055.
ACCESSION AR087353
VERSION AR087353.1 GI:10014116
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.Peter.
TITLE CDK2 interactions
JOURNAL Patent: US 5986055-A 5 16-NOV-1999;
FEATURES
source
1..1260
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x AR087353 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 13
CO812312
LOCUS CO812312 linear PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CO812312
VERSION CO812312.1 GI:47601932
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Wittig,R., Poustka,A., Mollenhauer,J. and Schadendorf,D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 64 06-MAY-2004;
DEUTSCHES Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES
source
1..1260
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature
1..1260
/note="D50310"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x CO812312 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||

RESULT 14
AR281918
LOCUS AR281918 linear PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION AR281918.1 GI:29717848
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1260)
AUTHORS Yang,M., Nandabalan,K. and Schultz,V.P.
TITLE HsReq*1 and HsReq*2 proteins and use thereof to detect CDK2
JOURNAL Patent: US 6521412-A 5 18-FEB-2003;
FEATURES
source
1..1260
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.: 0.000362 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB:
US-09-736-250-5 (1-14) x AR281918 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068
|||||
```

DEFINITION Sequence 899 from patent US 6607879.
 ACCESSION AR380354
 VERSION AR380354.1 GI:40087988
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1260)
 AUTHORS Cocks B.G., Stuart S.G. and Seilhamer J.J.
 TITLE Compositions for the detection of blood cell and immunological
 response gene expression
 JOURNAL Patent: US 6607879-A 899 19-AUG-2003;
 FEATURES
 source
 1..1260
 /organism="unknown"
 /mol_type="genomic DNA"
 ORIGIN
 Alignment Scores:
 Pred. No.: 0.000362 Length: 1260
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 6 Gaps: 0
 US-09-736-250-5 (1-14) x AR380354 (1-1260)
 QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 DB 1027 GAAGATATATGTCACAGAAATGTGGGTTCTGTGTGGCACT 1068

Search completed: February 11, 2005, 05:55:28
 Job time : 288.586 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:18:45 ; Search time 35.2327 Seconds
(without alignments)
2352.255 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCGT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgm2_1/USPTO_epool/US09736250/runat_07022005_154923_20396/app_query.fasta_1.718
-DB=N Geneseq_16Dec04 -QWTF=fastcap -SUPFIX=ring -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=prc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1.1 586 @runat_07022005_154923_20396 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N Geneseq_16Dec04:*

```
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	AAQ76921	AaQ76921 Human gen
c 2	74	100.0	351	8 AAD51549	Aad51549 Human BCA
3	74	100.0	389	10 ADK61066	Adk61066 Ovarian c
c 4	74	100.0	444	6 ABK45862	Abk45862 cDNA enco
5	74	100.0	447	4 AAS25071	Aas25071 Human ova

c 6	74	100.0	447	5 AAH83716	Aah83716 Human ova
c 7	74	100.0	597	10 ADK61065	Adk61065 Ovarian c
c 8	74	100.0	804	2 AAX40003	Aax40003 Prostate
9	74	100.0	903	12 ADN01156	Adn01156 Human cel
10	74	100.0	1260	3 AAZ37836	Aaz37836 Human cyc
11	74	100.0	1260	6 ABK83672	Abk83672 Human cDN
12	74	100.0	1260	10 ADK61064	Adk61064 Ovarian c
13	74	100.0	1260	11 ADI31573	Adi31573 Human cDN
14	74	100.0	1260	13 ADR25465	Adr25465 Breast ca
15	74	100.0	1328	2 AAT73937	Aat73937 DNA enco
16	74	100.0	1384	8 ACC47339	Acc47339 Human pro
17	74	100.0	1493	2 AAZ41284	Aaz41284 Human nor
18	74	100.0	1651	9 AAD57247	Aad57247 Human CGD
19	74	100.0	1889	6 ABL87929	Abi87929 Human ova
20	74	100.0	1890	12 ADP10653	Adp10653 Reference
21	74	100.0	1890	13 ACN38124	Acn38124 Tumour-as
22	74	100.0	2146	5 ADL63082	Adl63082 Human ova
23	74	100.0	2755	5 ADL63374	Adl63374 Human ova
24	69	93.2	304	3 AAC25819	Aac25819 Human sec
25	65	87.8	420	8 ABX44645	Abx44645 Bovine ES
c 26	50	67.6	3039	4 ABL09675	Abi09675 Drosophil
c 27	50	67.6	5856	4 ABL09674	Abi09674 Drosophil
c 28	46	62.2	293	12 ADQ19591	Adq19591 Human sof
c 29	46	62.2	379	4 AAI89415	Aai89415 Human pol
c 30	46	62.2	381	4 AAI87049	Aai87049 Human pol
c 31	46	62.2	564	2 AAV49573	Aav49573 Human sco
c 32	46	62.2	601	13 ACN60174	Acn60174 Cotton gy
c 33	46	62.2	798	13 ADR65695	Adr65695 Cotton CD
c 34	46	62.2	840	8 ACF64409	Acf64409 Human IP1
c 35	46	62.2	1138	5 ABV22730	Abv22730 Human pro
c 36	46	62.2	1138	5 ABV28557	Abv28557 Human pro
c 37	46	62.2	1175	12 ADL91836	Adl91836 Human PRO
c 38	46	62.2	1186	2 AAV49572	Aav49572 Human sco
c 39	46	62.2	1186	11 ADP65828	Adp65828 Human mRN
c 40	46	62.2	1186	11 ADP65750	Adp65750 Human put
c 41	46	62.2	1187	2 AAX28650	Aax28650 Nucleotid
c 42	46	62.2	1187	3 AAA40570	Aaa40570 Human fet
c 43	46	62.2	1206	13 ACN37541	Acn37541 Tumour-as
c 44	46	62.2	1264	4 AAS21244	Aas21244 Human cDN
c 45	46	62.2	1264	8 ACA03603	Aca03603 cDNA enco

ALIGNMENTS

RESULT 1
AAQ76921
ID AAQ76921 standard; DNA; 136 BP.

XX AAQ76921;

XX 25-MAR-2003 (revised)

DT 23-SEP-1994 (first entry)

XX Human genome fragment.

XX Brain; placenta; bone marrow; genetic analysis; gene mapping; detection;

KW homology; human; adrenal tissue; ds.

XX Homo sapiens.

OS W09401548-A2.

XX 20-JAN-1994.

XX 13-JUL-1993; 93WO-GB001467.

XX 13-JUL-1992; 92GB-00014857.

XX (MEDI-) MEDICAL RES COUNCIL.

XX Sibson DR, Gross J, Hadfield KM, Howells D, Starkey M, Kelly M;

PI Shaw D;

XX

DR WPI; 1994-035056/04.
 XX
 PT New nucleic acid fragment encoding gene products - can be used for
 PT genetic analysis and mapping.
 XX
 PS Claim 1; Page 272; 616pp; English.
 XX
 CC Human nucleic acid fragments, isolated from brain adrenal tissue, the
 CC placenta or bone marrow comprise any of: (A) a sequence selected from
 CC (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in
 CC (A), or (C) a sequence complementary to (A) or (B). (Updated on 25-MAR-
 CC 2003 to correct FN field.)
 XX
 SQ Sequence 136 BP; 36 A; 28 C; 29 G; 43 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 5,39e-05 Length: 136
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x AAQ76921 (1-136)
 QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 DB 24 GAAGATAATGCTCTCAGAAATGTCGGTCTCTGTGTGGCACT 65

RESULT 2
 AAD51549/c
 ID AAD51549 standard; cDNA; 351 BP.
 XX
 AC AAD51549;
 DT 16-APR-2003 (first entry)
 XX
 DE Human BCA7 cDNA.
 XX
 KW Human; breast cancer-associated gene; BCA-related disorder; lymphoma;
 KW infectious disease; eating disorder; cancer; Ewing's tumour; allergy;
 KW tumour; polycythaemia vera; forensic biology; gene therapy; leukaemia;
 KW bone disease; sarcoma; vaccine; gene; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT CDS
 FT Location/Qualifiers
 FT 1..351
 FT /*tag= a
 FT /product= "BCA protein"
 FT /transl_except= (pos:22..24, aa:Xaa)
 FT /transl_except= (pos:28..30, aa:Xaa)
 FT /transl_except= (pos:202..204, aa:Xaa)
 FT /transl_except= (pos:313..315, aa:Xaa)
 FT /transl_except= (pos:334..336, aa:Xaa)
 FT /note= "Xaa corresponds to in-frame stop codon; No start
 FT and stop codon"
 FT /partial
 XX
 PN WO200287507-A2.
 XX
 PD 07-NOV-2002.
 XX
 XX 29-APR-2002; 2002WO-US013584.
 XX
 PF 27-APR-2001; 2001US-0287170P.
 XX
 PR (SUNN-) SUNNYBROOK & WOMEN'S COLLEGE HEALTH SCI.
 XX
 PA Seth A;
 XX
 PI WPI; 2003-120443/11.
 XX
 DR P-PSDB; AAE33644.
 DR

XX New breast cancer-associated (BCA) genes and polypeptides, useful for
 PT preventing, treating, diagnosing or staging breast cancer, or other BCA-
 PT related disorders, e.g. prostate cancer, sarcoma, Ewing's tumor, leukemia
 PT or lymphomas.
 XX
 PS Disclosure; Page 188; 195pp; English.
 XX
 CC The invention relates to human breast cancer-associated (BCA) genes and
 CC polypeptides. BCA sequences are useful for preventing or treating breast
 CC cancer. Other BCA-related disorders that may be treated include allergy,
 CC bone disease, eating disorder, infectious disease, ovarian cancer,
 CC prostate cancer, skin cancer or brain cancer, malignant or non-malignant
 CC tumours, sarcoma, Ewing's tumour, leukaemia, lymphomas, or polycythaemia
 CC vera. BCA sequences are also useful in forensic biology, diagnostic
 CC assays, prognostic assays or pharmacogenomics or for monitoring clinical
 CC trials. The invention is useful in gene therapy and as vaccines. The
 CC present sequence is human BCA cDNA
 XX
 SQ Sequence 351 BP; 98 A; 77 C; 60 G; 116 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 0.000163 Length: 351
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 8 Gaps: 0

US-09-736-250-5 (1-14) x AAD51549 (1-351)
 QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 DB 308 GAAGATAATGCTCTCAGAAATGTCGGTCTCTGTGTGGCACT 267

RESULT 3
 ADK61066
 ID ADK61066 standard; DNA; 389 BP.
 XX
 AC ADK61066;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Ovarian cancer-related DNA #221 with altered ovarian cancer expression.
 XX
 KW ds; Gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
 KW gene expression; primer; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO2003068054-A2.
 XX
 PD 21-AUG-2003.
 XX
 PF 13-FEB-2003; 2003WO-US004688.
 XX
 PR 13-FEB-2002; 2002US-0357031P.
 XX
 PA (USSH) SLOAN KETTERING INST CANCER RES.
 XX
 PI Jazaeri AA, Boyd J, Liu ET;
 XX
 DR WPI; 2003-689589/65.
 XX
 CC Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
 PT like tumor by determining a pattern of expression in the ovarian tumor of
 PT several markers.
 XX
 PS Disclosure; SEQ ID NO 236; 137pp; English.
 XX
 CC The invention relates to a method of classifying an ovarian tumor as a
 CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a

CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

XX SQ Sequence 389 BP; 97 A; 99 C; 84 G; 100 T; 0 U; 9 Other;

Alignment Scores:
Pred. No.: 0.000184 Length: 389
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61066 (1-389)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
Db 286 GAAGATAATGCTCAGAAATGTGGGTCTGTGTGTCGACT 327

RESULT 4
ABK45862/c

ID ABK45862 standard; cDNA; 444 BP.

XX AC ABK45862;

XX DT 05-JUN-2002 (first entry)

XX DE cDNA encoding colon tumour protein, SEQ ID No 1413.

XX KW Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
XX gene; ss.

XX OS Homo sapiens.

XX PN WO200212328-A2.

XX PD 14-FEB-2002.

XX PF 31-JUL-2001; 2001WO-US024218.

XX PR 03-AUG-2000; 2000US-0223283P.

XX PR 28-MAR-2001; 2001US-0279763P.

XX PR 29-JUN-2001; 2001US-0302051P.

XX PA (CORI-) CORIXA CORP.

XX PI King GE, Meagher MJ, Xu J, Secretist H;

XX DR WPI; 2002-241739/29.

XX PT New colon cancer polypeptides and polynucleotides, useful as vaccines,
XX for diagnosing, preventing, and treating colon cancer, and as markers for
XX the progression of cancer.

XX PS Claim 1; SEQ ID NO 1413; 147pp; English.

XX CC The invention relates to polynucleotides encoding colon tumour proteins.
XX The polynucleotides and encoded polypeptides are useful in pharmaceutical
XX compositions, such as vaccines, for the diagnosis, prevention, and
XX treatment of colon cancer. Polynucleotide sequences may be used as
XX hybridisation probes or primers, and in the design and preparation of
XX ribozyme molecules for inhibiting expression of tumour polypeptides and
XX proteins in tumour cells. The compositions are useful for stimulating an
XX immune response against cancer, particularly for the immunotherapy of

CC colon cancer, and as markers for the progression of cancer. ABK44450-
CC ABK46237 represent coding sequences of human colon tumour proteins of the
CC invention. Note: With the exception of SEQ ID No 1 and 2, the sequence
CC data for this patent did not form part of the printed specification but
CC was supplied by the European Patent Office

XX SQ Sequence 444 BP; 134 A; 81 C; 74 G; 155 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000215 Length: 444
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK45862 (1-444)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14

Db 436 GAAGATAATGCTCAGAAATGTGGGTCTGTGTGTCGACT 395

RESULT 5

AAS25071

ID AAS25071 standard; cDNA; 447 BP.

XX AC AAS25071;

XX DT 07-NOV-2001 (first entry)

XX DE Human ovarian PCR-subtracted cDNA library clone #1252.

XX KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
XX Gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
XX primer; probe.

XX OS Homo sapiens.

XX PN WO200157207-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003733.

XX PR 04-FEB-2000; 2000US-0180403P.

XX PR 28-MAR-2000; 2000US-0192745P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Mannion J;

XX DR WPI; 2001-488879/53.

XX PT New polynucleotides encoding ovarian tumor proteins, useful for treating
XX ovarian cancer, and as probes, primers, and markers of cancer
XX progression.

XX PS Example 1; Page 304; 378pp; English.

XX CC The invention comprises compositions used for the therapy and diagnosis
XX of ovarian cancer. The compositions comprise one or more ovarian tumour
XX proteins, their associated polynucleotides, or immunogenic portions of
XX the proteins. The ovarian tumour polynucleotides and polypeptides are
XX useful for stimulating and/or expanding T cells specific for a tumour
XX protein. They are also useful for inhibiting the development of cancer in
XX a patient with an ovarian tumour DNA or protein by incubating isolated T-
XX cells allowing them to proliferate, and administering to the patient. The
XX sequences can be used as markers for cancer, for example, to monitor
XX ovarian cancer progression. Probes and primers are useful in nucleic acid
XX hybridisation, in detecting the presence of complementary sequences in a
XX given sample, for preparing mutant species and for preparing other
XX genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
XX represent human ovarian tumour protein cDNA clones

```
XX SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 0.000217 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-736-250-5 (1-14) x AAS25071 (1-447)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 134
RESULT 6
AAH83716
ID AAH83716 standard; cDNA; 447 BP.
XX
AC AAH83716;
XX
DT 25-SEP-2001 (first entry)
XX
DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1340.
XX
KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
KW immunogenic; vaccine; ss.
XX
OS Homo sapiens.
XX
PN WO200151513-A2.
XX
PD 19-JUL-2001.
XX
PF 16-JAN-2001; 2001WO-US001575.
XX
PR 14-JAN-2000; 2000US-0176722P.
XX
PA (CORI-) CORIXA CORP.
XX
PI Algate PA;
XX
DR WPI; 2001-425866/45.
XX
PT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
XX treat and diagnose cancers, particularly ovarian cancer.
XX Claim 5; Page 308; 338pp; English.
XX
CC AAH82377 to AAH83878 represent human ovarian tumour-associated
CC polynucleotide sequences which encode ovarian tumour proteins. The
CC ovarian tumour protein and polynucleotide sequences have cytostatic
CC activity, and can be used in gene therapy and vaccine production. The
CC ovarian tumour proteins and polynucleotides can be used to inhibit the
CC development of cancer, particularly ovarian cancer. They can also be used
CC to diagnose the onset and progression of cancer
XX
SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;
Alignment Scores:
Pred. No.: 0.000217 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0
US-09-736-250-5 (1-14) x AAH83716 (1-447)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 134
RESULT 7
ADK61065/c
ID ADK61065 standard; DNA; 597 BP.
XX
AC ADK61065;
XX
DT 06-MAY-2004 (first entry)
XX
DE Ovarian cancer-related DNA #220 with altered ovarian cancer expression.
XX
KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
KW gene expression; primer; cancer.
XX
OS Homo sapiens.
XX
PN WO2003068054-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004688.
XX
PR 13-FEB-2002; 2002US-0357031P.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK ) SLOAN KETTERING INST CANCER RES.
XX
PI Jazaeri AA, Boyd J, Liu ET;
XX
DR WPI; 2003-689589/65.
XX
PT Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.
XX
PS Disclosure; SEQ ID NO 235; 137pp; English.
XX
CC The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 597 BP; 152 A; 126 C; 143 G; 171 T; 0 U; 5 Other;
Alignment Scores:
Pred. No.: 0.000304 Length: 597
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-736-250-5 (1-14) x ADK61065 (1-597)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 303 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 262
RESULT 8
AAX40003/c
ID AAX40003 standard; DNA; 804 BP.
XX
AC AAX40003;
```

XX	01-JUL-2004 (first entry)	
DT	Human cell growth, differentiation, and death-associated coding seq #15.	
DE	human; cell growth; cell differentiation; cell death; CGDD;	
DE	cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;	
KW	cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;	
KW	developmental disorder; Cushing's syndrome; hypothyroidism;	
KW	neurological disorder; epilepsy; stroke; Alzheimer's disease;	
KW	Pick's disease; Huntington's disease; Parkinson's disease;	
KW	multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;	
KW	allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;	
KW	reproductive disorder; infertility; endometriosis; uterine fibroid; gene;	
KW	ds.	
XX	Homo sapiens.	
OS		
XX	WO2004031364-A2.	
PN		
XX	15-APR-2004.	
PD		
XX	03-OCT-2003; 2003WO-US031441.	
PF		
XX	03-OCT-2002; 2002US-0416205P.	
PR		
XX	25-OCT-2002; 2002US-0421521P.	
PR		
XX	21-NOV-2002; 2002US-0428376P.	
PR		
XX	23-DEC-2002; 2002US-0436258P.	
PR		
XX	10-JAN-2003; 2002US-0439292P.	
PR		
XX	13-FEB-2003; 2003US-0447578P.	
PR		
XX	(INCY-) INCYTE CORP.	
PA	(BURR/) BURRILL J D.	
PA		
XX		
XX	Elllott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;	
PI	Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;	
PI	Tran UK, Bhatia UG, Lee S, Blake JU, Ho A, Zheng W, Gao J, Tran B;	
PI	Yang YG, Gietzen KJ, Hafalia AJA;	
PI		
XX	WPI: 2004-330172/30.	
DR	P-PSDB; ADN01131.	
DR		
XX		
XX	New isolated polypeptides associated with cell growth, differentiation	
PT	and death, useful for diagnosing, treating or preventing e.g.	
PT	atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anaemia,	
PT	diabetes mellitus or infertility.	
PT		
XX	Claim 5; SEQ ID NO 40; 213pp; English.	
PS		
XX		
CC	The invention comprises the amino acid and coding sequences of human	
CC	proteins that are associated with cell growth, differentiation, and death	
CC	(CGDD). The DNA and protein sequences of the invention are useful for	
CC	diagnosing, treating or preventing disorders associated with aberrant	
CC	expression of CGDD, such as: cell proliferative disorders (e.g.	
CC	arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,	
CC	polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.	
CC	Cushing's syndrome and hypothyroidism), neurological disorders (e.g.	
CC	epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's	
CC	disease, Parkinson's disease and multiple sclerosis),	
CC	autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,	
CC	contact dermatitis and diabetes mellitus), and reproductive disorders	
CC	(e.g. infertility, endometriosis and uterine fibroid). The present DNA	
CC	sequence encodes a human CGDD-associated protein of the invention.	
XX		
SQ	Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;	
	Alignment Scores:	
	Pred. No.:	Length: 903
	Score:	74.00
	Percent Similarity:	100.00%
	Best Local Similarity:	100.00%
	Query Match:	100.00%
	DB:	12
		Gaps: 0
		Indels: 0
		Mismatches: 0
		Conservative: 14
		Matches: 14

The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile

CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK83672 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAATGTGGGTCTGTGTGGCACT 1068
|||||

RESULT 12

ADK61064
ID ADK61064 standard; DNA; 1260 BP.

XX
AC ADK61064;

XX
DT 06-MAY-2004 (first entry)

XX
DE Ovarian cancer-related DNA #219 with altered ovarian cancer expression.

XX
KW ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;

XX
KW gene expression; primer; cancer.

XX
XX Homo sapiens.

XX
FN WO2003068054-A2.

XX
PD 21-AUG-2003.

XX
PF 13-FEB-2003; 2003WO-US004688.

XX
PR 13-FEB-2002; 2002US-0357031P.

XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX
PA (SLOK) SLOAN KETTERING INST CANCER RES.

XX
PI Jazaeri AA, Boyd J, Liu ET;

XX
XX WPI; 2003-689589/65.

XX
PT Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
PT several markers.

XX
PS Disclosure; SEQ ID NO 234; 137pp; English.

XX
XX The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a

CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61064 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAATGTGGGTCTGTGTGGCACT 1068
|||||

RESULT 13

AD131573

ID AD131573 standard; cDNA; 1260 BP.

XX
AC AD131573;

XX
DT 17-JUN-2004 (first entry)

XX
DE Human cDNA #899.

XX
KW Human; gene; ss; immunological response; immunopathological condition;
KW Crohn's disease; asthma; ulcerative colitis; hyper eosinophilia;

XX
KW irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;

XX
KW acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;

XX
KW osteopathic; antiarthritic; antirheumatic; cytostatic.

XX
OS Homo sapiens.

XX
FN US6607879-B1.

XX
PD 19-AUG-2003.

XX
PF 09-FEB-1998; 98US-00023655.

XX
PR 09-FEB-1998; 98US-00023655.

XX
PA (INCY-) INCYTE CORP.

XX
PI Cocks BG, Stuart SG, Seilhamer JJ;

XX
XX WPI; 2003-895307/82.

XX
PT A composition comprising a plurality of cDNAs, useful for detecting
PT altered expression of genes in an immunological response or for
PT diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
PT or osteoarthritis.

XX
PS Claim 1; SEQ ID NO 899; 50pp; English.

XX
CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under

CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hyperesinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensic or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x ADI31573 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGGTTCTGTGTGGCACT 1068

RESULT 14
ID ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX AC ADR25465;
XX 21-OCT-2004 (first entry)
XX Breast cancer prognosis marker #1326.
XX ds; breast cancer; prognosis; gene expression; diagnosis.
XX Homo sapiens.
XX WO2004065545-A2.
XX 05-AUG-2004.
XX 15-JAN-2004; 2004WO-US001100.
XX 15-JAN-2003; 2003US-00342887.
XX (ROSE-) ROSETTA INPHARMATICS LLC.
XX (NECA-) NETHERLANDS CANCER INST.
XX Van't Veer LJ, He Y;
XX WPI; 2004-593473/57.

Classifying a breast cancer patient according to prognosis comprises
determining the similarity between the level of expression of each of
five genes in a cell sample taken from patient, to control levels.
Disclosure; SEQ ID NO 1326; 226pp; English.

CC The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 0.000729 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x ADR25465 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTGGGTTCTGTGTGGCACT 1068

RESULT 15
ID AAT73937
ID AAT73937 standard; DNA; 1328 BP.
XX AC AAT73937;
XX 02-DEC-1997 (first entry)
XX DNA encoding human cyclin I.
XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.
XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 69..1202
XX /*tag= a
XX WO9712973-A1.
XX 10-APR-1997.
XX 07-OCT-1996; 96WO-JP002905.
XX 05-OCT-1995; 95JP-00284663.
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX Nakamura T;
XX WPI; 1997-226217/20.
XX P-PSDB; AAW21965.

Human cyclin I protein and related (anti:sense) DNA - used for neuron
labelling method and cancer cell detection.

Example 1; Fig 1; 45pp; Japanese.

This sequence encodes human cyclin I. Antisense polynucleotides are
useful for as probes and can be labelled and used for detection of
neurons by hybridisation with mRNA for cyclin I (contained in the
neurons and arising by the expression of the cyclin I gene in these
cells). The gene can be used for detection of cancer cells by detecting
the expression of the cyclin I gene in these cells. Also antibodies
specific for the fragments of the protein (especially AAW21966) can be
used for detection

```

XX
SQ Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      0.000775      Length:      1328
Score:          74.00         Matches:     14
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00%  Mismatches:  0
Query Match:      2          Indels:      0
DB:                2          Gaps:       0

US-09-736-250-5 (1-14) x AAT73937 (1-1328)

Qy      1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db      1095 GAAGATAATGTCACAAAAATGTGGGTTCTGTGTGTGGCACT 1136

Search completed: February 11, 2005, 03:41:49
Job time : 39.2327 secs

```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:24:00 ; Search time 11.2072 Seconds
(without alignments)
2044.039 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154924_20422/app_query.fasta_1.718
-DB=Issued Patents NA -QWMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pct -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250 @CEN 1 1 93 @runat_07022005_154924_20422 -NCPU=6 -ICPU=3
-NO.MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	1133	3	US-09-054-492B-2
2	74	100.0	1260	2	Sequence 2, Appli
3	74	100.0	1260	4	Sequence 5, Appli
4	74	100.0	1260	4	Sequence 338-125-5
5	69	93.2	304	4	Sequence 899, App
6	44	59.5	2080	4	Sequence 28894, A
7	44	59.5	5299	4	Sequence 7092, App
8	44	59.5	53165	4	Sequence 540-7092
9	43	58.1	601	4	US-09-214-808-1
10	43	58.1	601	4	Sequence 11, Appli
11	43	58.1	601	4	Sequence 17099, A
12	43	58.1	601	4	Sequence 164761, Sequence 164762,

c 13	58.1	601	4	US-09-949-016-164763	Sequence 164763,
14	58.1	2614	4	US-09-999-699A-3	Sequence 3, Appli
15	58.1	113042	4	US-09-949-016-12343	Sequence 12343, A
16	58.1	113042	4	US-09-949-016-15246	Sequence 15246, A
17	58.1	1136917	4	US-09-949-016-16369	Sequence 16369, A
18	56.8	601	4	US-09-949-016-187338	Sequence 187338,
19	56.8	601	4	US-09-949-016-187339	Sequence 187339,
20	56.8	601	4	US-09-949-016-187340	Sequence 187340,
21	56.8	78269	4	US-09-949-016-17099	Sequence 17099, A
22	56.8	78269	4	US-09-949-016-12497	Sequence 12497, A
23	56.8	392000	4	US-10-027-983-11	Sequence 11, Appl
24	55.4	601	4	US-09-949-016-68033	Sequence 68033, A
25	55.4	601	4	US-09-949-016-147945	Sequence 147945,
26	55.4	601	4	US-09-949-016-196181	Sequence 196181,
27	55.4	942	4	US-09-543-681A-1078	Sequence 1078, Ap
28	55.4	1128	4	US-09-270-767-14909	Sequence 14909, A
29	55.4	1938	4	US-09-270-767-12995	Sequence 12995, A
30	55.4	2061	1	US-08-472-028A-7	Sequence 7, Appli
31	55.4	2061	2	US-08-808-931-7	Sequence 7, Appli
32	55.4	2061	3	US-08-808-323-7	Sequence 7, Appli
33	55.4	2061	3	US-09-050-603A-7	Sequence 7, Appli
34	55.4	2061	3	US-09-102-420B-7	Sequence 7, Appli
35	55.4	2061	3	US-09-071-296-7	Sequence 7, Appli
36	55.4	2061	3	US-09-196-268-7	Sequence 7, Appli
37	55.4	2061	3	US-09-015-683-7	Sequence 7, Appli
38	55.4	2061	3	US-09-191-998-7	Sequence 7, Appli
39	55.4	2061	3	US-09-497-698-7	Sequence 7, Appli
40	55.4	2061	4	US-09-730-525-7	Sequence 7, Appli
41	55.4	2276	3	US-08-946-026-11	Sequence 11, Appl
42	55.4	2983	3	US-09-058-489-86	Sequence 86, Appl
43	55.4	4134	3	US-09-182-021B-1	Sequence 1, Appli
44	55.4	4134	3	US-09-687-477-17	Sequence 17, Appl
45	55.4	4134	4	US-09-687-476-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-054-492B-2
Sequence 2, Application US/09054492B
Patent No. 6218115
GENERAL INFORMATION:
APPLICANT: TAKESHI NAKAMURA
TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: PILLSBURY, MADISON & SUTRO
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,492B
FILING DATE: APRIL 3, 1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PAUL E. WHITE, JR.
REGISTRATION NUMBER: 32,011
REFERENCE/DOCKET NUMBER: 7898/252159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627CUSH
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1133
TYPE: nucleic acid

```

; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-492B-2
Alignment Scores:
Pred. No.: 2.83e-05 Length: 1133
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-736-250-5 (1-14) x US-09-054-492B-2 (1-1133)
QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
DB 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 2
US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-09-736-250-5
Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-969-106-5
QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
DB 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 3
US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-09-338-125-5
Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-338-125-5 (1-1260)
QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
DB 1027 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 1068

RESULT 4
US-09-023-655-899
```

Sequence 899, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023.655
FILING DATE: HERewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 899:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
CLONE: g1183161
US-09-023-655-899

Alignment Scores:
Pred. No.: 3.24e-05 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-023-655-899 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATATGTCACAGAAATGGGTTCTGTGTGGCACT 1068

RESULT 5
US-09-513-999C-29894
Sequence 29894, Application US/09513999C
Patent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513.999C

CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29894
LENGTH: 304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 231
OTHER INFORMATION: n-a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 268
OTHER INFORMATION: w-a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 5.23e-05 Length: 304
Score: 69.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.24% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-513-999C-29894 (1-304)

Qy 2 AspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 2 GATAATGTCACAGAAATGGGTTCTGTGTGGCACT 40

RESULT 6
US-09-902-540-7092
Sequence 7092, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 7092
LENGTH: 2080
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-7092

Alignment Scores:
Pred. No.: 65.2 Length: 2080
Score: 44.00 Matches: 8
Percent Similarity: 75.00% Conservative: 1
Best Local Similarity: 66.67% Mismatches: 3
Query Match: 59.46% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-902-540-7092 (1-2080)

Qy 2 AspAsnValSerGluAsnValGlySerValCysGly 13
Db 649 GACAACGTGGCGACAAACGTGGGTGACGTGCCGCG 684

1

US-09-736-250-5 (1-14) x US-09-949-016-124453 (1-601)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 325 GAAGATTCAATGAATGAACGTAAGTAGTTGTGC 360

RESULT 11

US-09-949-016-164761/c
; Sequence 164761, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164761
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164761

Alignment Scores:
Pred. No.: 20.9 Length: 601
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164761 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 437 CAGAGCAACTGCAGCCAGAAATCTGGGTTCAGTATGC 402

RESULT 12

US-09-949-016-164762/c
; Sequence 164762, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164762
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164762

Alignment Scores:
Pred. No.: 20.9 Length: 601

Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164762 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 96 CAGAGCAACTGCAGCCAGAAATCTGGGTTCAGTATGC 61

RESULT 13

US-09-949-016-164763/c
; Sequence 164763, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164763
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-164763

Alignment Scores:
Pred. No.: 20.9 Length: 601
Score: 43.00 Matches: 7
Percent Similarity: 83.33% Conservative: 3
Best Local Similarity: 58.33% Mismatches: 2
Query Match: 58.11% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-164763 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCys 12
Db 84 CAGAGCAACTGCAGCCAGAAATCTGGGTTCAGTATGC 49

RESULT 14

US-09-999-699A-3
; Sequence 3, Application US/09999699A
; Patent No. 6794139
; GENERAL INFORMATION:
; APPLICANT: SCHIEMANN, Sabine
; APPLICANT: WEIDLE, Ulrich
; TITLE OF INVENTION: BREAST CARCINOMA-ASSOCIATED GENE
; FILE REFERENCE: 20221US1
; CURRENT APPLICATION NUMBER: US/09/999,699A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: PCT/EP97/04785
; PRIOR FILING DATE: 1997-09-02
; PRIOR APPLICATION NUMBER: EP 96114098.5
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: US 09/254,129
; PRIOR FILING DATE: 2002-05-12
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 2614
; TYPE: DNA
; ORGANISM: Murinae gen. sp.

```
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (90)..(569)
US-09-999-699A-3

Alignment Scores:
Pred. NO.:      139      Length:      2614
Score:          43.00    Matches:      9
Percent Similarity: 52.17% Conservative: 3
Best Local Similarity: 39.13% Mismatches: 1
Query Match:      58.11% Indels:      10
DB:               4      Gaps:       1

US-09-736-250-5 (1-14) x US-09-999-699A-3 (1-2614)

Qy      1 GluAepAenValSerGluAenValGlySer----- 10
Db      1377 GATGATATATGCTCACAAACATAGGTCAAAGCATATGCCACCGCAGTGCTATAGTAA 1436

Qy      11 ValCysGly 13
Db      1437 GTTTGTGGG 1445

RESULT 15
US-09-949-016-12343
; Sequence 12343, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12343
; LENGTH: 113042
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12343

Alignment Scores:
Pred. NO.:      1.79e+04      Length:      113042
Score:          43.00    Matches:      7
Percent Similarity: 91.67% Conservative: 4
Best Local Similarity: 58.33% Mismatches: 1
Query Match:      58.11% Indels:      0
DB:               4      Gaps:       0

US-09-736-250-5 (1-14) x US-09-949-016-12343 (1-113042)

Qy      1 GluAepAenValSerGluAenValGlySerValCys 12
Db      101983 GAAGATTCAATGAATGAACGTAAGTAGTTGTGC 102018

Search completed: February 11, 2005, 07:42:13
Job time : 41.2072 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model
Run on: February 11, 2005, 05:55:30 ; Search time 59.9028 Seconds
(without alignments)
1379.008 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 74
Sequence: 1 EDVSENVGSVCGT 14

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Total number of hits satisfying chosen parameters: 10757346

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_spool/US09736250/runat 07022005 154926 20490/app query.fasta_1.718
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloums62
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09736250 @CGN 1 1 582 @runat 07022005 154926 20490
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
12: /cgn2_6/ptodata/1/pubpna/US09A_NEW_PUB.seq*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	288	17	US-10-242-535A-57578
2	74	100.0	288	17	US-10-085-783A-57578
3	74	100.0	350	17	US-10-242-535A-20816
4	74	100.0	350	17	US-10-085-783A-20816
c 5	74	100.0	444	9	US-09-920-300A-1413
c 6	74	100.0	444	13	US-10-033-528-1413
c 7	74	100.0	444	16	US-10-099-926-1413
8	74	100.0	447	9	US-09-777-564-1252
9	74	100.0	447	14	US-10-015-219-1252
10	74	100.0	1134	12	US-09-736-250-2
11	74	100.0	1260	17	US-10-172-118-1326
12	74	100.0	1260	17	US-10-342-887-1326
13	74	100.0	1260	17	US-10-641-643-899
14	74	100.0	1889	9	US-09-867-701-10907
15	74	100.0	2145	10	US-09-814-353-21294
16	74	100.0	2755	10	US-09-814-353-21586
17	70	94.6	308	17	US-10-242-535A-41781
18	70	94.6	308	17	US-10-085-783A-41781
19	65	87.8	420	9	US-09-960-352-9810
20	49	66.2	200	17	US-10-242-535A-5568
21	49	66.2	200	17	US-10-085-783A-5568
c 22	46	62.2	293	18	US-10-723-860-2410
c 23	46	62.2	401	17	US-10-242-535A-3486
c 24	46	62.2	401	17	US-10-085-783A-3486
c 25	46	62.2	474	17	US-10-242-535A-57273
c 26	46	62.2	474	17	US-10-085-783A-57273
c 27	46	62.2	564	10	US-09-284-320-37
c 28	46	62.2	601	18	US-10-021-323-14955
c 29	46	62.2	798	18	US-10-767-795-6476
c 30	46	62.2	1110	18	US-10-842-740-40
c 31	46	62.2	1138	18	US-10-357-930-22723
c 32	46	62.2	1138	18	US-10-357-930-28570
c 33	46	62.2	1186	10	US-09-284-320-62
c 34	46	62.2	1264	14	US-10-028-072-1
c 35	46	62.2	1264	14	US-10-140-808-1
c 36	46	62.2	1264	14	US-10-121-049-1
c 37	46	62.2	1264	14	US-10-123-904-1
c 38	46	62.2	1264	14	US-10-140-470-1
c 39	46	62.2	1264	14	US-10-175-746-1
c 40	46	62.2	1264	14	US-10-176-918-1
c 41	46	62.2	1264	14	US-10-137-865-1
c 42	46	62.2	1264	14	US-10-140-474-1
c 43	46	62.2	1264	14	US-10-142-431-1
c 44	46	62.2	1264	14	US-10-143-114-1
c 45	46	62.2	1264	14	US-10-143-114-1

ALIGNMENTS

RESULT 1
US-10-242-535A-57578
; Sequence 57578, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR FILING DATE: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994

; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57578

Alignment Scores:
Pred. No.: 4.01e-05 Length: 288
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-57578 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 104

RESULT 2

US-10-085-783A-57578
; Sequence 57578, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-57578

Alignment Scores:
Pred. No.: 4.01e-05 Length: 288
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-57578 (1-288)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 104

RESULT 3

US-10-242-535A-20816
; Sequence 20816, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28

; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-20816

Alignment Scores:
Pred. No.: 5.03e-05 Length: 350
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 170

RESULT 4

US-10-085-783A-20816
; Sequence 20816, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-20816

Alignment Scores:
Pred. No.: 5.03e-05 Length: 350
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 170

RESULT 5

US-09-920-300A-1413/c
; Sequence 1413, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.

```

; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-099-926-1413

Alignment Scores:
Pred. No.: 5.63e-05 Length: 444
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-736-250-5 (1-14) x US-10-099-926-1413 (1-444)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
DB 436 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 395
|||||

RESULT 8
US-09-777-564-1252
; Sequence 1252, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: Fast-SEQ for Window Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1252

Alignment Scores:
Pred. No.: 6.69e-05 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-777-564-1252 (1-447)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
DB 93 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 134
|||||

RESULT 9
US-10-015-219-1252
; Sequence 1252, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:

```

; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493C1
; CURRENT APPLICATION NUMBER: US/10/015,219
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 1739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 424, 428, 437, 440
; OTHER INFORMATION: n = A,T,C or G
US-10-015-219-1252

Alignment Scores:
Pred. No.: 6.69e-05 Length: 447
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0
US-09-736-250-5 (1-14) x US-10-015-219-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 134

RESULT 10

US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; PRIOR FILING DATE: 1995-10-05
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 0.000197 Length: 1134
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-5 (1-14) x US-09-736-250-2 (1-1134)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 1068

RESULT 11

US-10-172-118-1326

; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 0.000223 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0
US-09-736-250-5 (1-14) x US-10-172-118-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 1068

RESULT 12

US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1326

Alignment Scores:
Pred. No.: 0.000223 Length: 1260

Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-342-887-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1027 GAAGATAATGCTCAGAAATGTTGGTCTCTGTGTGGCACT 1068
|||||

RESULT 13
US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :
US-10-641-643-899

Alignment Scores:
Pred. No.: 0.000223 Length: 1260
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-641-643-899 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||

Db 1027 GAAGATAATGCTCAGAAATGTTGGTCTCTGTGTGGCACT 1068
|||||

RESULT 14
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907

Alignment Scores:
Pred. No.: 0.000356 Length: 1889
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-867-701-10907 (1-1889)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 1570 GAAGATAATGCTCAGAAATGTTGGTCTCTGTGTGGCACT 1611
|||||

RESULT 15
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294

Alignment Scores:
Pred. No.: 0.000413 Length: 2146

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x US-09-814-353-21294 (1-2146)

QY 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 1213 GAAGATATATGCTCAGAAAATGTGGTCTCTGTGTGGCACT 1254

Search completed: February 11, 2005, 10:20:38
 Job time : 61.9028 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 03:23:50 ; Search time 218.235 Seconds
(without alignments)
2441.859 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 74

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO/US09736250/runat 07022005 154924 20414/app query.fasta_1.718
-DB-EST_QFMT-fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250 -CGN 1 1 4385 @runat 07022005 154924 20414 -NCPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hsc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	136	7	Z20123
2	74	100.0	139	1	A2678060
3	74	100.0	139	1	AA094874
4	74	100.0	197	1	AA659220
5	74	100.0	234	1	AA058781
6	74	100.0	246	4	BG180306
7	74	100.0	251	5	BQ327548
8	74	100.0	251	5	BQ327560
9	74	100.0	265	7	R85184

C 10	74	100.0	269	1	AA680208
C 11	74	100.0	275	1	AA011113
C 12	74	100.0	278	1	AA0778982
C 13	74	100.0	296	7	F32546
C 14	74	100.0	302	4	BI493342
C 15	74	100.0	302	7	N84129
C 16	74	100.0	321	7	R87368
C 17	74	100.0	323	2	BE245492
C 18	74	100.0	325	1	AI383113
C 19	74	100.0	328	2	BE675114
C 20	74	100.0	331	2	BF109323
C 21	74	100.0	340	2	AW993907
C 22	74	100.0	340	4	BI491010
C 23	74	100.0	340	7	R83731
C 24	74	100.0	341	1	AA055821
C 25	74	100.0	341	2	AW019986
C 26	74	100.0	341	5	BM894061
C 27	74	100.0	343	2	BF901867
C 28	74	100.0	344	1	AI735109
C 29	74	100.0	346	7	H80782
C 30	74	100.0	347	1	AA248313
C 31	74	100.0	347	6	CB135564
C 32	74	100.0	348	1	AA018692
C 33	74	100.0	348	4	BG943235
C 34	74	100.0	348	5	BM894332
C 35	74	100.0	349	1	AI857246
C 36	74	100.0	350	1	AA730298
C 37	74	100.0	350	7	R88164
C 38	74	100.0	351	2	AW225340
C 39	74	100.0	352	2	BE539946
C 40	74	100.0	352	7	H38301
C 41	74	100.0	353	1	AA558174
C 42	74	100.0	357	7	H84151
C 43	74	100.0	357	7	N45919
C 44	74	100.0	358	2	AW408405
C 45	74	100.0	358	6	CD678566

ALIGNMENTS

RESULT 1

LOCUS	Z20123	136 bp	mrna	linear	EST 07-FEB-1995
DEFINITION	HSAAABALIE P, Human foetal Brain Whole tissue Homo sapiens CDNA,				
ACCESSION	Z20123				
VERSION	Z20123.1	GI:26868			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 136)				
AUTHORS	MRC Human Genome Mapping Project Resource Centre.				
TITLE	The UK-HGMP CDNA program				
JOURNAL	Unpublished (1993)				
COMMENT	Contact: MRC Human Genome Mapping Project Resource Centre Clinical Research Centre Watford Road, Harrow, Middlesex HA1 3UJ, U.K. Email: biohelp@hgm.mrc.ac.uk single read.				
FEATURES	Location/Qualifiers				
source	1. .136				
	/organism="Homo sapiens"				
	/mol_type="mrna"				
	/db_xref="taxon:9606"				
	/clone_lib="P, Human foetal Brain Whole tissue"				
	/notes="vector: Bluescript; clone_library=P, Human foetal Brain Whole tissue; cloning vector is Bluescript."				

ORIGIN

Alignment Scores: 0.000573 Length: 136
Pred. No.: 136

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x Z20123 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 24 GAAGATAATGTCCTCAGAAATGCGGTCTCTGTGTGGCACT 65

RESULT 2

AA678060/c
 LOCUS AA678060 139 bp mRNA linear EST 19-DEC-1997
 DEFINITION z125f08.s1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA
 clone IMAGE:431847 3' similar to TR:G1183162 G1183162 CYCLIN I. ;
 mRNA sequence.

ACCESSION AA678060.1 GI:2658582

VERSION AA678060

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisels, G., Jost, S.,
 Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
 Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
 Theising, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R.
 WashU-NCI human EST Project
 Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LNL ; contact the

IMAGE Consortium (info@image.lnl.gov) for further information.

Possible reversed clone: similarity on wrong strand

Seq primer: -40m3 fwd. ET from Amer-sham

High quality sequence status: 1.

FEATURES

source

1..139
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:431847"
 /sex="male"
 /dev_stage="20 week-post conception fetus"
 /lab_host="DH10B (ampicillin resistant)"
 /clone_lib="Soares fetal liver spleen INFLS S1"
 /note="Organ: Liver and Spleen; Vector: p773D (Pharmacia)
 with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
 This is a subtracted version of the original Soares fetal
 liver spleen INFLS library. 1st strand cDNA was primed
 with a Pac I - oligo(dT) primer [5'
 RACTGGAGATTATTAAAGATCTTTTCTTTTCTTTT 3']
 double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with Pac I and cloned into the Pac I
 and Eco RI sites of the modified p773 vector. Library
 went through one round of normalization. Library
 constructed by Bento Soares and M.Patima Bonaldo."

ORIGIN

Alignment Scores:
 Pred. No.: 0.000587 Length: 139
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA678060 (1-139)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 103 GAAGATAATGTCCTCAGAAATGCGGTCTCTGTGTGGCACT 62

RESULT 3

LOCUS

AA094874
 DEFINITION cp2090.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens
 cDNA 5', mRNA sequence.

ACCESSION AA094874.1 GI:1640491

VERSION AA094874

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Liew, C.C.

CDNAs from fetal heart (1996)

Unpublished (1996)

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliew@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCCAAGCTCGAATTAACCCCTCACTAAAGG 3'

BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGCG 3'

Seq primer: 5' GAAATTAACCCCTCACTAAAGG 3'.

FEATURES

source

1..139
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /lab_host="E. coli XL1-Blue"
 /clone_lib="Human fetal heart, Lambda ZAP Express"
 /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:
 XhoI; mRNA was purified from human fetal hearts (8-10
 weeks). cDNA was synthesized using a XhoI-Oligo dT
 adaptor-primer. EcoRI adaptors were ligated, followed by
 digestion with XhoI, for directional cloning into
 predigested lambda ZAP Express."

ORIGIN

Alignment Scores:
 Pred. No.: 0.000587 Length: 139
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA094874 (1-139)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 50 GAAGATAATGTCCTCAGAAATGCGGTCTCTGTGTGGCACT 91

RESULT 4

LOCUS

AA659220
 DEFINITION nt92c11.s1 NCI CGAP Pr12 Homo sapiens cDNA clone IMAGE:1205972
 similar to TR:G1183162 G1183162 CYCLIN I. ; mRNA sequence.

ACCESSION

AA659220

VERSION AA659220.1 GI:2595374

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Email: cgapbs@mail.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LAM10189 row: c column: 13
 High quality sequence stop: 243.
 Location/Qualifiers
 1. 246
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:4432452"
 /tissue_type="adenocarcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_91"
 /note="Organ: prostate; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.4 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 0.00112 Length: 246
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BG180306 (1-246)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 44 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 85

RESULT 7

BQ327548

LOCUS BQ327548 251 bp mRNA linear EST 17-MAY-2002

DEFINITION

CMO-RT0017-211100-702-e07 RT0017 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BQ327548

VERSION

BQ327548.1 GI:20944770

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBLISHED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(<http://www.ludwig.org.br/scripts/gethtml2.pl?t1=CM0&t2=CM0-RT0017-211100-702-e07&t3=2000-11-21&t4=1>)
 Seq primer: puc 18 forward
 High quality sequence start: 7
 High quality sequence stop: 25.
 Location/Qualifiers
 1. 251
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_lib="RT0017"
 /note="Organ: kidney tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORGSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

FEATURES

source

ORIGIN

Alignment Scores:
 Pred. No.: 0.00114 Length: 251
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327548 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 |||||
 Db 163 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 204

RESULT 8

BQ327560

LOCUS BQ327560 251 bp mRNA linear EST 17-MAY-2002

DEFINITION

CMO-RT0017-221100-705-e07 RT0017 Homo sapiens cDNA, mRNA sequence.

ACCESSION

BQ327560

VERSION

BQ327560.1 GI:20944806

EST.

KEYWORDS

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

20202663

PUBLISHED

10737800

COMMENT

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

FEATURES
source

Location/Qualifiers
1..251
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="RT0017"
/note="Organ: kidney_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Alignment Scores:
Pred. No.: 0.00114 Length: 251
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 5 Gaps: 0

US-09-736-250-5 (1-14) x BQ327560 (1-251)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
|||||
Db 163 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 204
|||||

RESULT 9
R85184/c

LOCUS R85184 265 bp mRNA linear EST 14-AUG-1995
DEFINITION yo43f02.x1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180699 5', mRNA sequence.

ACCESSION
R85184

VERSION R85184.1 GI:943590

KEYWORDS
EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

TITLE
The WashU-Merck EST Project

JOURNAL

COMMENT

Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1058

High quality sequence stops: 220

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1058 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 220.

FEATURES

source

Location/Qualifiers
1..265
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3827349"
/db_xref="taxon:9606"
/clone="IMAGE:180699"
/sex="Male"
/dev_stage="55-year old"

/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares adult brain N2b4HB55Y"

/note="Organ: brain; Vector: p773D (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGAGCGCGCGCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified p773 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 53. Library constructed by Bento
Soares and M.Fatima Bonaldo. The adult brain RNA was
provided by Dr. Donald H. Gilden. Tissue was acquired
17-18 hours after death which occurred in consequence of a
ruptured aortic aneurysm. RNA was prepared from a pool of
tissues representing the following areas of the brain:
frontal, parietal, temporal and occipital cortex from the
left and right hemispheres, subcortical white matter,
basal ganglia, thalamus, cerebellum, midbrain, pons and
medulla."

ORIGIN

Alignment Scores:
Pred. No.: 0.00121 Length: 265
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x R85184 (1-265)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
|||||
Db 234 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 193
|||||

RESULT 10

AA680208/c

LOCUS

DEFINITION

ac82dl1.s1 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:869109 3' similar to TR:G1183162 G1183162 CYCLIN I. ;, mRNA
sequence.

ACCESSION
AA680208

VERSION AA680208.1 GI:2656176

KEYWORDS
EST.

SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.

TITLE
WashU-NCI human EST Project

JOURNAL

COMMENT

Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham

High quality sequence stop: 215.

FEATURES

source

Location/Qualifiers
1..269
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:869109"

```

/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/notes="Organ: lung; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo dt. normal lung. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGCAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 0.00123 Length: 269
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA680208 (1-269)

Qy 1 GluspaenValSerGluAsnValGlySerValCysGlyThr 14
Db 116 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 75

RESULT 11
LOCUS AA011113 275 bp mRNA linear EST 29-JUL-1996
DEFINITION ze34d03.r1 Soares retina N2b4HR Homo sapiens cDNA clone
IMAGE:360869 5', mRNA sequence.
ACCESSION AA011113.1 GI:1472160
VERSION AA011113.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 275)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Ellison,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Travaskis,E., Waterston,R., Williamson,A., Woldmann,P. and
Wilson,R.
The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: mob.REG+ET
High quality sequence stop: 165.
Location/Qualifiers
1..275
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1277414"
/db_xref="taxon:9606"
/clone="IMAGE:360869"
/sex="male"
/tissue_type="retina"
/dev_stage="55 years old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N2b4HR"
/notes="Organ: eye; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dt) primer (5'
TGTTACCATCTGAGTGGAGCGCGCGCTTTTTTTTTTTTTTTT 3'),
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into

```

```

the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). The retinas were obtained from a 55 year old
Caucasian and total cellular poly(A)+ RNA was extracted 6
hrs after their removal. The retina RNA was kindly
provided by Roderick R. McInnes M.D. Ph.D. from the
University of Toronto. Library constructed by Bento
Soares and M.Fatima Bonaldo. "

ORIGIN
Alignment Scores:
Pred. No.: 0.00127 Length: 275
Score: 74.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA011113 (1-275)

Qy 1 GluspaenValSerGluAsnValGlySerValCysGlyThr 14
Db 234 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 193

RESULT 12
LOCUS AA778982/c
DEFINITION AA778982 278 bp mRNA linear EST 05-FEB-1998
ACCESSION AA778982.1 GI:2838313
VERSION AA778982.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 278)
AUTHORS Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M.,
Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 177.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:858661"
/dev_stage="hnt neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hnt neuron (#937233)"
/notes="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dt.
Differentiated, post mitotic hnt neurons. Average insert
size: 1.5 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'
GAATTCGGCAGCAG 3' -3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN
Alignment Scores:
Pred. No.: 0.00128 Length: 278

```

Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA778982 (1-278)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 188 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 147

RESULT 13

LOCUS F32546 HSPD25369 HM3 Homo sapiens cDNA clone s3000040A06, mRNA sequence.
 DEFINITION F32546
 ACCESSION F32546
 VERSION F32546.1 GI:4818172
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 296)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Lanfranchi, G., Muraro, T., Caldara, F., Pacchioni, B., Pallavicini, A.,
 Pandolfo, D., Toppo, S., Trevisan, S., Scarso, S. and Valle, G.
 TITLE Identification of 4370 expressed sequence tags from a
 3'-end-specific cDNA library of human skeletal muscle by DNA
 sequencing and filter hybridization
 JOURNAL Genome Res. 6 (1), 35-42 (1996)
 MEDLINE 96276048
 PUBMED 8681137

COMMENT Contact: Valle G.
 CRIBI Biotechnology Centre
 University of Padua
 Via Trieste 75, 35121 Padua, Italy
 ABI Chromatograms and other information are available on WWW at
 http://grup.bio.unipd.it.

FEATURES
 source
 Location/Qualifiers
 1..296

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="s3000040A06"
 /sex="female"
 /tissue_type="pectoral muscle (after mastectomy)"
 /clone_lib="HM3"
 /note="Vector: pCDNAII (Invitrogen); Site 1: BstXI;
 Site 2: NotI; The library was constructed by G.
 Lanfranchi. This library is not subtracted nor normalized.
 The first strand cDNA was primed with a biotinylated
 oligo-dT-NotI primer
 (5'-biotin-AACCGCTCGAGCGCGCTTTTCTTTTCTTTT-3'). The
 ds cDNA was sonicated and size-selected in the range
 350-550 bp. The 3' specific fragments were selected by
 streptavidin coated magnetic beads, ligated to
 non-palindromic BstXI adapters, NotI digested and
 directionally cloned into BstXI-NotI cut pCDNAII vector."

ORIGIN

Alignment Scores:
 Pred. No.: 0.00137 Length: 296
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x F32546 (1-296)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 82 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 123

RESULT 14

BI493342/c

LOCUS BI493342

DEFINITION df100a06.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
 IMAGE:2540459 3', mRNA sequence.
 ACCESSION BI493342.1 GI:15332686
 VERSION BI493342.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 302)
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R.
 and Morton, C.C.
 TITLE Isolation of novel and known genes from a human fetal cochlear cDNA
 library using subtractive hybridization and differential screening
 JOURNAL Genomics 23, 42-50 (1994)
 MEDLINE 95130111
 PUBMED 7829101

COMMENT Contact: Morton, C. C.
 Departments of Pathology and Obstetrics, Gynecology and
 Reproductive Biology
 Brigham and Women's Hospital
 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
 Tel: 617 732 7980
 Fax: 617 738 6996
 Email: cmorton@rics.bwh.harvard.edu
 DNA sequencing and analyses were performed by National Institutes
 of Health Intramural Sequencing Center (NISC; see
 http://www.nisc.nih.gov).
 This clone is available royalty-free through LLNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Plate: LIAM6328 row: B column: 12
 Seq primer: T7 primer.

FEATURES
 source
 Location/Qualifiers
 1..302

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2540459"
 /tissue_type="cochlea"
 /dev_stage="16-22 week fetus"
 /lab_host="SOLR cells (kanamycin resistant)"
 /clone_lib="Morton Fetal Cochlea"
 /note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;
 Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned
 unidirectionally. Primer: Oligo df. Fetal cochlea, normal.
 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP
 XR Vector. Library constructed by N. Robertson, C. Morton.
 -5' adaptor sequence: 5' GAATTGGCAGCG 3' -3' adaptor
 sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'"

ORIGIN

Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservatives: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x BI493342 (1-302)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
 |||||
 Db 259 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 218

RESULT 15

N84129

LOCUS N84129

DEFINITION KK6088F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA

clone KK6088 5' similar to EST (VP97B03.S1), mRNA sequence.

ACCESSION N84129
 VERSION N84129.1 GI:1259754
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 302)
 AUTHORS Liew, C.C.
 TITLE cDNAs from fetal heart (1996)
 JOURNAL Unpublished (1996)
 COMMENT Contact: Liew CC
 Brigham and Women's Hospital
 Harvard Medical School
 75 Francis St., Boston, MA 02115, USA
 Tel: 6177328915
 Fax: 6179750995
 Email: cliew@rics.bwh.harvard.edu
 Seq primer: GAAATTAACCTCACTAAAGG.

FEATURES
 source
 1..302
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="KK6088"
 /lab_host="E. coli XL1-Blue"
 /clone_lib="Human fetal heart, Lambda ZAP Express"
 /note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2: XhoI; mRNA was purified from human fetal hearts (8-10 weeks). cDNA was synthesized using a XhoI-Oligo dt adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into predigested lambda ZAP Express."

ORIGIN

Alignment Scores:
 Pred. No.: 0.00141 Length: 302
 Score: 74.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 7 Gaps: 0
 US-09-736-250-5 (1-14) x N84129 (1-302)
 Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 Db 50 GAAGATAATGTCAGAAAATGGGGTCTGTGTGGCACT 91

Search completed: February 11, 2005, 07:36:35
 Job time : 225.235 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:05:54 ; Search time 3.93862 Seconds
(without alignments)
1374.757 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:
OLIGO
Gapex 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	100.0	14	2	AAW21966 Human cyc
2	14	100.0	300	8	ADN01131 Human cel
3	14	100.0	334	7	AAE37938 Human CGD
4	14	100.0	377	2	AAW21965 Human cyc
5	14	100.0	377	3	AAW52185 Human cyc
6	14	100.0	377	6	ABR39934 Human pro
7	14	100.0	377	8	ADP12615 Protein e
8	14	100.0	377	8	ABM80569 Tumour-as
9	7	50.0	446	5	ADP35708 Fungal ZB
10	7	50.0	446	8	ADJ93495 RDS2. 5/2
11	7	50.0	556	4	ABB69870 Drosophil
12	7	50.0	1068	6	ABP78187 N. gonorr
13	7	50.0	1190	8	ADS29513 Bacterial
14	6	42.9	13	2	AAW74214 Internal
15	6	42.9	63	4	ABG23791 Novel hum
16	6	42.9	63	4	AAW29530 Human cyc
17	6	42.9	81	5	ABP42754 Human Cr2
18	6	42.9	118	5	ABB49682 Listeria
19	6	42.9	169	8	ADS28328 Bacterial
20	6	42.9	194	4	ABB65029 Drosophil
21	6	42.9	219	6	ADA54813 Human pro
22	6	42.9	224	5	ABU05664 M. tuberc
23	6	42.9	231	8	ADN23823 Bacterial
24	6	42.9	233	5	ABB49740 Listeria
25	6	42.9	233	6	ABU32874 Protein e

26	6	42.9	248	3	AAG10786 Arabidops
27	6	42.9	249	3	AAG47125 Arabidops
28	6	42.9	260	3	AAG47124 Arabidops
29	6	42.9	260	3	AAG10785 Arabidops
30	6	42.9	278	6	AAO16277 Human CD2
31	6	42.9	282	2	AAW74217 Bryodin-2
32	6	42.9	310	3	AAV53037 Human sec
33	6	42.9	330	8	ADO41954 Human CD5
34	6	42.9	334	8	ADO41950 Human CR2
35	6	42.9	381	5	ABB49806 Listeria
36	6	42.9	381	6	ABU32409 Protein e
37	6	42.9	383	7	ADM25476 Hyperther
38	6	42.9	419	4	AAW75602 Human sec
39	6	42.9	419	4	AAW75601 Gene 45 h
40	6	42.9	456	4	ABG21589 Novel hum
41	6	42.9	495	8	ADO41948 Human CR2
42	6	42.9	510	8	ADO41963 Human CR2
43	6	42.9	518	8	ADO41952 Human DAF
44	6	42.9	603	6	ABU20315 Protein e
45	6	42.9	634	6	ABU20978 Protein e
46	6	42.9	709	8	ADI40865 Human kin
47	6	42.9	721	8	ADI40866 Human kin
48	6	42.9	732	4	AAW67574 Amino aci
49	6	42.9	733	7	ABM85399 Human pro
50	6	42.9	745	6	ABR41368 Human DIT
51	6	42.9	785	8	ADN72669 Thale cre
52	6	42.9	794	5	ABBS7307 Mouse lsc
53	6	42.9	794	7	ADD48931 Rat Prote
54	6	42.9	794	7	ADD47982 Rat Prote
55	6	42.9	794	7	ADD47984 Human pro
56	6	42.9	794	7	ADD48933 Human pro
57	6	42.9	794	8	ADQ39213 Human myo
58	6	42.9	819	4	ABG13725 Novel hum
59	6	42.9	875	6	ABU24883 Protein e
60	6	42.9	884	6	ABU25371 Protein e
61	6	42.9	890	6	ABU25357 Protein e
62	6	42.9	892	8	ADO62059 Transcrip
63	6	42.9	1033	7	ADM67538 Human Ly1
64	6	42.9	1033	8	ADI05797 Human com
65	6	42.9	1033	8	ADO41968 Human com
66	6	42.9	1033	8	ADO41971 Human com
67	6	42.9	1033	8	ADP56042 Human PRO
68	6	42.9	1048	4	ABBS9245 Drosophil
69	6	42.9	1066	4	AAW67418 Amino aci
70	6	42.9	1066	6	ABG72693 Fruit fly
71	6	42.9	1066	7	ADG98862 Fruit fly
72	6	42.9	1084	8	ADM90837 Human pha
73	6	42.9	1087	2	AAW11139 B lymphoc
74	6	42.9	1367	4	ABG25023 Novel hum
75	6	42.9	1415	7	ABO77692 Pseudomon
76	6	42.9	2520	8	ADN11586 Human CD9
77	6	42.9	2565	8	ADN11585 Human CD9
78	6	42.9	3029	8	ADP25433 Plasmodiu
79	6	42.9	4183	7	ABM85419 Human pro
80	6	42.9	4419	8	ADN11590 Human CD9
81	6	42.9	4419	8	ADN11588 Human CD9
82	6	42.9	4464	8	ADN11587 Human CD9
83	6	42.9	4464	8	ADN11589 Human CD9
84	6	42.9	4529	5	AAU81016 Mouse alp
85	6	42.9	4544	2	AAW47861 Alpha 2-M
86	6	42.9	4544	2	AAW60517 Human alp
87	6	42.9	4544	4	AAW79091 Human pro
88	6	42.9	4544	5	AAU81019 Human alp
89	6	42.9	4544	6	ABP56839 Human LRP
90	6	42.9	4544	6	ABU89744 Protein d
91	6	42.9	4544	7	ADD14025 Human src
92	6	42.9	4544	8	ADI27167 Human LRP
93	6	42.9	4544	8	ADL15636 Human lip
94	6	42.9	4544	8	ADN11584 Human CD9
95	6	42.9	4545	5	AAU74797 Mouse alp
96	6	42.9	4545	8	ADI27166 Mouse LRP
97	6	42.9	4545	8	ADI27170 Mouse LRP
98	6	42.9	4545	8	ADT49882 Murine LR

99	6	42.9	4563	4	ABBI1353	Abbi1353 Human LDL	172	5	35.7	68	5	ABR04908	Abb04908 LRPB huma
100	6	42.9	4599	6	ABP56837	Abp56837 Human LRP	173	5	35.7	70	5	ABG44988	Abg44988 Human pep
101	6	42.9	4599	8	ADI27168	Adi27168 Mouse LRP	174	5	35.7	70	7	ADC94966	Adc94966 E. faeciu
102	6	42.9	4599	8	ADI27169	Adi27169 Mouse LRP	175	5	35.7	70	7	ADC94965	Adc94965 E. faeciu
103	6	42.9	4636	4	AAE11937	AAe11937 Human CG1	176	5	35.7	77	3	AGG1601	Agg1601 Arabidops
104	6	42.9	4636	8	ADS10474	AdS10474 Human the	177	5	35.7	77	3	AGG15499	Agg15499 Arabidops
105	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	178	5	35.7	77	4	AAU47724	Aau47724 Propionib
106	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	179	5	35.7	77	4	AAU47724	Aau47724 Propionib
107	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	180	5	35.7	78	4	AAU47171	Aau47171 Propionib
108	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	181	5	35.7	78	4	AAU47171	Aau47171 Propionib
109	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	182	5	35.7	78	4	AAU47171	Aau47171 Propionib
110	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	183	5	35.7	79	6	ABM43690	Abm43690 Propionib
111	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	184	5	35.7	81	4	ABU00345	Abu00345 Human nov
112	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	185	5	35.7	81	4	ABU00345	Abu00345 Human nov
113	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	186	5	35.7	81	4	ABU00345	Abu00345 Human nov
114	5	35.7	9	4	AAAG6836	Aaag6836 Human pep	187	5	35.7	81	4	ABU00345	Abu00345 Human nov
115	5	35.7	11	6	ABO10711	AbO10711 Murine J4	188	5	35.7	81	4	ABU00345	Abu00345 Human nov
116	5	35.7	11	6	ABR44655	AbR44655 Murine J4	189	5	35.7	81	4	ABU00345	Abu00345 Human nov
117	5	35.7	11	8	ADQ09078	AdQ09078 Mouse com	190	5	35.7	81	4	ABU00345	Abu00345 Human nov
118	5	35.7	12	8	ADP21839	AdP21839 Branched	191	5	35.7	81	4	ABU00345	Abu00345 Human nov
119	5	35.7	15	7	ADK82700	AdK82700 Beta-amy1	192	5	35.7	81	4	ABU00345	Abu00345 Human nov
120	5	35.7	15	7	ADM64487	AdM64487 human zin	193	5	35.7	81	4	ABU00345	Abu00345 Human nov
121	5	35.7	16	7	ADM35232	AdM35232 Human LY1	194	5	35.7	81	4	ABU00345	Abu00345 Human nov
122	5	35.7	28	5	RAAB47915	RAab47915 EETI-2 va	195	5	35.7	81	4	ABU00345	Abu00345 Human nov
123	5	35.7	30	7	ADM35227	AdM35227 Human LY1	196	5	35.7	81	4	ABU00345	Abu00345 Human nov
124	5	35.7	30	7	ADM35226	AdM35226 Human LY1	197	5	35.7	81	4	ABU00345	Abu00345 Human nov
125	5	35.7	35	2	RAY05330	Ray05330 Inflammat	198	5	35.7	81	4	ABU00345	Abu00345 Human nov
126	5	35.7	37	4	AAAM88488	Aaam88488 Human imm	199	5	35.7	81	4	ABU00345	Abu00345 Human nov
127	5	35.7	37	6	ABP80484	AbP80484 N. gonorr	200	5	35.7	81	4	ABU00345	Abu00345 Human nov
128	5	35.7	37	6	ABP77386	AbP77386 N. gonorr	201	5	35.7	81	4	ABU00345	Abu00345 Human nov
129	5	35.7	39	6	AAW03644	AaW03644 Rat FC5R	202	5	35.7	81	4	ABU00345	Abu00345 Human nov
130	5	35.7	39	6	ABP77797	AbP77797 N. gonorr	203	5	35.7	81	4	ABU00345	Abu00345 Human nov
131	5	35.7	42	6	ABP97890	AbP97890 Amino aci	204	5	35.7	81	4	ABU00345	Abu00345 Human nov
132	5	35.7	44	7	ADC24831	AdC24831 Human bre	205	5	35.7	81	4	ABU00345	Abu00345 Human nov
133	5	35.7	46	8	ADM63393	AdM63393 Tobamovir	206	5	35.7	81	4	ABU00345	Abu00345 Human nov
134	5	35.7	47	4	AAAM18291	AaM18291 Peptide #	207	5	35.7	81	4	ABU00345	Abu00345 Human nov
135	5	35.7	47	4	ABB37326	AbB37326 Peptide #	208	5	35.7	81	4	ABU00345	Abu00345 Human nov
136	5	35.7	47	4	AAAM30779	AaM30779 Peptide #	209	5	35.7	81	4	ABU00345	Abu00345 Human nov
137	5	35.7	47	4	ABB32074	AbB32074 Peptide #	210	5	35.7	81	4	ABU00345	Abu00345 Human nov
138	5	35.7	47	4	ABB22616	AbB22616 Protein #	211	5	35.7	81	4	ABU00345	Abu00345 Human nov
139	5	35.7	47	4	AAAM58019	AaM58019 Human bra	212	5	35.7	81	4	ABU00345	Abu00345 Human nov
140	5	35.7	47	4	ABG52143	AbG52143 Human liv	213	5	35.7	81	4	ABU00345	Abu00345 Human nov
141	5	35.7	47	4	ABG52143	AbG52143 Human liv	214	5	35.7	81	4	ABU00345	Abu00345 Human nov
142	5	35.7	47	4	ABG40095	AbG40095 Human pep	215	5	35.7	81	4	ABU00345	Abu00345 Human nov
143	5	35.7	49	7	ADBE7025	AdB7025 Human pan	216	5	35.7	81	4	ABU00345	Abu00345 Human nov
144	5	35.7	51	4	AAU43192	Aau43192 Propionib	217	5	35.7	81	4	ABU00345	Abu00345 Human nov
145	5	35.7	51	4	ABM39711	AbM39711 Propionib	218	5	35.7	81	4	ABU00345	Abu00345 Human nov
146	5	35.7	53	4	ABB15233	AbB15233 Human ner	219	5	35.7	81	4	ABU00345	Abu00345 Human nov
147	5	35.7	56	4	AAAM92619	AaM92619 Human dig	220	5	35.7	81	4	ABU00345	Abu00345 Human nov
148	5	35.7	56	4	AAU22613	Aau22613 Novel hum	221	5	35.7	81	4	ABU00345	Abu00345 Human nov
149	5	35.7	56	8	ADN63392	AdN63392 Tobamovir	222	5	35.7	81	4	ABU00345	Abu00345 Human nov
150	5	35.7	60	4	AAAG69147	AaG69147 M. catarr	223	5	35.7	81	4	ABU00345	Abu00345 Human nov
151	5	35.7	61	3	AAAG55738	AaG55738 Arabidops	224	5	35.7	81	4	ABU00345	Abu00345 Human nov
152	5	35.7	62	8	ADL05381	AdL05381 M. catarr	225	5	35.7	81	4	ABU00345	Abu00345 Human nov
153	5	35.7	62	2	AAAY11422	Aay11422 Human 5'	226	5	35.7	81	4	ABU00345	Abu00345 Human nov
154	5	35.7	65	4	AAAM19963	AaM19963 Peptide #	227	5	35.7	81	4	ABU00345	Abu00345 Human nov
155	5	35.7	65	4	ABB40009	AbB40009 Peptide #	228	5	35.7	81	4	ABU00345	Abu00345 Human nov
156	5	35.7	65	4	AAAM33630	AaM33630 Peptide #	229	5	35.7	81	4	ABU00345	Abu00345 Human nov
157	5	35.7	65	4	ABB24530	AbB24530 Protein #	230	5	35.7	81	4	ABU00345	Abu00345 Human nov
158	5	35.7	65	4	AAAM73428	AaM73428 Human bon	231	5	35.7	81	4	ABU00345	Abu00345 Human nov
159	5	35.7	65	4	AAAM60756	AaM60756 Human bra	232	5	35.7	81	4	ABU00345	Abu00345 Human nov
160	5	35.7	65	4	ABG55151	AbG55151 Human liv	233	5	35.7	81	4	ABU00345	Abu00345 Human nov
161	5	35.7	65	5	ABG43287	AbG43287 Human pep	234	5	35.7	81	4	ABU00345	Abu00345 Human nov
162	5	35.7	65	8	ADR96312	AdR96312 Novel S.	235	5	35.7	81	4	ABU00345	Abu00345 Human nov
163	5	35.7	66	2	AAAG60064	AaG60064 Human end	236	5	35.7	81	4	ABU00345	Abu00345 Human nov
164	5	35.7	68	3	AAAG51691	AaG51691 Arabidops	237	5	35.7	81	4	ABU00345	Abu00345 Human nov
165	5	35.7	68	4	AAAM20583	AaM20583 Peptide #	238	5	35.7	81	4	ABU00345	Abu00345 Human nov
166	5	35.7	68	4	ABB41716	AbB41716 Peptide #	239	5	35.7	81	4	ABU00345	Abu00345 Human nov
167	5	35.7	68	4	AAAM35513	AaM35513 Peptide #	240	5	35.7	81	4	ABU00345	Abu00345 Human nov
168	5	35.7	68	4	ABB25478	AbB25478 Protein #	241	5	35.7	81	4	ABU00345	Abu00345 Human nov
169	5	35.7	68	4	AAAM75400	AaM75400 Human bon	242	5	35.7	81	4	ABU00345	Abu00345 Human nov
170	5	35.7	68	4	AAAM62590	AaM62590 Human bra	243	5	35.7	81	4	ABU00345	Abu00345 Human nov
171	5	35.7	68	4	ABG57156	AbG57156 Human liv	244	5	35.7	81	4	ABU00345	Abu00345 Human nov

245 5 35.7 107 6 ABR44621 Murine J4
246 5 35.7 107 6 ABR44679 Murine J4
247 5 35.7 107 6 ABR44681 Murine J4
248 5 35.7 107 6 ABR44671 Murine J4
249 5 35.7 107 8 ADQ90815 Deimmunis
250 5 35.7 107 8 ADQ90801 Deimmunis
251 5 35.7 107 8 ADQ90819 Deimmunis
252 5 35.7 107 8 ADQ90813 Deimmunis
253 5 35.7 107 8 ADQ90814 Deimmunis
254 5 35.7 107 8 ADQ90816 Deimmunis
255 5 35.7 108 6 AAO03463 Human pol
256 5 35.7 108 6 ABU10451 Immunolog
257 5 35.7 108 8 ADS80905 Mammalian
258 5 35.7 109 2 AAU77680 Staphyloc
259 5 35.7 111 3 AAG31059 Arabidops
260 5 35.7 111 5 ABP32915 Human gly
261 5 35.7 112 4 AAM23547 Human EST
262 5 35.7 112 7 ADE09154 Novel pro
263 5 35.7 112 7 ADF06990 Bacterial
264 5 35.7 114 3 AAG31058 Arabidops
265 5 35.7 114 4 AAM99734 Human exc
266 5 35.7 114 4 AAM42397 Human pol
267 5 35.7 114 4 AAM42549 Human kid
268 5 35.7 116 3 AAG01391 Human sec
269 5 35.7 117 2 AAY35533 Chlamydia
270 5 35.7 117 4 AAU65135 Propionib
271 5 35.7 117 6 ABM61654 Propionib
272 5 35.7 118 2 AAR90845 Partial h
273 5 35.7 118 4 AAR31838 Novel hum
274 5 35.7 118 7 ADH10109 Human IL-
275 5 35.7 118 7 ADG48163 Human IL-
276 5 35.7 119 8 ADR96302 Novel S.
277 5 35.7 120 4 AEG20367 Bacterial
278 5 35.7 120 7 ADF06977 Bacterial
279 5 35.7 124 6 ADA34000 Acinetoba
280 5 35.7 124 7 ADM04257 Human pro
281 5 35.7 125 3 AAG58327 Arabidops
282 5 35.7 125 3 AAG59802 Arabidops
283 5 35.7 125 4 AAU31404 Novel hum
284 5 35.7 127 3 AAG00143 Human sec
285 5 35.7 127 5 AAU10999 Kringle p
286 5 35.7 127 6 ABP80865 N. gonorr
287 5 35.7 127 6 ABP80891 N. gonorr
288 5 35.7 127 6 ABP80485 N. gonorr
289 5 35.7 127 6 ABP77395 N. gonorr
290 5 35.7 127 6 ABP79509 N. gonorr
291 5 35.7 128 6 ABU17286 Protein e
292 5 35.7 128 6 ABU28715 Protein e
293 5 35.7 128 6 ABU32227 Protein e
294 5 35.7 132 4 ABM63892 Drosophil
295 5 35.7 132 7 ABO65227 Klebsiell
296 5 35.7 133 4 AAU44627 Propionib
297 5 35.7 133 5 ABB09893 Amino aci
298 5 35.7 133 6 ABM41146 Propionib
299 5 35.7 137 3 AAG31057 Arabidops
300 5 35.7 137 6 ADA36428 Acinetoba
301 5 35.7 137 8 ADP84570 Human bre
302 5 35.7 138 4 ABG13457 Novel hum
303 5 35.7 138 4 ABG12342 Novel hum
304 5 35.7 138 8 ADR99911 Immune Re
305 5 35.7 139 3 AAG37154 Arabidops
306 5 35.7 140 4 AAU27759 Human ful
307 5 35.7 140 5 ABP54681 Metastati
308 5 35.7 140 8 ABP54680 Metastati
309 5 35.7 140 8 ADN04734 Antipsori
310 5 35.7 140 8 ADN04249 Antipsori
311 5 35.7 140 8 ADP23986 PRO polyp
312 5 35.7 141 3 AAG29979 Arabidops
313 5 35.7 142 6 ABU43688 Protein e
314 5 35.7 143 3 AAG29978 Arabidops
315 5 35.7 143 3 AAG08646 Arabidops
316 5 35.7 143 4 AAB70795 A. thalia
317 5 35.7 145 3 AAG08645 Arabidops

318 5 35.7 145 8 ADN73803 Thale cre
319 5 35.7 146 5 ABG23799 Novel hum
320 5 35.7 146 5 ADR41557 Human CD-
321 5 35.7 147 4 ABG12343 Novel hum
322 5 35.7 147 4 ABG23801 Novel hum
323 5 35.7 147 6 ABU10250 Mammalian
324 5 35.7 147 8 ADS80904 Mammalian
325 5 35.7 148 7 ABM73894 DNA clone
326 5 35.7 149 3 AAG00176 Human sec
327 5 35.7 150 4 AAG23800 Novel hum
328 5 35.7 151 3 AAG56381 Arabidops
329 5 35.7 151 3 AAG50992 Arabidops
330 5 35.7 151 3 AAG37153 Arabidops
331 5 35.7 151 4 AAB99315 Human pro
332 5 35.7 154 3 AAG38476 Arabidops
333 5 35.7 154 5 ABB49339 Listeria
334 5 35.7 156 3 AAB58936 Breast an
335 5 35.7 156 3 AAG60991 Arabidops
336 5 35.7 156 3 AAG56380 Arabidops
337 5 35.7 159 3 AAG08644 Arabidops
338 5 35.7 160 3 AAG29977 Arabidops
339 5 35.7 160 8 ADQ65870 Novel hum
340 5 35.7 160 8 ADN2897 Bacterial
341 5 35.7 161 6 ABP77628 N. gonorr
342 5 35.7 162 2 AAR25124 Hepatilis
343 5 35.7 163 2 AAU56730 Human dis
344 5 35.7 163 2 AAM64463 Human sec
345 5 35.7 163 3 AAB19038 Amino aci
346 5 35.7 163 3 AAB19037 Amino aci
347 5 35.7 163 3 AAY93601 Protein e
348 5 35.7 163 7 ADC38660 Human sec
349 5 35.7 163 7 ADI63102 Human apo
350 5 35.7 163 7 ADN95501 Human BEC
351 5 35.7 163 8 ADO55179 Protein #
352 5 35.7 163 8 ADQ20841 Human sof
353 5 35.7 163 8 ADP23602 PRO polyp
354 5 35.7 164 7 ADB65642 Human pro
355 5 35.7 166 3 AAG38475 Arabidops
356 5 35.7 166 4 AAU16609 Human nov
357 5 35.7 166 6 ABU10452 Immunolog
358 5 35.7 166 6 ABU55678 Human nov
359 5 35.7 166 8 ADS80906 Mammalian
360 5 35.7 168 3 AAG20163 Arabidops
361 5 35.7 168 4 AAU45536 Propionib
362 5 35.7 168 6 ABM42055 Propionib
363 5 35.7 170 4 ABG23793 Novel hum
364 5 35.7 171 3 AAG60990 Arabidops
365 5 35.7 171 3 AAG56379 Arabidops
366 5 35.7 172 4 AAU53524 Propionib
367 5 35.7 172 6 ABM50043 Propionib
368 5 35.7 173 4 AAU25771 Human pro
369 5 35.7 174 7 ADD13208 C. glutam
370 5 35.7 174 7 AAG90845 C. glutam
371 5 35.7 175 3 AAG59801 Arabidops
372 5 35.7 175 3 AAG58326 Arabidops
373 5 35.7 180 3 AAG20162 Arabidops
374 5 35.7 185 7 ADF06164 Bacterial
375 5 35.7 186 2 AAW81026 PAS domai
376 5 35.7 188 6 ADA89678 Staphyloc
377 5 35.7 188 6 ADA89666 Staphyloc
378 5 35.7 190 3 AAG59800 Arabidops
379 5 35.7 190 8 ABO58830 Human gen
380 5 35.7 191 7 ADM03992 Human pro
381 5 35.7 193 2 AAR33985 HCT23 E1
382 5 35.7 193 6 ADB11810 Alloiococ
383 5 35.7 194 7 ADC00075 Enterobae
384 5 35.7 198 6 AAO16405 Human nuc
385 5 35.7 199 4 ABG23794 Novel hum
386 5 35.7 203 6 ADB11808 Alloiococ
387 5 35.7 204 5 ABB04904 Meg human
388 5 35.7 205 4 ABG25323 Novel hum
389 5 35.7 205 5 ABP39921 Staphyloc
390 5 35.7 205 8 ADS08697 Staphyloc

391	5	35.7	206	6	ADB11806	Adb11806 Alloiococ	464	258	2	AAW10154	Aaw10154 Callose
392	5	35.7	207	2	AAR97213	Aar97213 Human cal	465	258	6	ABR52901	AbR52901 Protein s
393	5	35.7	207	2	AAW26770	AAW26770 Calcium s	466	258	7	ADK62442	AdK62442 Disease t
394	5	35.7	212	6	ADA34545	Ada34545 Acinetoba	466	258	8	Adn62547	Adn62547 A. thalia
395	5	35.7	213	2	AY42374	Ay42374 Amino aci	468	258	8	ADS43390	AdS43390 Bacterial
396	5	35.7	214	8	ADL22485	AdL22485 Human tau	469	260	2	AAM52944	Aam52944 Agkistrod
397	5	35.7	214	8	ADL22485	AdL22485 Human tau	470	260	8	ADL65425	AdL65425 DNA gyrase
398	5	35.7	216	2	AAV73908	Aav73908 Human pro	471	261	7	ADM34373	Adm34373 Human LV1
399	5	35.7	216	3	AAW24648	Aaw24648 Plant SDF	472	261	7	ADM35281	Adm35281 Human LV1
400	5	35.7	216	3	AAW25090	Aaw25090 Plant SDF	472	261	8	ADR96378	Adr96378 Novel S.
401	5	35.7	217	8	ADN21492	Adn21492 Bacterial	473	262	3	ABR52508	AbR52508 Plant SDF
402	5	35.7	218	5	ABB09590	Abb09590 Deinagkis	474	262	3	ABR52508	AbR52508 Plant SDF
403	5	35.7	219	2	AAV34450	Aav34450 Porphyrom	475	262	3	ABR52508	AbR52508 Plant SDF
404	5	35.7	221	4	ABG30016	Abg30016 Novel hum	476	262	3	ABR52508	AbR52508 Plant SDF
405	5	35.7	223	4	ABR65564	AbR65564 Drosophil	477	262	6	AAE38420	Aae38420 Arabidops
406	5	35.7	224	7	ADM25534	Adm25534 Hyperther	478	266	3	AAE38420	Aae38420 Arabidops
407	5	35.7	225	2	AAAR09846	Aaar09846 Hybrid co	479	266	3	AAE38420	Aae38420 Arabidops
408	5	35.7	225	7	ADH10110	Adh10110 Human IL-	480	266	3	AAE38420	Aae38420 Arabidops
409	5	35.7	225	7	ADG48164	Adg48164 Human IL-	481	266	3	AAE38420	Aae38420 Arabidops
410	5	35.7	226	4	AAU60973	Aau60973 Propionib	482	266	3	AAE38420	Aae38420 Arabidops
411	5	35.7	226	6	ABM57492	Abm57492 Propionib	483	266	3	AAE38420	Aae38420 Arabidops
412	5	35.7	226	6	ABM57492	Abm57492 Propionib	484	266	3	AAE38420	Aae38420 Arabidops
413	5	35.7	227	3	ABM70168	Abm70168 Photorhab	485	266	3	AAE38420	Aae38420 Arabidops
414	5	35.7	227	6	ABP78057	Abp78057 N. gonorr	486	266	3	AAE38420	Aae38420 Arabidops
415	5	35.7	227	6	ABB48998	Abb48998 Listeria	487	266	3	AAE38420	Aae38420 Arabidops
416	5	35.7	228	5	ABR08510	AbR08510 A recombi	488	266	3	AAE38420	Aae38420 Arabidops
417	5	35.7	230	3	ABR08511	AbR08511 Biosynthe	489	266	3	AAE38420	Aae38420 Arabidops
418	5	35.7	231	2	AAW76538	Aaw76538 A. contor	490	266	3	AAE38420	Aae38420 Arabidops
419	5	35.7	231	2	AAW76538	Aaw76538 A. contor	491	266	3	AAE38420	Aae38420 Arabidops
420	5	35.7	231	2	AAW76538	Aaw76538 A. contor	492	266	3	AAE38420	Aae38420 Arabidops
421	5	35.7	233	4	AAW52946	Aaw52946 Batroxobi	493	266	3	AAE38420	Aae38420 Arabidops
422	5	35.7	233	4	AAW52946	Aaw52946 Batroxobi	494	266	3	AAE38420	Aae38420 Arabidops
423	5	35.7	234	4	ADM19989	Adm19989 Protein e	495	266	3	AAE38420	Aae38420 Arabidops
424	5	35.7	234	4	ADM19989	Adm19989 Protein e	496	266	3	AAE38420	Aae38420 Arabidops
425	5	35.7	234	4	ADM19989	Adm19989 Protein e	497	266	3	AAE38420	Aae38420 Arabidops
426	5	35.7	234	4	ADM19989	Adm19989 Protein e	498	266	3	AAE38420	Aae38420 Arabidops
427	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	499	266	3	AAE38420	Aae38420 Arabidops
428	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	500	266	3	AAE38420	Aae38420 Arabidops
429	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	501	266	3	AAE38420	Aae38420 Arabidops
430	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	502	266	3	AAE38420	Aae38420 Arabidops
431	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	503	266	3	AAE38420	Aae38420 Arabidops
432	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	504	266	3	AAE38420	Aae38420 Arabidops
433	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	505	266	3	AAE38420	Aae38420 Arabidops
434	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	506	266	3	AAE38420	Aae38420 Arabidops
435	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	507	266	3	AAE38420	Aae38420 Arabidops
436	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	508	266	3	AAE38420	Aae38420 Arabidops
437	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	509	266	3	AAE38420	Aae38420 Arabidops
438	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	510	266	3	AAE38420	Aae38420 Arabidops
439	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	511	266	3	AAE38420	Aae38420 Arabidops
440	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	512	266	3	AAE38420	Aae38420 Arabidops
441	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	513	266	3	AAE38420	Aae38420 Arabidops
442	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	514	266	3	AAE38420	Aae38420 Arabidops
443	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	515	266	3	AAE38420	Aae38420 Arabidops
444	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	516	266	3	AAE38420	Aae38420 Arabidops
445	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	517	266	3	AAE38420	Aae38420 Arabidops
446	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	518	266	3	AAE38420	Aae38420 Arabidops
447	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	519	266	3	AAE38420	Aae38420 Arabidops
448	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	520	266	3	AAE38420	Aae38420 Arabidops
449	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	521	266	3	AAE38420	Aae38420 Arabidops
450	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	522	266	3	AAE38420	Aae38420 Arabidops
451	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	523	266	3	AAE38420	Aae38420 Arabidops
452	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	524	266	3	AAE38420	Aae38420 Arabidops
453	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	525	266	3	AAE38420	Aae38420 Arabidops
454	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	526	266	3	AAE38420	Aae38420 Arabidops
455	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	527	266	3	AAE38420	Aae38420 Arabidops
456	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	528	266	3	AAE38420	Aae38420 Arabidops
457	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	529	266	3	AAE38420	Aae38420 Arabidops
458	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	530	266	3	AAE38420	Aae38420 Arabidops
459	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	531	266	3	AAE38420	Aae38420 Arabidops
460	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	532	266	3	AAE38420	Aae38420 Arabidops
461	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	533	266	3	AAE38420	Aae38420 Arabidops
462	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	534	266	3	AAE38420	Aae38420 Arabidops
463	5	35.7	235	3	AAW52946	Aaw52946 Batroxobi	535	266	3	AAE38420	Aae38420 Arabidops

537	5	35.7	320	3	AAy84613	Aay84613	Amino aci	610	5	35.7	367	3	AAg06096	Ag06096	Arabidops
538	5	35.7	320	3	AABo1829	Ab01829	Haemophil	611	5	35.7	367	3	AAg49374	Ag49374	Arabidops
539	5	35.7	320	3	ADm35267	Adm35267	Human LY1	612	5	35.7	367	6	AAu35480	Au35480	Protein e
540	5	35.7	320	8	ABm83639	Abm83639	Human dia	613	5	35.7	367	3	ADm35275	Am35275	Human LY1
541	5	35.7	320	8	ADr99912	Adr99912	Immune Re	614	5	35.7	370	3	AAg49396	Ag49396	Arabidops
542	5	35.7	323	7	ADd24330	Ad24330	Mouse PST	615	5	35.7	371	5	ABp73608	Ap73608	Candida a
543	5	35.7	323	7	ABw02023	Abw02023	Murine mu	616	5	35.7	371	8	ADG27332	Dg27332	Candida a
544	5	35.7	323	7	ABw02020	Abw02020	Murine PS	617	5	35.7	371	8	ADN21175	Dn21175	Bacterial
545	5	35.7	323	8	ADJ48543	Adj48543	Oil-associ	618	5	35.7	374	4	ABg42328	Bg42328	Human ORF
546	5	35.7	324	3	AAg39403	Ag39403	Arabidops	619	5	35.7	374	4	ABg00048	Bg00048	Novel hum
547	5	35.7	325	8	ADs25592	Ad25592	Bacterial	620	5	35.7	375	7	ADm26000	Dm26000	Hyperther
548	5	35.7	325	8	ADs26043	Ad26043	Bacterial	621	5	35.7	376	7	ABO80426	Bo80426	Pseudomon
549	5	35.7	328	4	AB63244	Ab63244	Human bre	622	5	35.7	376	7	ABO71181	Bo71181	Pseudomon
550	5	35.7	328	4	ABG13237	Abg13237	Novel hum	623	5	35.7	377	2	AAw98246	Aw98246	H. pylori
551	5	35.7	328	4	ABG13476	Abg13476	Novel hum	624	5	35.7	377	3	AAy75615	Ay75615	Neisseria
552	5	35.7	329	3	AAg49375	Ag49375	Arabidops	625	5	35.7	379	5	ABu50882	Bu50882	Helicobac
553	5	35.7	329	3	AAg06097	Ag06097	Arabidops	626	5	35.7	379	7	ADd30156	Dd30156	Plant yie
554	5	35.7	331	6	ABr58009	Br58009	Mouse GI	627	5	35.7	379	7	ADe31537	De31537	Plant yie
555	5	35.7	331	8	ADN20053	Dn20053	Bacterial	628	5	35.7	379	8	ADi41953	Di41953	Plant tra
556	5	35.7	332	3	AAg49397	Ag49397	Arabidops	629	5	35.7	381	5	AAU98989	Au98989	Oestrogen
557	5	35.7	332	8	ADs29795	Ad29795	Bacterial	630	5	35.7	381	8	ADK16395	Dk16395	Nanoarcha
558	5	35.7	334	5	ABu51084	Bu51084	Helicobac	631	5	35.7	382	4	AAE08001	E08001	Rat neuro
559	5	35.7	335	6	ABu16367	Bu16367	Protein e	632	5	35.7	382	6	ABU45726	BU45726	Protein e
560	5	35.7	335	6	AAW77400	Aw77400	Absidia b	633	5	35.7	384	4	AAg70863	Ag70863	C albican
561	5	35.7	337	2	AAW26688	Aw26688	Absidia b	634	5	35.7	385	8	ADs27721	Ds27721	Bacterial
562	5	35.7	337	4	AAU34121	Au34121	Staphyloc	635	5	35.7	386	8	ADs24119	Ds24119	Bacterial
563	5	35.7	337	4	AAU37283	Au37283	Staphyloc	636	5	35.7	389	5	ABU51383	Bu51383	Helicobac
564	5	35.7	337	4	AAU36946	Au36946	Staphyloc	637	5	35.7	389	5	AAU75907	AU75907	Human epi
565	5	35.7	337	6	ABU42965	Bu42965	Protein e	638	5	35.7	391	6	ADA55534	Ad55534	Human pro
566	5	35.7	337	6	ABU43809	Bu43809	Protein e	639	5	35.7	391	8	ADs44135	Ds44135	Bacterial
567	5	35.7	337	6	ABU16072	Bu16072	Protein e	640	5	35.7	392	6	ABU45725	Bu45725	Protein e
568	5	35.7	337	6	ABM72240	Bm72240	Staphyloc	641	5	35.7	395	2	AAW43408	Aw43408	Mouse neu
569	5	35.7	339	3	AAg41814	Ag41814	Arabidops	642	5	35.7	395	2	AAW23347	Aw23347	Novel mur
570	5	35.7	340	7	ADf05682	Df05682	Bacterial	643	5	35.7	395	3	AAy77536	Ay77536	Murine ne
571	5	35.7	340	8	ADi67230	Di67230	Lactobaci	644	5	35.7	395	3	AAy53254	Ay53254	Mouse neu
572	5	35.7	341	8	ADf89714	Df89714	Human can	645	5	35.7	395	4	ABG69176	Bg69176	Murine ne
573	5	35.7	343	6	ABU33511	Bu33511	Protein e	646	5	35.7	395	6	ADa47992	A47992	Rice prot
574	5	35.7	345	4	ABE67087	Be67087	Drosophil	647	5	35.7	395	8	ADH10676	Dh10676	Murine fr
575	5	35.7	347	6	ABP78216	Bp78216	N. gonorr	648	5	35.7	395	8	ADJ76268	Dj76268	Marker ge
576	5	35.7	349	4	AAb79726	Ab79726	Corynebac	649	5	35.7	395	8	ADP98875	Dp98875	C. albica
577	5	35.7	349	4	AAU71897	Au71897	C. glutami	650	5	35.7	396	8	ADr01259	Dr01259	Farnesyl
578	5	35.7	349	4	AAg90683	Ag90683	C. glutami	651	5	35.7	397	2	AAy28292	Ay28292	Amino aci
579	5	35.7	350	4	ABE84724	Be84724	DNA polym	652	5	35.7	398	3	AAg29822	Ag29822	Arabidops
580	5	35.7	350	5	ABE84804	Be84804	Aquifex a	653	5	35.7	400	3	AAy81929	Ay81929	Human EST
581	5	35.7	350	5	ABE84812	Be84812	DNA polym	654	5	35.7	400	8	ADN46344	Dn46344	Thermococ
582	5	35.7	350	8	ADJ67894	Dj67894	A. aeolic	655	5	35.7	404	7	ADK68537	Dk68537	Mycoplasma
583	5	35.7	350	8	ADJ67894	Dj67894	A. aeolic	656	5	35.7	404	7	ADK68536	Dk68536	Mycoplasma
584	5	35.7	350	8	ADK01184	Dk01184	DNA polym	657	5	35.7	406	3	AAg37979	Ag37979	Arabidops
585	5	35.7	350	8	ADJ79403	Dj79403	A. aeolic	658	5	35.7	407	3	ABs20939	Bs20939	Drosophil
586	5	35.7	350	8	ADJ84843	Dj84843	A. aeolic	659	5	35.7	407	7	ADD15320	Dd15320	Fruitfly
587	5	35.7	350	8	ADm77631	Dm77631	DNA polym	660	5	35.7	408	2	AAW71465	Aw71465	Glycosylt
588	5	35.7	350	8	ADm66298	Dm66298	A. aeolic	661	5	35.7	408	3	AAy67549	Ay67549	A. Orient
589	5	35.7	350	8	ADm04351	Dm04351	A. aeolic	662	5	35.7	411	5	ABb97295	Bb97295	Novel hum
590	5	35.7	350	8	ADP82428	Dp82428	Aquifex a	663	5	35.7	413	2	AAW46822	Aw46822	Amino aci
591	5	35.7	351	3	AAg39402	Ag39402	Arabidops	664	5	35.7	413	6	ADa32940	A32940	Acinetoba
592	5	35.7	352	8	ADs41644	Ds41644	Bacterial	665	5	35.7	413	7	ADm35265	Dm35265	Human LY1
593	5	35.7	353	5	ABP40666	Bp40666	Staphyloc	666	5	35.7	415	2	AAW71595	Aw71595	Murine ty
594	5	35.7	353	8	ADs07922	Ds07922	Staphyloc	667	5	35.7	415	3	AAb53180	B53180	Macaca mu
595	5	35.7	354	6	ADa34348	D34348	Acinetoba	668	5	35.7	415	3	AAy81928	Ay81928	Murine PS
596	5	35.7	355	3	ADa33610	D33610	Arabidops	669	5	35.7	415	3	ABb08486	Bb08486	A murine
597	5	35.7	355	8	ABO58499	Bo58499	Human gen	670	5	35.7	415	7	ADm35266	Dm35266	Human LY1
598	5	35.7	356	5	ABU51625	Bu51625	Helicobac	671	5	35.7	416	2	AAy28291	Ay28291	Amino aci
599	5	35.7	358	5	ABG77256	Bg77256	Selected	672	5	35.7	416	3	AAy68782	Ay68782	Amino aci
600	5	35.7	358	5	ABJ11127	Bj11127	Yeast sel	673	5	35.7	416	4	ABG28750	BG28750	Novel hum
601	5	35.7	359	2	AAr88871	Ar88871	Sardinian	674	5	35.7	416	6	ABM67905	Bm67905	Photorhab
602	5	35.7	359	2	AAr88870	Ar88870	Sardinian	675	5	35.7	416	7	ADD24329	Dd24329	Human CD2
603	5	35.7	359	2	AAr88872	Ar88872	Sardinian	676	5	35.7	416	7	ADD24348	Dd24348	Human CD2
604	5	35.7	359	2	AAy05667	Ay05667	Maize cin	677	5	35.7	416	7	ADD24350	Dd24350	Human CD2
605	5	35.7	360	7	ADc61397	Dc61397	Nicotiana	678	5	35.7	416	7	ABW02019	Bw02019	Human CD2
606	5	35.7	361	8	ADp29940	Dp29940	Human sec	679	5	35.7	416	7	ABW02022	Bw02022	Human CD2
607	5	35.7	362	5	ABb05006	Bb05006	Mouse ser	680	5	35.7	416	8	ADL22901	Dl22901	Human MP2
608	5	35.7	365	7	ADm35272	Dm35272	Human LY1	681	5	35.7	416	8	ADs29579	Ds29579	Bacterial
609	5	35.7	366	7	ABm74139	Bm74139	DNA clone	682	5	35.7	419	4	ABb58148	Bb58148	Drosophil

683	5	35.7	419	5	AAU99075	Aau99075 Human Pro	756	5	35.7	473	8	ADQ65367	Novel hum
684	5	35.7	420	5	ABU51367	Abu51367 Helicobac	757	5	35.7	473	8	ABM83797	Human dia
685	5	35.7	420	5	ABB48624	Abb48624 Listeria	758	5	35.7	473	8	ADN21319	Bacterial
686	5	35.7	422	5	ABU51614	Abu51614 Helicobac	759	5	35.7	474	3	AAU56509	Human Jur
687	5	35.7	423	3	AAU37978	Aag37978 Arabidops	760	5	35.7	475	6	ABU43179	Protein e
688	5	35.7	424	2	AAW23818	Aaw23818 Arabidops	761	5	35.7	478	3	AAU44073	Arabidops
689	5	35.7	424	2	AAW45512	Aaw45512 LEAFY gen	762	5	35.7	478	3	AAU47163	Arabidops
690	5	35.7	424	2	AAW43332	Aaw43332 Arabidops	763	5	35.7	479	4	ABBS1020	Escherich
691	5	35.7	424	2	AAW39138	Aaw39138 Arabidops	764	5	35.7	479	7	ADU7046	Bacterial
692	5	35.7	424	3	AAU67557	Aay67557 A. thalia	765	5	35.7	479	8	ADN24682	Bacterial
693	5	35.7	424	3	AAU13248	Abu13248 Amino aci	766	5	35.7	481	4	ABM62987	Drosophil
694	5	35.7	424	3	AAU78886	Aay78886 A. thalia	767	5	35.7	481	8	ABM83796	Human dia
695	5	35.7	424	6	ABR42687	Abu42687 Arabidops	768	5	35.7	482	6	ABU31996	Protein e
696	5	35.7	424	7	ADU56541	Adf56541 Thale cre	769	5	35.7	483	8	ADU44061	Bacterial
697	5	35.7	424	8	ADG47860	Adg47860 Arabidops	770	5	35.7	485	6	ABU37935	Protein e
698	5	35.7	426	8	ADU61643	Adu61643 Transcript	771	5	35.7	485	6	ABU37322	Protein e
699	5	35.7	426	8	ADU42621	Adu42621 Bacterial	772	5	35.7	488	5	ABP39401	Staphyloc
700	5	35.7	428	2	AAU05332	Aay05332 Inflammat	773	5	35.7	488	8	ADU04592	Staphyloc
701	5	35.7	428	6	ABP71709	Abp71709 M161 anti	774	5	35.7	489	7	ADU74316	Human FCR
702	5	35.7	428	7	ADK68538	Adk68538 Mycoplasma	775	5	35.7	490	2	AAU05375	Human HCM
703	5	35.7	428	7	ADK68531	Adk68531 Mycoplasma	776	5	35.7	490	7	ADU76387	Novel hum
704	5	35.7	429	2	AAU22727	Aaw22727 Membrane	777	5	35.7	490	8	ADU75340	Marker ge
705	5	35.7	430	4	ABM60505	Abm60505 Drosophil	778	5	35.7	490	8	ADL61272	Human int
706	5	35.7	432	3	AAU48078	Aag48078 Arabidops	779	5	35.7	490	8	ADN06003	Antipsori
707	5	35.7	432	8	ADK60819	Adk60819 Lycopersi	780	5	35.7	490	8	ADO24395	Human PRO
708	5	35.7	432	8	ABM83798	Abm83798 Human dia	781	5	35.7	490	8	ADQ19383	Human sof
709	5	35.7	433	3	AAU41651	Aag41651 Arabidops	782	5	35.7	490	8	ADL14255	Human NF-
710	5	35.7	433	3	AAU43025	Aag43025 Arabidops	783	5	35.7	491	4	AAU33137	Novel hum
711	5	35.7	433	5	ABM92056	Abm92056 Herbicida	784	5	35.7	493	4	ABG75409	Xenopus B
712	5	35.7	433	6	ABR52885	Abu52885 Protein s	785	5	35.7	494	3	AAU44072	Arabidops
713	5	35.7	433	7	ADU79808	Adu79808 Mouse put	786	5	35.7	494	8	ADO19013	Amino aci
714	5	35.7	433	7	ADK62398	Adk62398 Disease t	787	5	35.7	495	3	AAU94280	Corri hist
715	5	35.7	435	3	AAU29821	Aay29821 Arabidops	788	5	35.7	497	2	AAU74187	Human pro
716	5	35.7	436	2	AAU04391	Aay04391 Human ori	789	5	35.7	500	6	ABP78407	N. gonorr
717	5	35.7	436	8	ABM80350	Abm80350 Tumour-as	790	5	35.7	502	8	ADS42440	Bacterial
718	5	35.7	437	5	ABM97913	Abm97913 Human sec	791	5	35.7	503	6	AAO23320	Rhesus mo
719	5	35.7	437	8	ADN24334	Adn24334 Bacterial	792	5	35.7	503	6	AAO23312	Cynomolg
720	5	35.7	438	8	ADN01257	Adn01257 Farnesyl	793	5	35.7	503	6	ABU28414	Protein e
721	5	35.7	442	8	ADN04828	Adn04828 Antipsori	794	5	35.7	504	3	ABU18228	Plasmodi
722	5	35.7	442	8	ABM81629	Abm81629 Tumour-as	795	5	35.7	505	3	AAU17004	Arabidops
723	5	35.7	444	4	AAU40722	Aam40722 Human pol	796	5	35.7	505	6	AAO23316	Rhesus mo
724	5	35.7	445	6	ABU23382	Abu23382 Protein e	797	5	35.7	506	4	ABM64792	Drosophil
725	5	35.7	446	8	ADN73299	Adn73299 Thale cre	798	5	35.7	506	7	ADU75344	Prostate
726	5	35.7	447	3	AAU74915	Aay74915 Neisseria	799	5	35.7	506	8	ADM74217	Human NOV
727	5	35.7	447	3	AAU41813	Aag41813 Arabidops	800	5	35.7	506	8	ADM74215	Human NOV
728	5	35.7	447	4	ABM61990	Abm61990 Drosophil	801	5	35.7	506	8	ADR14579	Human NF-
729	5	35.7	447	7	ADU64482	Adu64482 human zin	802	5	35.7	506	8	ADS24106	Bacterial
730	5	35.7	448	8	ADS23705	Adg23705 Bacterial	803	5	35.7	507	4	ABM96433	Putative
731	5	35.7	451	3	AAU74916	Aay74916 Neisseria	804	5	35.7	508	4	ABM82317	Human imm
732	5	35.7	451	3	AAU74914	Aay74914 Neisseria	805	5	35.7	508	7	ADM35239	Human LY1
733	5	35.7	451	3	AAU43024	Aag43024 Arabidops	806	5	35.7	508	7	ADM35264	Human LY1
734	5	35.7	451	6	ABU79400	Abu79400 Taxane sy	807	5	35.7	508	8	ADR99715	Human can
735	5	35.7	451	6	ABU40758	Abu40758 Protein e	808	5	35.7	508	8	ADL06539	Human tum
736	5	35.7	453	4	ABM59823	Abm59823 Drosophil	809	5	35.7	509	2	AAU43215	Bacillus
737	5	35.7	455	7	ADC31345	Adc31345 Human nov	810	5	35.7	509	2	AAU41138	Zea may
738	5	35.7	456	4	AAU35277	Aau35277 Enterococ	811	5	35.7	509	3	AAU44603	Maize MLO
739	5	35.7	457	6	ABP80604	Abp80604 N. gonorr	812	5	35.7	509	4	ABM30697	Amino aci
740	5	35.7	458	3	AAU41812	Aag41812 Arabidops	813	5	35.7	509	5	ABP73880	Candida a
741	5	35.7	459	6	ABM71447	Abm71447 Staphyloc	814	5	35.7	510	3	AAU17003	Arabidops
742	5	35.7	460	7	ADM35273	Adm35273 Human LY1	815	5	35.7	511	3	AAU52005	Arabidops
743	5	35.7	464	6	ABU20568	Abu20568 Protein e	816	5	35.7	511	4	AAU62624	Human cel
744	5	35.7	464	8	ADU28122	Adu28122 Bacterial	817	5	35.7	512	8	ABM83795	Human dia
745	5	35.7	465	5	ABG96348	Abg96348 Human ova	818	5	35.7	513	8	ADK13898	Human PSK
746	5	35.7	466	7	ABO61137	Abu61137 Klebsiell	819	5	35.7	518	7	ABO82898	Pseudomon
747	5	35.7	467	5	ABG96349	Abg96349 Human ova	820	5	35.7	520	8	ADR86188	Aspergill
748	5	35.7	468	6	ABU50430	Abu50430 Protein e	821	5	35.7	520	8	ADR86430	Aspergill
749	5	35.7	468	7	ABG39829	Abg39829 Protein s	822	5	35.7	520	2	AAU47207	Homoe sapi
750	5	35.7	469	3	AAU48077	Aag48077 Arabidops	823	5	35.7	527	3	AAU29820	Arabidops
751	5	35.7	470	6	ABM69001	Abm69001 Phototrab	824	5	35.7	528	8	ADN37289	Barley st
752	5	35.7	470	8	ADJ37217	Adj37217 Human nuc	825	5	35.7	529	6	AAO23295	Chimpanze
753	5	35.7	471	8	ADN21925	Adn21925 Bacterial	826	5	35.7	530	6	AAO23292	Chimpanze
754	5	35.7	473	5	ABM47872	Abm47872 Listeria	827	5	35.7	531	6	AAO23298	Chimpanze
755	5	35.7	473	6	AAE32081	Aae32081 Human TRI	828	5	35.7	533	4	ABG25433	Novel hum

975 5 35.7 883 6 ABM69376 Photorhab
976 5 35.7 885 6 ABM69449 Photorhab
977 5 35.7 887 4 ABM39431 Human pol
978 5 35.7 887 6 ABU54626 Human NOV
979 5 35.7 887 6 ABU40971 Protein e
980 5 35.7 888 5 AAU83013 Human hom
981 5 35.7 888 8 ADO79411 KIAA0783
982 5 35.7 889 8 ADJ50234 OIL-asso
983 5 35.7 891 4 AAU34554 E. coli c
984 5 35.7 891 6 ABU28609 Protein e
985 5 35.7 891 6 ABU49944 Protein e
986 5 35.7 892 4 AAU38250 Salmonell
987 5 35.7 892 6 ABU47096 Protein e
988 5 35.7 892 6 ABU48057 Protein e
989 5 35.7 894 6 ABU49454 Protein e
990 5 35.7 894 7 ADF04439 Bacterial
991 5 35.7 898 7 ABO63805 Klebsiell
992 5 35.7 901 4 AAU41217 Human pol
993 5 35.7 901 6 ABU15843 Protein e
994 5 35.7 904 4 AAU36814 Staphyloc
995 5 35.7 904 6 ABM71629 Staphyloc
996 5 35.7 906 7 ADC96823 E. faeciu
997 5 35.7 910 8 ADI45391 Rice isop
998 5 35.7 913 6 ABU54625 Human NOV
999 5 35.7 943 5 ABG91056 Neisseria
1000 5 35.7 943 8 ADP08381 Neisseria

ALIGNMENTS

RESULT 1
AAW21966
ID AAW21966 standard; protein; 14 AA.
AC AAW21966;
XX
XX
DT 02-DEC-1997 (first entry)
XX
DE Human cyclin I peptide fragment.
XX
KW human; cyclin I; antisense; probe; neurone; cancer; antibody.
XX
XX Homo sapiens.
XX
XX WO9712973-A1.
XX
XX 10-APR-1997.
XX
XX 07-OCT-1996; 96WO-JP002905.
XX
XX 05-OCT-1995; 95JP-00284663.
XX
XX (SUME) SUMITOMO ELECTRIC IND CO.
XX
XX Nakamura T;
XX
XX WPI; 1997-226217/20.
XX
XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
PT labelling method and cancer cell detection.
XX
XX Claim 7; Page 30; 45pp; Japanese.

XX
XX This peptide is a fragment of human cyclin I which can be specifically
CC recognised by antibodies of the invention. The antibodies are used to
CC detect the presence of cyclin I. Antisense cyclin I polynucleotides are
CC useful for as probes and can be labelled and used for detection of
CC neurones by hybridisation with mRNA for cyclin I (contained in the
CC neurones and arising by the expression of the cyclin I gene in these
CC cells). The gene can be used for detection of cancer cells by detecting
CC the expression of the cyclin I gene in these cells

SQ Sequence 14 AA;
Query Match 100.0%; Score 14; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 1,le-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCCT 14
Db 1 EDNVSENVGVCCT 14
|||||
RESULT 2
ADN01131
ID ADN01131 standard; protein; 300 AA.
XX
AC ADN01131;
XX
DT 01-JUL-2004 (first entry)
XX
DE Human cell growth, differentiation, and death-associated protein #15.
XX
KW human; cell growth; cell differentiation; cell death; CGDD;
KW cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
KW cirrhosis; hepatitis; polycythaemia vera; psoriasis; cancer;
KW developmental disorder; Cushing's syndrome; hypothyroidism;
KW neurological disorder; epilepsy; stroke; Alzheimer's disease;
KW Pick's disease; Huntington's disease; Parkinson's disease;
KW multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
KW allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
KW reproductive disorder; infertility; endometriosis; uterine fibroid.
XX
XX Homo sapiens.
XX
XX WO2004031364-A2.
XX
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
XX 03-OCT-2002; 2002US-0416205P.
XX
XX 25-OCT-2002; 2002US-0421521P.
XX
XX 21-NOV-2002; 2002US-0428376P.
XX
XX 23-DEC-2002; 2002US-0436258P.
XX
XX 10-JAN-2003; 2003US-0439292P.
XX
XX 13-FEB-2003; 2003US-0447578P.
XX
XX (INCY-) INCYTE CORP.
XX
XX (BURR/) BURRILL J D.
XX
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
XX Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
XX Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
XX Yang YG, Gietzen KJ, Hafalia AJA;
XX
XX WPI; 2004-330172/30.
XX
XX N-PSDB; ADN01156.
XX
XX New isolated polypeptides associated with cell growth, differentiation
PT and death, useful for diagnosing, treating or preventing e.g.
PT atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
PT diabetes mellitus or infertility.
XX
XX Claim 1; SEQ ID NO 15; 213pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
CC proteins that are associated with cell growth, differentiation, and death
CC (CGDD). The DNA and protein sequences of the invention are useful for
CC diagnosing, treating or preventing disorders associated with aberrant
CC expression of CGDD, such as: cell proliferative disorders (e.g.
CC arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
CC polycythaemia vera, psoriasis and cancers), developmental disorders (e.g.
CC Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
CC epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
| | | | | | | | | |
Db 343 EDNVSENVGVCVT 356

RESULT 5
AAY52185
ID AAY52185 standard; protein; 377 AA.

XX AC AAY52185;

XX DT 09-FEB-2000 (first entry)

XX DE Human cyclin I amino acid sequence.

XX KW Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
XX ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
XX KW atherosclerosis; tumour.

XX OS Homo sapiens.

XX FN WO9925829-A2.

XX PD 27-MAY-1999.

XX PF 12-NOV-1998; 98WO-US024095.

XX PR 13-NOV-1997; 97US-00969106.

XX PA (CURA-) CURAGEN CORP.

XX PI Yang M, Nandabalan K, Schulz VP;

XX WPI; 2000-061923/05.

XX DR N-PSDB; AAZ37836.

XX PT New complexes of the cyclin-dependent kinase 2 protein with its
interacting proteins, used to treat, e.g. atherosclerosis.

XX PS Example; Fig 2; 90pp; English.

XX CC This is the human Cyclin I amino acid sequence. Cyclin I is expressed at
almost constant levels throughout the cell cycle, and is implicated in
controlling cell cycle progression and transcriptional control. Cyclins
form complexes with cyclin-dependent kinases. CDK2, cyclin-dependent
kinase 2, is used in the invention which relates to complexes of the CDK2
protein with other proteins, selected from cyclin I, ERH, hsReq, hsReq*-1
and hsReq*-2 (AAY52185-Y52188). CDK2 is expressed late in G1 or early in
S phase of the cell cycle, and is pivotal for G1/S transition.

XX CC Compositions containing a CDK2 complex, an antibody targeting the
complex, and nucleotide sequences encoding CDK2 or its derivatives can be
used therapeutically. The complexes and their nucleotide sequences can be
used to treat diseases or disorders associated with increased or
decreased levels of the complex. Screening the complex, or a derivative
or a modulator of the complex for neoplastic activity by measuring the
survival or proliferation of cells from a malignant cell line when in
contact with the complex can be used to indicate if the complex has
anti-neoplastic activity. Screening for molecules that modulate the
formation of the complexes can be used for treating or preventing
atherosclerosis or atherosclerosis-associated disease by contacting cells
or using a test animal, in which tumour growth or regression is measured
to test whether anti-neoplastic activity is displayed. Diseases which can
be treated or prevented by molecule/s which modulate the function of the
complex include cancer, hyperproliferative disorders and atherosclerosis

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 14; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
| | | | | | | | | |
Db 343 EDNVSENVGVCVT 356

RESULT 6

ABR39934

ID ABR39934 standard; protein; 377 AA.

XX AC ABR39934;

XX DT 11-AUG-2003 (first entry)

XX DE Human prostate selective polypeptide Pr325.

XX KW Prostate; molecular marker; cancer; cytostatic; gene therapy; human.

XX OS Homo sapiens.

XX FN WO2003014298-A2.

XX PD 20-FEB-2003.

XX PF 02-AUG-2002; 2002WO-US024431.

XX PR 03-AUG-2001; 2001US-0309470P.

XX PR 30-OCT-2001; 2001US-0330747P.

XX PA (ORIG-) ORIGENE TECHNOLOGIES INC.

XX PI Sun Z, Li X, Jay G, Kovacs KF, Shu Y, Fan W;

XX WPI; 2003-256562/25.

XX DR N-PSDB; ACC47339.

XX PT New polynucleotide, useful for preparing a composition for treating
prostate disease, e.g., cancer.

XX PS Claim 5; Page 147-149; 212pp; English.

XX CC The invention relates to prostate selective polynucleotides and
polypeptides. The polynucleotides are expressed in prostate and are
useful as molecular markers, as drug targets, and for detecting,
monitoring, preventing or treating diseases and conditions related to
prostate, such as prostate cancers. The present sequence represents a
prostate specific polypeptide

XX SQ Sequence 377 AA;

Query Match 100.0%; Score 14; DB 6; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
| | | | | | | | | |
Db 343 EDNVSENVGVCVT 356

RESULT 7

ADP12615

ID ADP12615 standard; protein; 377 AA.

XX AC ADP12615;

XX DT 12-AUG-2004 (first entry)

XX DE Protein encoded by mRNA of the invention #225.

XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX OS Homo sapiens.

PN WO2004042346-A2.
PD 21-MAY-2004.
XX
XX 24-APR-2003; 2003WO-US012946.
XX
XX 24-APR-2002; 2002US-00131831.
PR 20-DEC-2002; 2002US-00325899.
XX
XX (EXPR-) EXPRESSION DIAGNOSTICS INC.
PA
XX Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
PI Rosenberg S;
PI
XX WPI; 2004-400724/37.
XX
XX Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
PT rejection, in an individual, comprises detecting the expression level of
PT the genes.
XX
XX Claim 65; SEQ ID NO 2624; 1762pp; English.
XX
XX The present invention relates to diagnosing or monitoring transplant
CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
CC comprises detecting the expression level of one or more genes. The
CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.
XX
XX Sequence 377 AA;
SQ
Query Match 100.0%; Score 14; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCVGT 14
Db 343 EDNVSENVGVCVGT 356
RESULT 8
ABM80569
ID ABM80569 standard; protein; 377 AA.
XX
XX AC ABM80569;
XX
XX 18-NOV-2004 (first entry)
XX
XX Tumour-associated antigenic target (TAT) polypeptide PRO4605, SEQ.1450.
XX
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX
XX Homo sapiens.
XX
XX WO2004030615-A2.
XX
XX 15-APR-2004.
XX
XX 29-SEP-2003; 2003WO-US028547.
XX

XX 02-OCT-2002; 2002US-0414971P.
PR (GETH) GENENTECH INC.
XX
XX Wu TD, Zhang Z, Zhou Y;
PI
XX WPI; 2004-347921/32.
DR N-PSDB; ACN38124.
XX
XX New tumor-associated antigenic target polypeptides and nucleic acids,
PT useful in preparing a medicament for treating or detecting a
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
PT prostate cancer or tumor.
XX
XX Claim 12; SEQ ID NO 1450; 7273pp; English.
XX
XX The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antagonists, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT polypeptide of the invention
XX
XX Sequence 377 AA;
SQ
Query Match 100.0%; Score 14; DB 8; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVGVCVGT 14
Db 343 EDNVSENVGVCVGT 356
RESULT 9
ABP35708
ID ABP35708 standard; protein; 446 AA.
XX
XX AC ABP35708;
XX
XX 24-JUL-2002 (first entry)
XX
XX Fungal ZBC protein sequence #134.
XX
XX Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein;
KW antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastatin;
KW mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine;
KW angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin;
KW fungal toxin; cell surface receptor; plant growth regulator; pigment;
KW insecticide; antineoplastic.
XX
XX Unidentified.
XX
XX WO200224865-A2.
XX
XX 28-MAR-2002.
XX
XX 19-SEP-2001; 2001WO-US029288.
XX

CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-AB130511), expressed DNA
CC sequences (AB101840-AB116175) and the encoded proteins (AB157737-
CC AB172072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 556 AA;

Query Match 50.0%; Score 7; DB 4; Length 556;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCGT 14
| | | | |
Db 131 VGSVCGT 137

RESULT 12
ABP78187
ID ABP78187 standard; protein; 1068 AA.
XX
AC ABP78187;
XX
XX 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 2904.
XX
KW Antibacterial; infection; vaccine; gene therapy.
XX
OS Neisseria gonorrhoeae.
XX
XX WO200279243-A2.
PN
XX
PD 10-OCT-2002.
XX
XX 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
XX (CHIR-) CHIRON SPA.
PA
XX Fontana MR, Pizza M, Masignani V, Monaci E;
PI
XX WPI; 2003-058415/05.
DR
DR N-PSDB; ABZ39157.

PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
PT medicament for treating or preventing N. gonorrhoeae infection.
XX

PS Disclosure; Page 401; 815pp; English.

XX The present invention relates to proteins from Neisseria gonorrhoeae.
CC Also disclosed are the nucleic acid molecules encoding the proteins and
CC antibodies that specifically bind to the proteins. The composition
CC comprising the protein, nucleic acid or antibody is useful for the
CC manufacture of a medicament for treating or preventing N. gonorrhoeae
CC infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
CC molecules of the invention
XX

SQ Sequence 1068 AA;

Query Match 50.0%; Score 7; DB 6; Length 1068;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGSV 11
| | | | |
Db 317 SENVGSV 323

RESULT 13

ADS29513
ID ADS29513 standard; protein; 1190 AA.

XX
AC ADS29513;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #18546.

XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.

PN US2003233675-A1.

XX 18-DEC-2003.

XX 20-FEB-2003; 2003US-00369493.

XX 21-FEB-2002; 2002US-0360039P.

XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.

XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI
XX WPI; 2004-061375/06.

DR

XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 18546; 122pp; English.

PS The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 1190 AA;

Query Match 50.0%; Score 7; DB 8; Length 1190;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SENVGSV 11
DB 106 SENVGSV 112
RESULT 14
AAR74214
ID AAR74214 standard; peptide; 13 AA.
AC AAR74214;
XX 25-MAR-2003 (revised)
DT 25-OCT-1995 (first entry)
XX
XX Internal fragment of bryodin-2.
XX
XX Ribosome inactivating protein; cell death; proliferation; tumour; cancer;
KW virus; malaria; trypanosomiasis; inflammation; autoimmune; disease;
KW purging; bone marrow.
XX
XX Bryonia dioica.
XX
XX WO9511977-A2.
XX
XX 04-MAY-1995.
XX
XX 25-OCT-1994; 94WO-US012382.
XX
XX 25-OCT-1993; 93US-00141891.
PR 20-OCT-1994; 94US-00324301.
XX
XX (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX Siegall CB, Gawlak SL, Marquardt H;
XX
XX WPI; 1995-178870/23.
DR
XX
XX New ribosome inactivating protein bryodin-2 and related conjugates - for
PT killing target cells, e.g. in treatment of cancer, also related nucleic
PT acid, vectors and transformed cells.
XX
XX Claim 4; Page 61; 81pp; English.
XX
XX The sequence is that of a fragment of a ribosome inactivating protein
CC termed 'bryodin-2', isolated from Bryonia dioica. Conjugates of the protein
CC with a ligand may be used to kill target cells (i.e. those to which the
CC ligand component binds specifically) or to inhibit proliferation of
CC tumour cells. Typical applications include the treatment of cancer, viral
CC infections, malaria, trypanosomiasis, inflammatory or autoimmune
CC diseases, including in vitro purging of e.g. bone marrow. See also
CC AAR74210-7. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 13 AA;
SQ
Query Match 42.9%; Score 6; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 VSENVG 9
DB 6 VSENVG 11
RESULT 15
ABG23791
ID ABG23791 standard; protein; 63 AA.
XX
XX ABG23791;
XX
XX 18-FEB-2002 (first entry)
DT
XX
XX Novel human diagnostic protein #23782.
DE

XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Dmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
DR N-PSDB; AAS87978.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
XX Claim 20; SEQ ID NO 54150; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG0010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 63 AA;
SQ
Query Match 42.9%; Score 6; DB 4; Length 63;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VGSVCG 13
DB 30 VGSVCG 35
Search completed: February 11, 2005, 03:16:41
Job time : 41.9386 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:39 ; Search time 1.21739 Seconds
(without alignments)
858.464 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGVCVT 14

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

- Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	14	3	US-09-054-492B-5
2	14	100.0	377	2	US-08-969-106-6
3	14	100.0	377	3	US-09-054-492B-1
4	14	100.0	377	4	US-09-338-125-6
5	7	50.0	446	4	US-09-538-092-781
6	6	42.9	13	1	US-08-324-301-5
7	6	42.9	282	1	US-08-324-301-15
8	6	42.9	1033	4	US-08-834-309-1
9	6	42.9	1066	3	US-09-541-782-8
10	6	42.9	1066	4	US-09-723-820-8
11	6	42.9	1066	4	US-10-270-085-8
12	6	42.9	1415	4	US-09-252-991A-26438
13	6	42.9	2362	4	US-09-949-016-8985
14	6	42.9	4544	1	US-08-469-486-52
15	6	42.9	4544	2	US-08-469-658-52
16	5	35.7	61	4	US-09-540-236-3067
17	5	35.7	65	4	US-09-107-433-4947
18	5	35.7	65	4	US-09-673-395A-264
19	5	35.7	68	4	US-09-562-737-131
20	5	35.7	70	4	US-09-107-532A-4592
21	5	35.7	70	4	US-09-107-532A-4593
22	5	35.7	87	4	US-09-328-352-4143
23	5	35.7	88	2	US-08-391-916A-10
24	5	35.7	91	4	US-09-489-039A-14306
25	5	35.7	94	4	US-09-465-558-20
26	5	35.7	97	4	US-09-562-737-126
27	5	35.7	98	4	US-09-543-681A-7281

28	5	35.7	104	4	US-09-465-558-24
29	5	35.7	108	4	US-09-270-767-46391
30	5	35.7	109	3	US-08-936-165A-440
31	5	35.7	112	4	US-09-543-681A-7275
32	5	35.7	113	4	US-09-949-016-9318
33	5	35.7	116	4	US-09-513-999C-5472
34	5	35.7	117	4	US-09-138-452A-951
35	5	35.7	118	1	US-08-300-903A-13
36	5	35.7	118	4	US-08-988-197-13
37	5	35.7	118	4	US-10-385-072-13
38	5	35.7	119	4	US-09-107-433-4937
39	5	35.7	120	4	US-09-543-681A-7262
40	5	35.7	124	4	US-09-328-352-5287
41	5	35.7	127	4	US-09-270-767-39006
42	5	35.7	127	4	US-09-270-767-54223
43	5	35.7	127	4	US-09-513-999C-4224
44	5	35.7	132	4	US-09-489-039A-11744
45	5	35.7	137	4	US-09-328-352-7715
46	5	35.7	149	4	US-09-513-999C-4257
47	5	35.7	158	4	US-09-270-767-32974
48	5	35.7	158	4	US-09-270-767-48191
49	5	35.7	162	3	US-08-078-271B-6
50	5	35.7	163	2	US-08-783-395-5
51	5	35.7	163	3	US-08-600-430-2
52	5	35.7	163	3	US-08-600-430-4
53	5	35.7	163	4	US-09-461-912A-44
54	5	35.7	163	4	US-09-949-016-6077
55	5	35.7	164	4	US-09-248-796A-19361
56	5	35.7	164	4	US-09-270-767-34036
57	5	35.7	168	4	US-09-270-767-49253
58	5	35.7	169	4	US-09-248-796A-27591
59	5	35.7	174	4	US-09-949-016-11208
60	5	35.7	175	4	US-09-418-710-65
61	5	35.7	175	4	US-09-839-479-64
62	5	35.7	176	4	US-09-418-710-66
63	5	35.7	176	4	US-09-839-479-65
64	5	35.7	183	4	US-09-270-767-47315
65	5	35.7	185	4	US-09-543-681A-6449
66	5	35.7	186	4	US-09-125-635-2
67	5	35.7	192	1	US-08-440-103-45
68	5	35.7	192	1	US-08-440-542-45
69	5	35.7	192	1	US-08-231-368-45
70	5	35.7	192	1	US-08-440-210-45
71	5	35.7	192	3	US-08-444-818-166
72	5	35.7	192	3	US-09-046-604-45
73	5	35.7	203	4	US-09-902-540-11721
74	5	35.7	204	4	US-09-562-737-127
75	5	35.7	205	3	US-09-134-001C-4766
76	5	35.7	207	3	US-08-652-877-13
77	5	35.7	207	3	US-08-476-515A-13
78	5	35.7	212	4	US-09-328-352-5832
79	5	35.7	212	4	US-09-270-767-32098
80	5	35.7	213	3	US-09-156-579C-2
81	5	35.7	225	1	US-08-300-903A-14
82	5	35.7	225	4	US-08-988-197-14
83	5	35.7	225	4	US-10-385-072-14
84	5	35.7	227	4	US-09-270-767-39404
85	5	35.7	227	4	US-09-270-767-54621
86	5	35.7	231	4	US-09-402-515A-16
87	5	35.7	232	2	US-08-738-413B-11
88	5	35.7	234	1	US-08-684-862-3
89	5	35.7	234	2	US-08-738-413B-12
90	5	35.7	236	1	US-08-684-862-4
91	5	35.7	236	2	US-08-684-862-5
92	5	35.7	236	2	US-08-738-413B-10
93	5	35.7	236	4	US-09-248-796A-16587
94	5	35.7	239	4	US-09-465-558-58
95	5	35.7	245	4	US-09-248-796A-14382
96	5	35.7	247	4	US-09-270-767-43996
97	5	35.7	251	2	US-08-665-647-7
98	5	35.7	258	4	US-09-538-092-728
99	5	35.7	261	4	US-09-107-433-5013
100	5	35.7	262	4	US-09-465-558-62

101	5	35.7	266	4	US-09-248-796A-17576	Sequence 17576, A	174	5	35.7	428	4	US-09-182-625F-9	Sequence 9, Appl
102	5	35.7	270	4	US-09-270-767-44001, A	Sequence 44001, A	175	5	35.7	428	4	US-09-182-625F-16	Sequence 16, Appl
103	5	35.7	271	4	US-09-252-991A-17292	Sequence 17292, A	176	5	35.7	432	4	US-09-103-331-40	Sequence 40, Appl
104	5	35.7	278	4	US-09-107-532A-6673	Sequence 6673, Ap	177	5	35.7	432	4	US-09-631-594-49	Sequence 49, Appl
105	5	35.7	289	4	US-09-252-991A-20221	Sequence 20221, A	178	5	35.7	433	4	US-09-248-796A-19799	Sequence 19799, A
106	5	35.7	289	4	US-09-543-681A-7998	Sequence 7998, Ap	179	5	35.7	436	3	US-09-150-213-4	Sequence 4, Appl
107	5	35.7	289	4	US-09-270-767-42634	Sequence 42634, A	180	5	35.7	448	4	US-09-949-016-9083	Sequence 9083, Ap
108	5	35.7	294	4	US-09-103-664A-5	Sequence 5, Appl	181	5	35.7	466	4	US-09-489-039A-7654	Sequence 7654, Ap
109	5	35.7	297	4	US-09-465-558-56	Sequence 56, Appl	182	5	35.7	474	4	US-09-081-385-148	Sequence 148, App
110	5	35.7	306	4	US-09-248-796A-16022	Sequence 16022, A	183	5	35.7	478	4	US-09-543-681A-7331	Sequence 7331, Ap
111	5	35.7	310	1	US-08-123-456A-37	Sequence 37, Appl	184	5	35.7	489	3	US-09-134-001C-4246	Sequence 4246, Ap
112	5	35.7	312	3	US-08-360-821B-36	Sequence 36, Appl	185	5	35.7	490	4	US-09-949-016-6091	Sequence 6091, Ap
113	5	35.7	312	4	US-09-851-026-36	Sequence 36, Appl	186	5	35.7	509	1	US-10-095-946-8	Sequence 8, Appl
114	5	35.7	313	4	US-09-583-110-4236	Sequence 4236, Ap	187	5	35.7	509	3	US-09-198-959-6	Sequence 6, Appl
115	5	35.7	313	4	US-09-107-433-3706	Sequence 3706, Ap	188	5	35.7	509	3	US-09-183-959-8	Sequence 8, Appl
116	5	35.7	316	4	US-09-538-032-397	Sequence 397, App	189	5	35.7	509	3	US-09-694-331-6	Sequence 6, Appl
117	5	35.7	319	4	US-08-835-279-2	Sequence 2, Appl	190	5	35.7	509	4	US-09-347-650-6	Sequence 6, Appl
118	5	35.7	320	3	US-09-166-205B-64	Sequence 64, Appl	191	5	35.7	509	4	US-10-072-152-6	Sequence 6, Appl
119	5	35.7	320	4	US-09-806-658-2	Sequence 2, Appl	192	5	35.7	509	4	US-09-535-315-8	Sequence 8, Appl
120	5	35.7	320	4	US-09-949-016-7144	Sequence 7144, Ap	193	5	35.7	509	4	US-09-949-016-7965	Sequence 7965, Ap
121	5	35.7	323	4	US-09-710-693-2	Sequence 2, Appl	194	5	35.7	518	4	US-09-252-991A-31644	Sequence 31644, A
122	5	35.7	326	2	US-08-784-651-4	Sequence 4, Appl	195	5	35.7	526	3	US-09-342-648-8	Sequence 8, Appl
123	5	35.7	339	3	US-08-444-818-150	Sequence 150, App	196	5	35.7	530	4	US-09-248-796A-15021	Sequence 15021, A
124	5	35.7	339	3	US-08-444-818-158	Sequence 158, App	197	5	35.7	534	4	US-09-103-664A-2	Sequence 2, Appl
125	5	35.7	340	4	US-09-543-681A-5967	Sequence 5967, Ap	198	5	35.7	541	2	US-08-540-804-16	Sequence 16, Appl
126	5	35.7	345	4	US-09-902-540-12122	Sequence 12122, A	199	5	35.7	541	2	US-08-218-265-16	Sequence 16, Appl
127	5	35.7	349	4	US-09-270-767-45401	Sequence 45401, A	200	5	35.7	541	3	US-08-521-872-16	Sequence 16, Appl
128	5	35.7	350	4	US-09-818-780-95	Sequence 95, Appl	201	5	35.7	541	3	US-08-590-399-16	Sequence 16, Appl
129	5	35.7	353	3	US-08-134-001C-5511	Sequence 5511, Ap	202	5	35.7	590	4	US-09-489-039A-10743	Sequence 10743, A
130	5	35.7	354	4	US-09-328-332-5635	Sequence 5635, Ap	203	5	35.7	610	1	US-08-212-188-2	Sequence 2, Appl
131	5	35.7	354	4	US-09-248-796A-19050	Sequence 19050, A	204	5	35.7	610	3	US-08-970-725-2	Sequence 2, Appl
132	5	35.7	359	3	US-08-809-103B-2	Sequence 2, Appl	205	5	35.7	610	5	PCT-US95-03708-2	Sequence 2, Appl
133	5	35.7	359	3	US-08-809-103B-4	Sequence 4, Appl	206	5	35.7	620	4	US-09-673-198-1	Sequence 1, Appl
134	5	35.7	359	3	US-08-809-103B-6	Sequence 6, Appl	207	5	35.7	626	4	US-09-489-039A-13113	Sequence 13113, A
135	5	35.7	359	3	US-08-809-103B-8	Sequence 8, Appl	208	5	35.7	630	3	US-08-973-462-9	Sequence 9, Appl
136	5	35.7	362	4	US-09-691-861A-4	Sequence 4, Appl	209	5	35.7	631	4	US-09-732-615-8	Sequence 8, Appl
137	5	35.7	362	4	US-09-634-238-417	Sequence 417, App	210	5	35.7	631	4	US-10-273-051-8	Sequence 8, Appl
138	5	35.7	362	4	US-09-248-796A-14994	Sequence 14994, A	211	5	35.7	645	4	US-09-543-681A-6140	Sequence 6140, Ap
139	5	35.7	366	4	US-09-248-796A-14679	Sequence 14679, A	212	5	35.7	648	4	US-09-328-352-7882	Sequence 7882, Ap
140	5	35.7	376	4	US-09-252-991A-19927	Sequence 19927, A	213	5	35.7	650	4	US-09-583-110-3221	Sequence 3221, Ap
141	5	35.7	376	4	US-09-252-991A-29172	Sequence 29172, A	214	5	35.7	650	4	US-09-107-433-3515	Sequence 3515, Ap
142	5	35.7	381	4	US-10-052-032-29	Sequence 29, Appl	215	5	35.7	686	2	US-08-849-480A-4	Sequence 4, Appl
143	5	35.7	382	2	US-08-555-268A-13	Sequence 13, Appl	216	5	35.7	704	3	US-08-792-832A-2	Sequence 2, Appl
144	5	35.7	395	3	US-08-991-426-2	Sequence 2, Appl	217	5	35.7	718	4	US-09-540-236-2753	Sequence 2753, Ap
145	5	35.7	395	3	US-09-143-470-2	Sequence 2, Appl	218	5	35.7	733	4	US-09-270-767-44442	Sequence 44442, A
146	5	35.7	395	4	US-09-771-023-8	Sequence 8, Appl	219	5	35.7	750	4	US-09-248-796A-14886	Sequence 14886, A
147	5	35.7	397	4	US-09-006-428A-2	Sequence 2, Appl	220	5	35.7	787	4	US-09-252-991A-26468	Sequence 26468, A
148	5	35.7	397	4	US-09-006-428A-19	Sequence 19, Appl	221	5	35.7	840	4	US-09-489-039A-11722	Sequence 11722, A
149	5	35.7	397	4	US-09-615-387C-2	Sequence 2, Appl	222	5	35.7	894	4	US-09-543-681A-4724	Sequence 4724, Ap
150	5	35.7	397	4	US-09-615-387C-19	Sequence 19, Appl	223	5	35.7	896	4	US-09-043-818-13	Sequence 13, Appl
151	5	35.7	400	3	US-08-938-830-29	Sequence 29, Appl	224	5	35.7	898	4	US-09-489-039A-10322	Sequence 10322, A
152	5	35.7	404	4	US-09-182-625F-14	Sequence 14, Appl	225	5	35.7	906	4	US-09-107-532A-6450	Sequence 6450, Ap
153	5	35.7	404	4	US-09-182-625F-15	Sequence 15, Appl	226	5	35.7	941	3	US-09-074-658-75	Sequence 75, Appl
154	5	35.7	407	4	US-09-431-577-78	Sequence 78, Appl	227	5	35.7	943	3	US-08-476-515A-12	Sequence 12, Appl
155	5	35.7	408	2	US-08-924-847A-2	Sequence 2, Appl	228	5	35.7	944	2	US-08-867-941-23	Sequence 23, Appl
156	5	35.7	408	3	US-09-120-052-2	Sequence 2, Appl	229	5	35.7	944	2	US-08-867-941-24	Sequence 24, Appl
157	5	35.7	413	4	US-09-328-352-4227	Sequence 4227, Ap	230	5	35.7	944	3	US-09-074-658-23	Sequence 23, Appl
158	5	35.7	415	3	US-08-938-830-1	Sequence 1, Appl	231	5	35.7	944	3	US-09-074-658-24	Sequence 24, Appl
159	5	35.7	415	3	US-09-020-222-1	Sequence 1, Appl	232	5	35.7	944	3	US-08-652-877-12	Sequence 12, Appl
160	5	35.7	416	3	US-09-457-040B-10	Sequence 10, Appl	233	5	35.7	945	4	US-09-543-681A-4200	Sequence 4200, Ap
161	5	35.7	416	4	US-09-006-428A-1	Sequence 1, Appl	234	5	35.7	1034	4	US-09-562-737-43	Sequence 43, Appl
162	5	35.7	416	4	US-09-006-428A-17	Sequence 17, Appl	235	5	35.7	1036	4	US-09-248-796A-16128	Sequence 16128, A
163	5	35.7	416	4	US-09-710-693-1	Sequence 1, Appl	236	5	35.7	1147	3	US-08-470-260-5	Sequence 5, Appl
164	5	35.7	416	4	US-09-710-693-19	Sequence 19, Appl	237	5	35.7	1147	3	US-08-471-491-5	Sequence 5, Appl
165	5	35.7	416	4	US-09-615-387C-1	Sequence 1, Appl	238	5	35.7	1147	3	US-08-466-662-5	Sequence 5, Appl
166	5	35.7	416	4	US-09-615-387C-17	Sequence 17, Appl	239	5	35.7	1181	1	US-08-053-614-4	Sequence 4, Appl
167	5	35.7	424	2	US-08-592-214A-16	Sequence 16, Appl	240	5	35.7	1181	1	US-08-316-397B-4	Sequence 4, Appl
168	5	35.7	424	3	US-08-659-188-16	Sequence 16, Appl	241	5	35.7	1181	2	US-09-034-306-4	Sequence 4, Appl
169	5	35.7	424	3	US-08-655-227-16	Sequence 16, Appl	242	5	35.7	1181	3	US-09-259-437-4	Sequence 4, Appl
170	5	35.7	424	3	US-08-655-241-16	Sequence 16, Appl	243	5	35.7	1181	5	PCT-US93-09782-4	Sequence 4, Appl
171	5	35.7	424	3	US-09-149-976-16	Sequence 16, Appl	244	5	35.7	1222	4	US-09-206-942-37	Sequence 37, Appl
172	5	35.7	424	3	US-09-398-326-16	Sequence 16, Appl	245	5	35.7	1228	4	US-09-206-942-34	Sequence 34, Appl
173	5	35.7	424	4	US-09-853-450-16	Sequence 16, Appl	246	5	35.7	1302	4	US-09-949-016-10852	Sequence 10852, A

247	5	35.7	1311	2	US-08-540-406-4	Sequence 4, Appli	320	4	28.6	13	2	US-08-482-142-68	Sequence 68, Appl
248	5	35.7	1311	3	US-08-656-055-4	Sequence 4, Appli	321	4	28.6	13	2	US-08-478-572-68	Sequence 68, Appl
249	5	35.7	1311	3	US-08-954-668-4	Sequence 4, Appli	322	4	28.6	13	3	US-08-448-194-36	Sequence 36, Appl
250	5	35.7	1311	4	US-08-918-658-4	Sequence 4, Appli	323	4	28.6	13	3	US-08-484-296-68	Sequence 36, Appl
251	5	35.7	1311	4	US-08-724-631-4	Sequence 4, Appli	324	4	28.6	13	3	US-08-867-921-36	Sequence 36, Appl
252	5	35.7	1311	4	US-08-954-701A-4	Sequence 4, Appli	325	4	28.6	13	4	US-09-878-281A-249	Sequence 249, App
253	5	35.7	1311	5	PCT-US95-13233-4	Sequence 4, Appli	326	4	28.6	14	1	US-07-794-288D-21	Sequence 21, Appl
254	5	35.7	1402	4	US-09-125-635-12	Sequence 12, Appl	327	4	28.6	14	1	US-07-794-288D-42	Sequence 42, Appl
255	5	35.7	1402	4	US-09-445-635E-2	Sequence 2, Appli	328	4	28.6	14	1	US-08-487-890A-49	Sequence 49, Appl
256	5	35.7	1420	4	US-09-125-635-4	Sequence 4, Appli	329	4	28.6	14	2	US-08-478-435-49	Sequence 49, Appl
257	5	35.7	1447	3	US-09-376-330-17	Sequence 17, Appl	330	4	28.6	14	2	US-08-337-483-49	Sequence 49, Appl
258	5	35.7	1463	4	US-09-949-016-11696	Sequence 11696, A	331	4	28.6	14	2	US-08-478-373-49	Sequence 49, Appl
259	5	35.7	1464	3	US-08-891-640-2	Sequence 2, Appli	332	4	28.6	14	3	US-08-474-671-49	Sequence 49, Appl
260	5	35.7	1464	4	US-09-949-016-6738	Sequence 6738, Ap	333	4	28.6	14	3	US-08-483-577A-49	Sequence 49, Appl
261	5	35.7	1507	4	US-09-944-259-37	Sequence 37, Appl	334	4	28.6	14	3	US-08-897-438-49	Sequence 49, Appl
262	5	35.7	1512	3	US-09-443-184-48	Sequence 48, Appl	335	4	28.6	14	3	US-08-637-654-49	Sequence 49, Appl
263	5	35.7	1786	3	US-08-973-462-8	Sequence 8, Appli	336	4	28.6	14	3	US-08-649-518-49	Sequence 49, Appl
264	5	35.7	1876	4	US-09-418-710-71	Sequence 71, Appl	337	4	28.6	15	1	US-07-720-189-9	Sequence 9, Appli
265	5	35.7	1876	4	US-09-839-479-70	Sequence 70, Appl	338	4	28.6	15	1	US-08-036-555B-49	Sequence 49, Appl
266	5	35.7	1878	4	US-09-418-710-13	Sequence 13, Appl	339	4	28.6	15	1	US-07-794-288D-20	Sequence 20, Appl
267	5	35.7	1878	4	US-09-839-479-13	Sequence 13, Appl	340	4	28.6	15	1	US-07-794-288D-41	Sequence 41, Appl
268	5	35.7	1969	4	US-09-418-710-72	Sequence 72, Appl	341	4	28.6	15	1	US-07-794-288D-210	Sequence 210, App
269	5	35.7	1969	4	US-09-839-479-71	Sequence 71, Appl	342	4	28.6	15	1	US-08-469-569-49	Sequence 49, Appl
270	5	35.7	1972	4	US-09-418-710-21	Sequence 21, Appl	343	4	28.6	15	1	US-08-222-619-9	Sequence 9, Appli
271	5	35.7	1972	4	US-09-839-479-21	Sequence 21, Appl	344	4	28.6	15	1	US-08-249-322A-49	Sequence 49, Appl
272	5	35.7	2048	3	US-08-268-347-48	Sequence 48, Appl	345	4	28.6	15	1	US-08-665-220-41	Sequence 41, Appl
273	5	35.7	2600	4	US-09-949-016-7309	Sequence 7309, Ap	346	4	28.6	15	1	US-08-665-220-46	Sequence 46, Appl
274	5	35.7	2697	4	US-10-144-198-12	Sequence 12, Appl	347	4	28.6	15	1	US-08-469-526A-49	Sequence 49, Appl
275	5	35.7	3135	1	US-08-323-170B-2	Sequence 2, Appli	348	4	28.6	15	2	US-08-618-408B-46	Sequence 46, Appl
276	5	35.7	3135	3	US-08-954-441-2	Sequence 2, Appli	349	4	28.6	15	2	US-08-734-591A-49	Sequence 49, Appl
277	5	35.7	3259	4	US-09-949-016-6507	Sequence 6507, Ap	350	4	28.6	15	2	US-08-469-660-49	Sequence 49, Appl
278	5	35.7	3289	2	US-08-477-451-2	Sequence 2, Appli	351	4	28.6	15	2	US-08-553-257A-3	Sequence 3, Appli
279	5	35.7	4654	3	US-08-476-515A-84	Sequence 84, Appl	352	4	28.6	15	3	US-09-091-001-2	Sequence 2, Appli
280	5	35.7	4655	3	US-08-652-877-84	Sequence 84, Appl	353	4	28.6	15	3	US-08-341-018-82	Sequence 82, Appl
281	5	35.7	4655	3	US-08-652-877-86	Sequence 86, Appl	354	4	28.6	15	3	US-08-470-335-49	Sequence 49, Appl
282	5	35.7	4655	3	US-08-652-877-88	Sequence 88, Appl	355	4	28.6	15	3	US-08-735-021-49	Sequence 49, Appl
283	5	35.7	4655	3	US-08-652-877-90	Sequence 90, Appl	356	4	28.6	15	3	US-08-734-664A-49	Sequence 49, Appl
284	4	28.6	4	2	US-08-667-001-8	Sequence 8, Appli	357	4	28.6	15	3	US-08-470-339-49	Sequence 49, Appl
285	4	28.6	6	5	PCT-US93-12679-13	Sequence 13, Appl	358	4	28.6	15	3	US-09-257-218-59	Sequence 59, Appl
286	4	28.6	8	1	US-08-477-727A-66	Sequence 66, Appl	359	4	28.6	15	3	US-09-311-760-59	Sequence 59, Appl
287	4	28.6	8	1	US-08-477-727A-68	Sequence 68, Appl	360	4	28.6	15	3	US-09-291-692-41	Sequence 41, Appl
288	4	28.6	8	3	US-08-444-818-335	Sequence 335, App	361	4	28.6	15	3	US-09-291-692-46	Sequence 46, Appl
289	4	28.6	8	3	US-08-444-818-336	Sequence 336, App	362	4	28.6	15	3	US-09-561-756-97	Sequence 97, Appl
290	4	28.6	8	3	US-09-139-802-157	Sequence 157, App	363	4	28.6	15	3	US-09-227-721-97	Sequence 97, Appl
291	4	28.6	8	4	US-09-659-786-157	Sequence 157, App	364	4	28.6	15	4	US-09-009-953-67	Sequence 67, Appl
292	4	28.6	8	4	US-09-926-914-157	Sequence 157, App	365	4	28.6	15	4	US-08-467-602-49	Sequence 49, Appl
293	4	28.6	9	2	US-08-177-109A-53	Sequence 53, Appl	366	4	28.6	15	4	US-08-865-579-59	Sequence 59, Appl
294	4	28.6	9	2	US-08-687-706-53	Sequence 53, Appl	367	4	28.6	15	4	US-09-441-992-3	Sequence 3, Appli
295	4	28.6	9	4	US-09-311-784A-440	Sequence 440, App	368	4	28.6	15	4	US-10-059-749-59	Sequence 59, Appl
296	4	28.6	10	1	US-07-794-288D-25	Sequence 25, Appl	369	4	28.6	15	4	US-09-954-697-97	Sequence 97, Appl
297	4	28.6	10	1	US-07-794-288D-46	Sequence 46, Appl	370	4	28.6	15	4	US-09-952-768-41	Sequence 41, Appl
298	4	28.6	10	1	US-07-794-288D-211	Sequence 211, App	371	4	28.6	15	4	US-09-952-768-46	Sequence 46, Appl
299	4	28.6	10	3	US-08-939-853A-20	Sequence 20, Appl	372	4	28.6	15	4	US-08-411-295F-113	Sequence 113, App
300	4	28.6	11	1	US-07-794-288D-24	Sequence 24, Appl	373	4	28.6	15	4	US-10-378-707-3	Sequence 3, Appli
301	4	28.6	11	1	US-07-794-288D-45	Sequence 45, Appl	374	4	28.6	15	5	PCT-US94-05083C-46	Sequence 46, Appl
302	4	28.6	11	1	US-07-794-288D-212	Sequence 212, App	375	4	28.6	15	5	PCT-US95-04075-9	Sequence 9, Appli
303	4	28.6	11	1	US-07-794-288D-217	Sequence 217, App	376	4	28.6	15	5	PCT-US95-06846A-49	Sequence 49, Appl
304	4	28.6	11	1	US-07-794-288D-222	Sequence 222, App	377	4	28.6	16	1	US-08-036-555B-37	Sequence 37, Appl
305	4	28.6	11	1	US-08-408-604A-104	Sequence 104, App	378	4	28.6	16	1	US-07-794-288D-19	Sequence 19, Appl
306	4	28.6	11	6	5260275-5	Patent No. 5260275	379	4	28.6	16	1	US-07-794-288D-40	Sequence 40, Appl
307	4	28.6	11	6	5260275-5	Patent No. 5260275	380	4	28.6	16	1	US-08-469-569-37	Sequence 37, Appl
308	4	28.6	12	1	US-07-794-288D-23	Sequence 23, Appl	381	4	28.6	16	1	US-08-222-619-30	Sequence 30, Appl
309	4	28.6	12	1	US-07-794-288D-44	Sequence 44, Appl	382	4	28.6	16	1	US-08-249-322A-37	Sequence 37, Appl
310	4	28.6	12	1	US-08-260-582-32	Sequence 32, Appl	383	4	28.6	16	1	US-08-307-724B-25	Sequence 25, Appl
311	4	28.6	12	2	US-08-406-330-40	Sequence 40, Appl	384	4	28.6	16	1	US-08-307-724B-25	Sequence 25, Appl
312	4	28.6	12	2	US-08-406-330-50	Sequence 50, Appl	385	4	28.6	16	1	US-08-459-526A-37	Sequence 37, Appl
313	4	28.6	12	2	US-08-556-557-50	Sequence 50, Appl	386	4	28.6	16	2	US-08-734-591A-37	Sequence 37, Appl
314	4	28.6	12	5	PCT-US95-05471-32	Sequence 32, Appl	387	4	28.6	16	2	US-08-469-660-37	Sequence 37, Appl
315	4	28.6	12	6	5378464-28	Patent No. 5378464	388	4	28.6	16	2	US-07-971-723-1	Sequence 1, Appli
316	4	28.6	12	6	5378464-28	Patent No. 5378464	389	4	28.6	16	3	US-08-470-335-37	Sequence 37, Appl
317	4	28.6	13	1	US-07-794-288D-22	Sequence 22, Appl	390	4	28.6	16	3	US-08-735-021-37	Sequence 37, Appl
318	4	28.6	13	1	US-07-794-288D-43	Sequence 43, Appl	391	4	28.6	16	3	US-08-734-664A-37	Sequence 37, Appl
319	4	28.6	13	1	US-08-681-812-4	Sequence 43, Appli	392	4	28.6	16	3	US-08-810-009-47	Sequence 47, Appl

333	4	28.6	16	3	US-08-470-339-37	Sequence 37, Appl	466	4	28.6	24	1	US-08-096-172A-17	Sequence 17, Appl
334	4	28.6	16	4	US-08-467-602-37	Sequence 37, Appl	467	4	28.6	24	1	US-08-096-172A-18	Sequence 18, Appl
335	4	28.6	16	4	US-09-776-490-47	Sequence 37, Appl	468	4	28.6	24	1	US-08-484-635-107	Sequence 107, Appl
336	4	28.6	16	5	PCT-US94-050830-37	Sequence 37, Appl	469	4	28.6	24	2	US-08-484-631-107	Sequence 107, Appl
337	4	28.6	16	5	PCT-US95-04075-30	Sequence 30, Appl	470	4	28.6	24	2	US-08-310-312A-70	Sequence 70, Appl
338	4	28.6	16	5	PCT-US95-06846A-37	Sequence 37, Appl	471	4	28.6	24	2	US-08-827-570-107	Sequence 107, Appl
339	4	28.6	17	1	US-07-798-776-24	Sequence 24, Appl	472	4	28.6	24	3	US-08-841-085-70	Sequence 70, Appl
340	4	28.6	17	1	US-07-794-288D-18	Sequence 18, Appl	473	4	28.6	24	3	US-09-301-089-70	Sequence 70, Appl
341	4	28.6	17	3	US-07-794-288D-39	Sequence 39, Appl	474	4	28.6	24	5	PCT-US94-08380-10	Sequence 10, Appl
342	4	28.6	17	3	US-08-251-288A-24	Sequence 24, Appl	475	4	28.6	24	5	PCT-US94-08380-11	Sequence 11, Appl
343	4	28.6	17	3	US-09-298-819A-24	Sequence 24, Appl	476	4	28.6	24	5	PCT-US94-08380-12	Sequence 12, Appl
344	4	28.6	17	4	US-09-586-563C-24	Sequence 24, Appl	477	4	28.6	24	5	PCT-US94-08380-13	Sequence 13, Appl
345	4	28.6	17	4	US-09-586-562C-24	Sequence 24, Appl	478	4	28.6	24	5	PCT-US94-08380-14	Sequence 14, Appl
346	4	28.6	17	6	5223424-4	Patent No. 5223424	479	4	28.6	24	5	PCT-US94-08380-15	Sequence 15, Appl
347	4	28.6	17	6	5223424-4	Patent No. 5223424	480	4	28.6	24	5	PCT-US94-08380-16	Sequence 16, Appl
348	4	28.6	18	1	US-07-794-288D-17	Sequence 17, Appl	481	4	28.6	24	5	PCT-US94-08380-17	Sequence 17, Appl
349	4	28.6	18	1	US-07-794-288D-38	Sequence 38, Appl	482	4	28.6	24	5	PCT-US94-08380-18	Sequence 18, Appl
350	4	28.6	18	1	US-07-794-288D-214	Sequence 214, Appl	483	4	28.6	24	5	PCT-US95-04570-70	Sequence 70, Appl
351	4	28.6	19	1	US-07-794-288D-16	Sequence 16, Appl	484	4	28.6	24	5	PCT-US95-04570-70	Sequence 70, Appl
352	4	28.6	19	1	US-07-794-288D-37	Sequence 37, Appl	485	4	28.6	24	5	US-07-794-288D-10	Sequence 10, Appl
353	4	28.6	19	1	US-07-794-288D-95	Sequence 95, Appl	486	4	28.6	25	1	US-07-794-288D-31	Sequence 31, Appl
354	4	28.6	19	1	US-07-794-288D-226	Sequence 226, Appl	487	4	28.6	25	1	US-07-794-288D-113	Sequence 113, Appl
355	4	28.6	19	1	US-08-446-632-68	Sequence 68, Appl	488	4	28.6	25	1	US-07-794-288D-120	Sequence 120, Appl
356	4	28.6	19	2	US-08-488-351A-68	Sequence 68, Appl	489	4	28.6	25	1	US-07-794-288D-137	Sequence 137, Appl
357	4	28.6	19	2	US-08-729-152-16	Sequence 16, Appl	490	4	28.6	25	1	US-07-794-288D-144	Sequence 144, Appl
358	4	28.6	19	3	US-09-329-350-29	Sequence 29, Appl	491	4	28.6	25	1	US-07-794-288D-206	Sequence 206, Appl
359	4	28.6	19	3	US-09-524-435-11	Sequence 11, Appl	492	4	28.6	25	1	US-08-096-172A-28	Sequence 28, Appl
360	4	28.6	19	4	US-09-441-502B-77	Sequence 77, Appl	493	4	28.6	25	1	US-08-096-172A-30	Sequence 30, Appl
361	4	28.6	19	4	US-08-841-636A-29	Sequence 29, Appl	494	4	28.6	25	1	US-08-096-172A-31	Sequence 31, Appl
362	4	28.6	20	1	US-07-794-288D-15	Sequence 15, Appl	495	4	28.6	25	1	US-08-096-172A-32	Sequence 32, Appl
363	4	28.6	20	1	US-07-794-288D-36	Sequence 36, Appl	496	4	28.6	25	1	US-08-096-172A-33	Sequence 33, Appl
364	4	28.6	20	1	US-07-794-288D-92	Sequence 92, Appl	497	4	28.6	25	1	US-08-096-172A-34	Sequence 34, Appl
365	4	28.6	20	1	US-07-794-288D-97	Sequence 97, Appl	498	4	28.6	25	1	US-08-096-172A-35	Sequence 35, Appl
366	4	28.6	20	1	US-07-794-288D-209	Sequence 209, Appl	499	4	28.6	25	1	US-08-096-172A-36	Sequence 36, Appl
367	4	28.6	20	2	US-08-934-915-13	Sequence 13, Appl	500	4	28.6	25	1	US-08-096-172A-37	Sequence 37, Appl
368	4	28.6	20	3	US-08-612-973-79	Sequence 79, Appl	501	4	28.6	25	1	US-08-096-172A-38	Sequence 38, Appl
369	4	28.6	20	3	US-08-612-973-80	Sequence 80, Appl	502	4	28.6	25	1	US-08-096-172A-39	Sequence 39, Appl
370	4	28.6	20	3	US-08-927-597-79	Sequence 79, Appl	503	4	28.6	25	1	US-08-096-172A-40	Sequence 40, Appl
371	4	28.6	20	3	US-08-927-597-80	Sequence 80, Appl	504	4	28.6	25	1	US-08-096-172A-41	Sequence 41, Appl
372	4	28.6	20	4	US-08-635-886C-35	Sequence 35, Appl	505	4	28.6	25	1	US-08-096-172A-42	Sequence 42, Appl
373	4	28.6	20	4	US-08-635-886C-36	Sequence 36, Appl	506	4	28.6	25	1	US-08-096-172A-43	Sequence 43, Appl
374	4	28.6	20	4	US-10-053-485-48	Sequence 48, Appl	507	4	28.6	25	1	US-08-096-172A-44	Sequence 44, Appl
375	4	28.6	20	4	US-08-974-690C-35	Sequence 35, Appl	508	4	28.6	25	1	US-08-096-172A-45	Sequence 45, Appl
376	4	28.6	20	4	US-08-974-690C-36	Sequence 36, Appl	509	4	28.6	25	1	US-08-096-172A-46	Sequence 46, Appl
377	4	28.6	20	4	US-08-974-685-35	Sequence 35, Appl	510	4	28.6	25	1	US-08-096-172A-47	Sequence 47, Appl
378	4	28.6	20	4	US-08-974-685-36	Sequence 36, Appl	511	4	28.6	25	1	US-08-096-172A-48	Sequence 48, Appl
379	4	28.6	20	4	US-09-667-857-407	Sequence 407, Appl	512	4	28.6	25	1	US-08-096-172A-49	Sequence 49, Appl
380	4	28.6	20	4	US-09-991-433-49	Sequence 49, Appl	513	4	28.6	25	1	US-08-096-172A-50	Sequence 50, Appl
381	4	28.6	20	4	US-09-991-433-50	Sequence 50, Appl	514	4	28.6	25	1	US-08-096-172A-51	Sequence 51, Appl
382	4	28.6	21	1	US-07-794-288D-14	Sequence 14, Appl	515	4	28.6	25	1	US-08-096-172A-52	Sequence 52, Appl
383	4	28.6	21	1	US-07-794-288D-35	Sequence 35, Appl	516	4	28.6	25	1	US-08-096-172A-53	Sequence 53, Appl
384	4	28.6	21	6	5171839-6	Patent No. 5171839	517	4	28.6	25	1	US-08-096-172A-54	Sequence 54, Appl
385	4	28.6	21	6	5171839-6	Patent No. 5171839	518	4	28.6	25	1	US-08-096-172A-55	Sequence 55, Appl
386	4	28.6	21	6	5171839-6	Patent No. 5171839	519	4	28.6	25	1	US-08-096-172A-56	Sequence 56, Appl
387	4	28.6	22	1	US-07-794-288D-13	Sequence 13, Appl	520	4	28.6	25	1	US-08-096-172A-57	Sequence 57, Appl
388	4	28.6	22	1	US-07-794-288D-34	Sequence 34, Appl	521	4	28.6	25	1	US-08-096-172A-58	Sequence 58, Appl
389	4	28.6	23	1	US-07-794-288D-12	Sequence 12, Appl	522	4	28.6	25	1	US-08-096-172A-59	Sequence 59, Appl
390	4	28.6	23	1	US-07-794-288D-33	Sequence 33, Appl	523	4	28.6	25	1	US-08-096-172A-60	Sequence 60, Appl
391	4	28.6	23	1	US-09-270-767-60883	Sequence 60883, A	524	4	28.6	25	1	US-08-096-172A-61	Sequence 61, Appl
392	4	28.6	24	1	US-07-794-288D-11	Sequence 11, Appl	525	4	28.6	25	1	US-08-096-172A-62	Sequence 62, Appl
393	4	28.6	24	1	US-07-794-288D-32	Sequence 32, Appl	526	4	28.6	25	1	US-08-096-172A-63	Sequence 63, Appl
394	4	28.6	24	1	US-07-794-288D-93	Sequence 93, Appl	527	4	28.6	25	1	US-08-096-172A-64	Sequence 64, Appl
395	4	28.6	24	1	US-07-794-288D-121	Sequence 121, Appl	528	4	28.6	25	1	US-08-096-172A-65	Sequence 65, Appl
396	4	28.6	24	1	US-07-794-288D-145	Sequence 145, Appl	529	4	28.6	25	1	US-08-096-172A-66	Sequence 66, Appl
397	4	28.6	24	1	US-07-794-288D-199	Sequence 199, Appl	530	4	28.6	25	1	US-08-096-172A-67	Sequence 67, Appl
398	4	28.6	24	1	US-07-794-288D-207	Sequence 207, Appl	531	4	28.6	25	1	US-08-096-172A-68	Sequence 68, Appl
399	4	28.6	24	1	US-07-794-288D-215	Sequence 215, Appl	532	4	28.6	25	1	US-08-096-172A-69	Sequence 69, Appl
400	4	28.6	24	1	US-08-096-172A-10	Sequence 10, Appl	533	4	28.6	25	1	US-08-096-172A-70	Sequence 70, Appl
401	4	28.6	24	1	US-08-096-172A-11	Sequence 11, Appl	534	4	28.6	25	1	US-08-096-172A-71	Sequence 71, Appl
402	4	28.6	24	1	US-08-096-172A-12	Sequence 12, Appl	535	4	28.6	25	1	US-08-096-172A-72	Sequence 72, Appl
403	4	28.6	24	1	US-08-096-172A-13	Sequence 13, Appl	536	4	28.6	25	1	US-08-096-172A-73	Sequence 73, Appl
404	4	28.6	24	1	US-08-096-172A-14	Sequence 14, Appl	537	4	28.6	25	1	US-08-096-172A-74	Sequence 74, Appl
405	4	28.6	24	1	US-08-096-172A-15	Sequence 15, Appl	538	4	28.6	25	1	US-08-096-172A-75	Sequence 75, Appl
406	4	28.6	24	1	US-08-096-172A-16	Sequence 16, Appl	539	4	28.6	25	1	US-08-096-172A-76	Sequence 76, Appl
407	4	28.6	24	1	US-08-096-172A-17	Sequence 17, Appl	540	4	28.6	25	1	US-08-096-172A-77	Sequence 77, Appl
408	4	28.6	24	1	US-08-096-172A-18	Sequence 18, Appl	541	4	28.6	25	1	US-08-096-172A-78	Sequence 78, Appl
409	4	28.6	24	1	US-08-096-172A-19	Sequence 19, Appl	542	4	28.6	25	1	US-08-096-172A-79	Sequence 79, Appl
410	4	28.6	24	1	US-08-096-172A-20	Sequence 20, Appl	543	4	28.6	25	1	US-08-096-172A-80	Sequence 80, Appl
411	4	28.6	24	1	US-08-096-172A-21	Sequence 21, Appl	544	4	28.6	25	1	US-08-096-172A-81	Sequence 81, Appl
412	4	28.6	24	1	US-08-096-172A-22	Sequence 22, Appl	545	4	28.6	25	1	US-08-096-172A-82	Sequence 82, Appl
413	4	28.6	24	1	US-08-096-172A-23	Sequence 23, Appl	546	4	28.6	25	1	US-08-096-172A-83	Sequence 83, Appl
414	4	28.6	24	1	US-08-096-172A-24	Sequence 24, Appl	547	4	28.6	25	1	US-08-096-172A-84	Sequence 84, Appl
415	4	28.6	24	1	US-08-096-172A-25	Sequence 25, Appl	548	4	28.6	25	1	US-08-096-172A-85	Sequence 85, Appl
416	4	28.6	24	1	US-08-096-172A-26	Sequence 26, Appl	549	4	28.6	25	1	US-08-096-172A-86	Sequence 86, Appl
417	4	28.6	24	1	US-08-096-172A-27	Sequence 27, Appl	550	4	28.6	25	1	US-08-096-172A-87	Sequence 87, Appl
418	4	28.6	24	1	US-08-096-172A-28	Sequence 28, Appl	551	4	28.6	25	1	US-08-096-172A-88	Sequence 88, Appl
419	4	28.6	24	1	US-08-096-172A-29	Sequence 29, Appl	552	4	28.6	25	1	US-08-096-172A-89	Sequence 89, Appl
420	4	28.6	24	1	US-08-096-172A-30	Sequence 30, Appl	553	4					

539	4	28.6	26	2	US-08-478-572-48	Sequence 48, Appl	612	4	28.6	30	3	US-08-504-538A-15	Sequence 15, Appl
540	4	28.6	26	2	US-08-478-572-66	Sequence 66, Appl	613	4	28.6	30	3	US-09-070-504-2	Sequence 2, Appl
541	4	28.6	26	2	US-08-478-572-67	Sequence 67, Appl	614	4	28.6	30	3	US-09-070-504-19	Sequence 19, Appl
542	4	28.6	26	2	US-08-478-572-112	Sequence 112, App	615	4	28.6	30	3	US-09-227-357-662	Sequence 662, App
543	4	28.6	26	3	US-08-484-296-48	Sequence 48, Appl	616	4	28.6	30	3	US-08-630-052-15	Sequence 15, Appl
544	4	28.6	26	3	US-08-484-296-66	Sequence 66, Appl	617	4	28.6	30	4	US-09-537-226-11	Sequence 11, Appl
545	4	28.6	26	3	US-08-484-296-67	Sequence 67, Appl	618	4	28.6	30	4	US-09-813-345C-1	Sequence 1, Appl
546	4	28.6	26	3	US-08-484-296-112	Sequence 112, App	619	4	28.6	30	4	US-09-813-345C-2	Sequence 2, Appl
547	4	28.6	26	3	US-09-227-357-579	Sequence 579, App	620	4	28.6	30	4	US-09-813-345C-18	Sequence 18, Appl
548	4	28.6	26	5	PCT-US95-04481-25	Sequence 25, Appl	621	4	28.6	30	4	US-09-813-345C-19	Sequence 19, Appl
549	4	28.6	27	1	US-07-794-288D-8	Sequence 8, Appl	622	4	28.6	30	5	PCT-US95-09307-15	Sequence 15, Appl
550	4	28.6	27	1	US-07-794-288D-29	Sequence 29, Appl	623	4	28.6	30	5	PCT-US95-09307-15	Sequence 15, Appl
551	4	28.6	27	1	US-07-794-288D-66	Sequence 66, Appl	624	4	28.6	30	6	5260275-4	Patent No. 5260275
552	4	28.6	27	1	US-07-794-288D-74	Sequence 74, Appl	625	4	28.6	30	6	5260275-4	Patent No. 5260275
553	4	28.6	27	1	US-07-794-288D-104	Sequence 104, App	626	4	28.6	31	3	US-08-504-538A-14	Sequence 14, Appl
554	4	28.6	27	1	US-07-794-288D-111	Sequence 111, App	627	4	28.6	31	3	US-09-070-504-18	Sequence 18, Appl
555	4	28.6	27	1	US-07-794-288D-128	Sequence 128, App	628	4	28.6	31	3	US-08-630-052-14	Sequence 14, Appl
556	4	28.6	27	1	US-07-794-288D-135	Sequence 135, App	629	4	28.6	31	5	PCT-US95-09307-14	Sequence 14, Appl
557	4	28.6	27	2	US-08-482-142-47	Sequence 47, Appl	630	4	28.6	31	6	5256643-14	Patent No. 5256643
558	4	28.6	27	2	US-08-482-142-111	Sequence 111, App	631	4	28.6	31	6	5256643-14	Patent No. 5256643
559	4	28.6	27	2	US-08-478-572-47	Sequence 47, Appl	632	4	28.6	32	1	US-08-190-802A-110	Sequence 110, App
560	4	28.6	27	2	US-08-478-572-111	Sequence 111, App	633	4	28.6	32	1	US-08-190-802A-114	Sequence 114, App
561	4	28.6	27	3	US-08-484-296-47	Sequence 47, Appl	634	4	28.6	32	1	US-08-477-727A-76	Sequence 76, Appl
562	4	28.6	27	3	US-08-484-296-111	Sequence 111, App	635	4	28.6	32	1	US-08-477-727A-78	Sequence 78, Appl
563	4	28.6	27	4	US-09-205-258-702	Sequence 702, App	636	4	28.6	32	3	US-08-477-346-110	Sequence 110, App
564	4	28.6	27	4	US-09-084-303B-293	Sequence 293, App	637	4	28.6	32	3	US-08-477-346-114	Sequence 114, App
565	4	28.6	27	5	PCT-US95-04481-24	Sequence 24, Appl	638	4	28.6	32	3	US-08-473-089-110	Sequence 110, App
566	4	28.6	28	1	US-07-794-288D-7	Sequence 7, Appl	639	4	28.6	32	4	US-08-487-072A-110	Sequence 110, App
567	4	28.6	28	1	US-07-794-288D-28	Sequence 28, App	640	4	28.6	32	4	US-08-487-072A-114	Sequence 114, App
568	4	28.6	28	1	US-07-794-288D-65	Sequence 65, Appl	641	4	28.6	33	1	US-07-927-755A-4	Sequence 4, Appl
569	4	28.6	28	1	US-07-794-288D-73	Sequence 73, Appl	642	4	28.6	33	1	US-07-927-755A-5	Sequence 5, Appl
570	4	28.6	28	1	US-07-794-288D-103	Sequence 103, App	643	4	28.6	33	1	US-07-927-755A-6	Sequence 6, Appl
571	4	28.6	28	1	US-07-794-288D-127	Sequence 127, App	644	4	28.6	33	1	US-07-927-755A-7	Sequence 7, Appl
572	4	28.6	28	4	US-08-469-260A-456	Sequence 456, App	645	4	28.6	33	1	US-07-927-755A-8	Sequence 8, Appl
573	4	28.6	28	4	US-08-488-446-456	Sequence 456, App	646	4	28.6	33	2	US-08-461-990B-9	Sequence 9, Appl
574	4	28.6	28	4	US-08-467-344A-456	Sequence 456, App	647	4	28.6	33	2	US-09-433-428D-41	Sequence 41, Appl
575	4	28.6	28	4	US-09-302-626B-156	Sequence 156, App	648	4	28.6	33	3	US-09-433-428D-45	Sequence 45, Appl
576	4	28.6	28	4	US-08-424-550B-456	Sequence 456, App	649	4	28.6	34	1	US-07-927-755A-1	Sequence 1, Appl
577	4	28.6	28	6	5248606-12	Patent No. 5248606	650	4	28.6	34	1	US-07-927-755A-2	Sequence 2, Appl
578	4	28.6	28	6	5248606-12	Patent No. 5248606	651	4	28.6	34	1	US-07-927-755A-3	Sequence 3, Appl
579	4	28.6	29	1	US-07-794-288D-6	Sequence 6, Appl	652	4	28.6	34	1	US-08-262-037-38	Sequence 38, Appl
580	4	28.6	29	1	US-07-794-288D-27	Sequence 27, Appl	653	4	28.6	35	2	US-08-482-142-113	Sequence 113, App
581	4	28.6	29	1	US-07-794-288D-64	Sequence 64, Appl	654	4	28.6	35	2	US-08-478-572-113	Sequence 113, App
582	4	28.6	29	1	US-07-794-288D-72	Sequence 72, Appl	655	4	28.6	35	2	US-08-460-890A-45	Sequence 45, Appl
583	4	28.6	29	1	US-07-794-288D-90	Sequence 90, Appl	656	4	28.6	35	3	US-08-167-641C-45	Sequence 45, Appl
584	4	28.6	29	1	US-07-794-288D-91	Sequence 91, Appl	657	4	28.6	35	3	US-08-460-971A-45	Sequence 45, Appl
585	4	28.6	29	1	US-07-794-288D-94	Sequence 94, Appl	658	4	28.6	35	3	US-08-462-040-45	Sequence 45, Appl
586	4	28.6	29	1	US-07-794-288D-96	Sequence 96, Appl	659	4	28.6	35	3	US-08-484-296-113	Sequence 113, App
587	4	28.6	29	1	US-07-794-288D-183	Sequence 183, App	660	4	28.6	35	4	US-09-431-705-24	Sequence 24, Appl
588	4	28.6	29	1	US-07-794-288D-184	Sequence 184, App	661	4	28.6	35	4	US-09-374-958C-13	Sequence 13, Appl
589	4	28.6	29	1	US-07-794-288D-185	Sequence 185, App	662	4	28.6	36	1	US-08-117-080-2	Sequence 2, Appl
590	4	28.6	29	1	US-07-794-288D-186	Sequence 186, App	663	4	28.6	36	1	US-08-117-080-4	Sequence 4, Appl
591	4	28.6	29	1	US-07-794-288D-187	Sequence 187, App	664	4	28.6	36	1	US-08-471-329-2	Sequence 2, Appl
592	4	28.6	29	1	US-07-794-288D-188	Sequence 188, App	665	4	28.6	36	1	US-08-471-329-4	Sequence 4, Appl
593	4	28.6	29	1	US-08-378-761A-28	Sequence 28, Appl	666	4	28.6	36	1	US-08-477-727A-79	Sequence 79, Appl
594	4	28.6	29	1	US-08-485-286-28	Sequence 28, Appl	667	4	28.6	36	1	US-08-477-727A-83	Sequence 83, Appl
595	4	28.6	29	3	US-08-471-675A-1	Sequence 1, Appl	668	4	28.6	36	1	US-08-477-727A-86	Sequence 86, Appl
596	4	28.6	29	3	US-09-177-249-189	Sequence 189, App	669	4	28.6	36	1	US-08-477-727A-88	Sequence 88, Appl
597	4	28.6	29	3	US-09-070-504-1	Sequence 1, Appl	670	4	28.6	36	1	US-08-477-727A-92	Sequence 92, Appl
598	4	28.6	29	4	US-09-812-283-189	Sequence 189, App	671	4	28.6	36	1	US-08-477-727A-98	Sequence 98, Appl
599	4	28.6	30	1	US-07-794-288D-5	Sequence 5, Appl	672	4	28.6	36	1	US-08-471-675A-5	Sequence 5, Appl
600	4	28.6	30	1	US-07-794-288D-26	Sequence 26, Appl	673	4	28.6	36	1	US-08-471-675A-7	Sequence 7, Appl
601	4	28.6	30	1	US-07-794-288D-175	Sequence 175, App	674	4	28.6	36	1	US-08-471-675A-10	Sequence 10, Appl
602	4	28.6	30	1	US-07-794-288D-176	Sequence 176, App	675	4	28.6	36	1	US-08-471-675A-11	Sequence 11, Appl
603	4	28.6	30	1	US-07-794-288D-177	Sequence 177, App	676	4	28.6	36	1	US-08-471-675A-14	Sequence 14, Appl
604	4	28.6	30	1	US-07-794-288D-178	Sequence 178, App	677	4	28.6	36	1	US-08-471-675A-20	Sequence 20, Appl
605	4	28.6	30	1	US-07-794-288D-179	Sequence 179, App	678	4	28.6	36	2	US-08-915-142-2	Sequence 2, Appl
606	4	28.6	30	1	US-07-794-288D-180	Sequence 180, App	679	4	28.6	36	2	US-08-915-142-4	Sequence 4, Appl
607	4	28.6	30	1	US-07-794-288D-195	Sequence 195, App	680	4	28.6	36	2	US-08-505-486-85	Sequence 85, Appl
608	4	28.6	30	1	US-07-794-288D-208	Sequence 208, App	681	4	28.6	36	2	US-08-892-549-7	Sequence 7, Appl
609	4	28.6	30	1	US-07-794-288D-218	Sequence 218, App	682	4	28.6	36	2	US-08-892-549-11	Sequence 11, Appl
610	4	28.6	30	1	US-07-794-288D-225	Sequence 225, App	683	4	28.6	36	2	US-08-892-549-14	Sequence 14, Appl
611	4	28.6	30	2	US-08-753-829A-8	Sequence 8, Appl	684	4	28.6	36	2	US-08-892-549-15	Sequence 15, Appl

685	4	28.6	36	2	US-08-892-549-18	Sequence 18, Appl	758	1	US-08-471-675A-12	Sequence 12, Appl
686	4	28.6	36	2	US-08-892-549-24	Sequence 24, Appl	759	1	US-08-471-675A-13	Sequence 13, Appl
687	4	28.6	36	2	US-08-892-549-39	Sequence 39, Appl	760	1	US-08-471-675A-15	Sequence 15, Appl
688	4	28.6	36	2	US-08-892-549-40	Sequence 40, Appl	761	1	US-08-471-675A-16	Sequence 16, Appl
689	4	28.6	36	3	US-08-801-028-85	Sequence 85, Appl	762	1	US-08-471-675A-17	Sequence 17, Appl
690	4	28.6	36	3	US-09-340-154-85	Sequence 85, Appl	763	1	US-08-471-675A-18	Sequence 18, Appl
691	4	28.6	36	3	US-08-302-069A-4	Sequence 4, Appl	764	1	US-08-471-675A-19	Sequence 19, Appl
692	4	28.6	36	3	US-08-302-069A-6	Sequence 6, Appl	765	1	US-08-471-675A-21	Sequence 21, Appl
693	4	28.6	36	3	US-08-302-069A-9	Sequence 9, Appl	766	1	US-08-471-675A-22	Sequence 22, Appl
694	4	28.6	36	3	US-08-302-069A-10	Sequence 10, Appl	767	1	US-08-471-675A-23	Sequence 23, Appl
695	4	28.6	36	3	US-08-302-069A-13	Sequence 13, Appl	768	1	US-08-259-762-1	Sequence 1, Appl
696	4	28.6	36	3	US-08-302-069A-19	Sequence 19, Appl	769	1	US-08-259-762-2	Sequence 2, Appl
697	4	28.6	36	3	US-09-482-611B-85	Sequence 85, Appl	770	1	US-08-259-762-3	Sequence 3, Appl
698	4	28.6	36	4	US-09-576-062A-4	Sequence 4, Appl	771	1	US-08-259-762-4	Sequence 4, Appl
699	4	28.6	36	4	US-09-576-062A-6	Sequence 6, Appl	772	1	US-08-259-762-5	Sequence 5, Appl
700	4	28.6	36	4	US-09-576-062A-9	Sequence 9, Appl	773	1	US-08-259-762-6	Sequence 6, Appl
701	4	28.6	36	4	US-09-576-062A-10	Sequence 10, Appl	774	1	US-08-259-762-7	Sequence 7, Appl
702	4	28.6	36	4	US-09-576-062A-13	Sequence 13, Appl	775	1	US-08-259-762-8	Sequence 8, Appl
703	4	28.6	36	4	US-09-576-062A-19	Sequence 19, Appl	776	1	US-08-259-762-9	Sequence 9, Appl
704	4	28.6	36	4	US-09-454-533-7	Sequence 7, Appl	777	1	US-08-801-863-8	Sequence 8, Appl
705	4	28.6	36	4	US-09-454-533-11	Sequence 11, Appl	778	1	US-08-801-863-9	Sequence 9, Appl
706	4	28.6	36	4	US-09-454-533-14	Sequence 14, Appl	779	1	US-08-801-863-10	Sequence 10, Appl
707	4	28.6	36	4	US-09-454-533-15	Sequence 15, Appl	780	1	US-08-486-596A-8	Sequence 8, Appl
708	4	28.6	36	4	US-09-454-533-18	Sequence 18, Appl	781	1	US-08-486-596A-9	Sequence 9, Appl
709	4	28.6	36	4	US-09-454-533-24	Sequence 24, Appl	782	1	US-08-486-596A-10	Sequence 10, Appl
710	4	28.6	36	4	US-09-454-533-39	Sequence 39, Appl	783	1	US-08-488-351A-66	Sequence 66, Appl
711	4	28.6	36	4	US-09-454-533-40	Sequence 40, Appl	784	1	US-08-313-185-3	Sequence 3, Appl
712	4	28.6	36	4	US-09-270-767-41321	Sequence 41321, A	785	1	US-08-459-499-6	Sequence 6, Appl
713	4	28.6	36	4	US-09-270-767-56537	Sequence 56537, A	786	1	US-09-004-713-8	Sequence 8, Appl
714	4	28.6	36	5	PCT-US95-09338-85	Sequence 85, Appl	787	1	US-09-004-713-9	Sequence 9, Appl
715	4	28.6	36	5	PCT-US95-09339-85	Sequence 85, Appl	788	1	US-09-004-713-10	Sequence 10, Appl
716	4	28.6	37	1	US-08-117-080-1	Sequence 1, Appl	789	1	US-08-619-841-1	Sequence 1, Appl
717	4	28.6	37	1	US-08-117-080-3	Sequence 3, Appl	790	1	US-08-619-841-2	Sequence 2, Appl
718	4	28.6	37	1	US-07-794-288D-1	Sequence 1, Appl	791	1	US-08-915-142-1	Sequence 1, Appl
719	4	28.6	37	1	US-07-794-288D-2	Sequence 2, Appl	792	1	US-08-915-142-3	Sequence 3, Appl
720	4	28.6	37	1	US-07-794-288D-3	Sequence 3, Appl	793	1	US-08-505-486-84	Sequence 84, Appl
721	4	28.6	37	1	US-07-929-206-6	Sequence 6, Appl	794	1	US-08-446-929A-1	Sequence 1, Appl
722	4	28.6	37	1	US-08-233-389C-8	Sequence 8, Appl	795	1	US-08-446-929A-2	Sequence 2, Appl
723	4	28.6	37	1	US-08-233-389C-9	Sequence 9, Appl	796	1	US-08-892-549-1	Sequence 1, Appl
724	4	28.6	37	1	US-08-233-389C-10	Sequence 10, Appl	797	1	US-08-892-549-2	Sequence 2, Appl
725	4	28.6	37	1	US-08-471-329-1	Sequence 1, Appl	798	1	US-08-892-549-3	Sequence 3, Appl
726	4	28.6	37	1	US-08-471-329-3	Sequence 3, Appl	799	1	US-08-892-549-4	Sequence 4, Appl
727	4	28.6	37	1	US-08-477-727A-4	Sequence 4, Appl	800	1	US-08-892-549-5	Sequence 5, Appl
728	4	28.6	37	1	US-08-477-727A-5	Sequence 5, Appl	801	1	US-08-892-549-8	Sequence 8, Appl
729	4	28.6	37	1	US-08-477-727A-17	Sequence 17, Appl	802	1	US-08-892-549-9	Sequence 9, Appl
730	4	28.6	37	1	US-08-477-727A-29	Sequence 29, Appl	803	1	US-08-892-549-10	Sequence 10, Appl
731	4	28.6	37	1	US-08-477-727A-30	Sequence 30, Appl	804	1	US-08-892-549-12	Sequence 12, Appl
732	4	28.6	37	1	US-08-477-727A-42	Sequence 42, Appl	805	1	US-08-892-549-13	Sequence 13, Appl
733	4	28.6	37	1	US-08-477-727A-75	Sequence 75, Appl	806	1	US-08-892-549-16	Sequence 16, Appl
734	4	28.6	37	1	US-08-477-727A-77	Sequence 77, Appl	807	1	US-08-892-549-17	Sequence 17, Appl
735	4	28.6	37	1	US-08-477-727A-80	Sequence 80, Appl	808	1	US-08-892-549-19	Sequence 19, Appl
736	4	28.6	37	1	US-08-477-727A-81	Sequence 81, Appl	809	1	US-08-892-549-20	Sequence 20, Appl
737	4	28.6	37	1	US-08-477-727A-82	Sequence 82, Appl	810	1	US-08-892-549-21	Sequence 21, Appl
738	4	28.6	37	1	US-08-477-727A-84	Sequence 84, Appl	811	1	US-08-892-549-22	Sequence 22, Appl
739	4	28.6	37	1	US-08-477-727A-85	Sequence 85, Appl	812	1	US-08-892-549-23	Sequence 23, Appl
740	4	28.6	37	1	US-08-477-727A-87	Sequence 87, Appl	813	1	US-08-892-549-25	Sequence 25, Appl
741	4	28.6	37	1	US-08-477-727A-89	Sequence 89, Appl	814	1	US-08-892-549-26	Sequence 26, Appl
742	4	28.6	37	1	US-08-477-727A-90	Sequence 90, Appl	815	1	US-08-892-549-27	Sequence 27, Appl
743	4	28.6	37	1	US-08-477-727A-91	Sequence 91, Appl	816	1	US-08-892-549-34	Sequence 34, Appl
744	4	28.6	37	1	US-08-477-727A-93	Sequence 93, Appl	817	1	US-08-892-549-35	Sequence 35, Appl
745	4	28.6	37	1	US-08-477-727A-94	Sequence 94, Appl	818	1	US-08-892-549-36	Sequence 36, Appl
746	4	28.6	37	1	US-08-477-727A-95	Sequence 95, Appl	819	1	US-08-892-549-37	Sequence 37, Appl
747	4	28.6	37	1	US-08-477-727A-96	Sequence 96, Appl	820	1	US-08-892-549-38	Sequence 38, Appl
748	4	28.6	37	1	US-08-477-727A-97	Sequence 97, Appl	821	1	US-08-892-549-41	Sequence 41, Appl
749	4	28.6	37	1	US-08-477-727A-99	Sequence 99, Appl	822	1	US-08-801-028-84	Sequence 84, Appl
750	4	28.6	37	1	US-08-477-727A-100	Sequence 100, App	823	1	US-09-053-197A-49	Sequence 49, Appl
751	4	28.6	37	1	US-08-477-727A-101	Sequence 101, App	824	1	US-09-340-154-84	Sequence 84, Appl
752	4	28.6	37	1	US-08-446-692-66	Sequence 66, Appl	825	1	US-08-784-582-51	Sequence 51, Appl
753	4	28.6	37	1	US-08-471-675A-2	Sequence 2, Appl	826	1	US-08-784-582-54	Sequence 54, Appl
754	4	28.6	37	1	US-08-471-675A-4	Sequence 4, Appl	827	1	US-08-302-069A-1	Sequence 1, Appl
755	4	28.6	37	1	US-08-471-675A-6	Sequence 6, Appl	828	1	US-08-302-069A-3	Sequence 3, Appl
756	4	28.6	37	1	US-08-471-675A-8	Sequence 8, Appl	829	1	US-08-302-069A-5	Sequence 5, Appl
757	4	28.6	37	1	US-08-471-675A-9	Sequence 9, Appl	830	1	US-08-302-069A-7	Sequence 7, Appl

831	4	28.6	37	3	US-08-302-069A-8	Sequence 8, Appli	Sequence 8, Appli	37	4	US-09-813-345C-8	Sequence 8, Appli
832	4	28.6	37	3	US-08-302-069A-11	Sequence 11, Appl	Sequence 11, Appl	37	4	US-09-813-345C-10	Sequence 10, Appl
833	4	28.6	37	3	US-08-302-069A-12	Sequence 12, Appl	Sequence 12, Appl	37	4	US-09-813-345C-11	Sequence 11, Appl
834	4	28.6	37	3	US-08-302-069A-14	Sequence 14, Appl	Sequence 14, Appl	37	4	US-09-813-345C-13	Sequence 13, Appl
835	4	28.6	37	3	US-08-302-069A-15	Sequence 15, Appl	Sequence 15, Appl	37	4	US-09-813-345C-16	Sequence 16, Appl
836	4	28.6	37	3	US-08-302-069A-16	Sequence 16, Appl	Sequence 16, Appl	37	4	US-09-813-345C-17	Sequence 17, Appl
837	4	28.6	37	3	US-08-302-069A-17	Sequence 17, Appl	Sequence 17, Appl	37	4	US-09-875-571A-1	Sequence 1, Appli
838	4	28.6	37	3	US-08-302-069A-18	Sequence 18, Appl	Sequence 18, Appl	37	5	PCT-US95-09338-84	Sequence 84, Appl
839	4	28.6	37	3	US-08-302-069A-20	Sequence 20, Appl	Sequence 20, Appl	37	5	PCT-US95-09339-84	Sequence 84, Appl
840	4	28.6	37	3	US-08-302-069A-21	Sequence 21, Appl	Sequence 21, Appl	37	6	5260275-1	Patent No. 5260275
841	4	28.6	37	3	US-08-302-069A-22	Sequence 22, Appl	Sequence 22, Appl	37	6	5424221-1	Patent No. 5424221
842	4	28.6	37	3	US-09-082-614A-3	Sequence 3, Appli	Sequence 3, Appli	37	6	5424221-4	Patent No. 5424221
843	4	28.6	37	3	US-09-070-504-3	Sequence 3, Appli	Sequence 3, Appli	37	6	5424221-5	Patent No. 5424221
844	4	28.6	37	3	US-09-070-504-4	Sequence 4, Appli	Sequence 4, Appli	37	6	5424221-6	Patent No. 5424221
845	4	28.6	37	3	US-09-070-504-5	Sequence 5, Appli	Sequence 5, Appli	37	6	5260275-1	Patent No. 5260275
846	4	28.6	37	3	US-09-070-504-6	Sequence 6, Appli	Sequence 6, Appli	37	6	5424221-1	Patent No. 5424221
847	4	28.6	37	3	US-09-070-504-7	Sequence 7, Appli	Sequence 7, Appli	37	6	5424221-4	Patent No. 5424221
848	4	28.6	37	3	US-09-070-504-8	Sequence 8, Appli	Sequence 8, Appli	37	6	5424221-5	Patent No. 5424221
849	4	28.6	37	3	US-09-070-504-10	Sequence 10, Appl	Sequence 10, Appl	37	6	5424221-6	Patent No. 5424221
850	4	28.6	37	3	US-09-070-504-11	Sequence 11, Appl	Sequence 11, Appl	38	1	US-07-776-272-19	Sequence 19, Appl
851	4	28.6	37	3	US-09-070-504-13	Sequence 13, Appl	Sequence 13, Appl	38	1	US-07-776-272-20	Sequence 20, Appl
852	4	28.6	37	3	US-09-070-504-16	Sequence 16, Appl	Sequence 16, Appl	38	1	US-07-776-272-21	Sequence 21, Appl
853	4	28.6	37	3	US-09-070-504-17	Sequence 17, Appl	Sequence 17, Appl	38	1	US-07-776-272-22	Sequence 22, Appl
854	4	28.6	37	3	US-09-085-761A-54	Sequence 54, Appl	Sequence 54, Appl	38	2	US-08-460-890A-44	Sequence 44, Appl
855	4	28.6	37	4	US-09-482-611B-84	Sequence 84, Appl	Sequence 84, Appl	38	3	US-08-167-641C-44	Sequence 44, Appl
856	4	28.6	37	4	US-09-576-062A-1	Sequence 1, Appli	Sequence 1, Appli	38	3	US-08-460-971A-44	Sequence 44, Appl
857	4	28.6	37	4	US-09-576-062A-3	Sequence 3, Appli	Sequence 3, Appli	38	3	US-08-462-040A-44	Sequence 44, Appl
858	4	28.6	37	4	US-09-576-062A-5	Sequence 5, Appli	Sequence 5, Appli	38	4	US-09-902-540-16576	Sequence 16576, A
859	4	28.6	37	4	US-09-576-062A-8	Sequence 8, Appli	Sequence 8, Appli	39	1	US-08-477-727A-3	Sequence 3, Appli
860	4	28.6	37	4	US-09-576-062A-16	Sequence 16, Appl	Sequence 16, Appl	39	4	US-09-439-410A-94	Sequence 94, Appl
861	4	28.6	37	4	US-09-576-062A-11	Sequence 11, Appl	Sequence 11, Appl	39	4	US-09-509-559B-14	Sequence 14, Appl
862	4	28.6	37	4	US-09-576-062A-12	Sequence 12, Appl	Sequence 12, Appl	40	4	US-09-270-767-57494	Sequence 57494, A
863	4	28.6	37	4	US-09-576-062A-14	Sequence 14, Appl	Sequence 14, Appl	40	4	US-09-270-767-58306	Sequence 58306, A
864	4	28.6	37	4	US-09-576-062A-15	Sequence 15, Appl	Sequence 15, Appl	41	1	US-08-781-020-9	Sequence 9, Appli
865	4	28.6	37	4	US-09-576-062A-16	Sequence 16, Appl	Sequence 16, Appl	41	3	US-09-038-935-9	Sequence 9, Appli
866	4	28.6	37	4	US-09-576-062A-17	Sequence 17, Appl	Sequence 17, Appl	41	3	US-09-690-454-206	Sequence 206, App
867	4	28.6	37	4	US-09-576-062A-18	Sequence 18, Appl	Sequence 18, Appl	42	1	US-08-293-778-15	Sequence 15, Appl
868	4	28.6	37	4	US-09-576-062A-20	Sequence 20, Appl	Sequence 20, Appl	42	1	US-08-262-037-1	Sequence 1, Appli
869	4	28.6	37	4	US-09-576-062A-21	Sequence 21, Appl	Sequence 21, Appl	42	4	US-09-462-917A-128	Sequence 128, App
870	4	28.6	37	4	US-09-576-062A-22	Sequence 22, Appl	Sequence 22, Appl	43	1	US-08-179-481-81	Sequence 81, Appl
871	4	28.6	37	4	US-09-454-533-1	Sequence 1, Appli	Sequence 1, Appli	43	2	US-08-488-161-80	Sequence 80, Appl
872	4	28.6	37	4	US-09-454-533-2	Sequence 2, Appli	Sequence 2, Appli	43	3	US-09-273-685-80	Sequence 80, Appl
873	4	28.6	37	4	US-09-454-533-3	Sequence 3, Appli	Sequence 3, Appli	43	4	US-07-757-022B-12	Sequence 12, Appl
874	4	28.6	37	4	US-09-454-533-4	Sequence 4, Appli	Sequence 4, Appli	43	4	US-09-057-363C-56	Sequence 56, Appl
875	4	28.6	37	4	US-09-454-533-5	Sequence 5, Appli	Sequence 5, Appli	43	4	US-09-057-363C-57	Sequence 57, Appl
876	4	28.6	37	4	US-09-454-533-8	Sequence 8, Appli	Sequence 8, Appli	43	4	US-09-057-363C-62	Sequence 62, Appl
877	4	28.6	37	4	US-09-454-533-9	Sequence 9, Appli	Sequence 9, Appli	43	4	US-09-057-363C-63	Sequence 63, Appl
878	4	28.6	37	4	US-09-454-533-10	Sequence 10, Appl	Sequence 10, Appl	43	4	US-09-057-363C-64	Sequence 64, Appl
879	4	28.6	37	4	US-09-454-533-12	Sequence 12, Appl	Sequence 12, Appl	43	4	US-09-265-107-56	Sequence 56, Appl
880	4	28.6	37	4	US-09-454-533-13	Sequence 13, Appl	Sequence 13, Appl	43	4	US-09-265-107-57	Sequence 57, Appl
881	4	28.6	37	4	US-09-454-533-16	Sequence 16, Appl	Sequence 16, Appl	43	4	US-09-265-107-62	Sequence 62, Appl
882	4	28.6	37	4	US-09-454-533-17	Sequence 17, Appl	Sequence 17, Appl	43	4	US-09-265-107-63	Sequence 63, Appl
883	4	28.6	37	4	US-09-454-533-19	Sequence 19, Appl	Sequence 19, Appl	43	4	US-09-265-107-64	Sequence 64, Appl
884	4	28.6	37	4	US-09-454-533-20	Sequence 20, Appl	Sequence 20, Appl	43	5	PCT-US95-11934-80	Sequence 80, Appl
885	4	28.6	37	4	US-09-454-533-21	Sequence 21, Appl	Sequence 21, Appl	44	1	US-08-421-661-4	Sequence 4, Appli
886	4	28.6	37	4	US-09-454-533-22	Sequence 22, Appl	Sequence 22, Appl	45	1	US-08-331-394-10	Sequence 10, Appl
887	4	28.6	37	4	US-09-454-533-23	Sequence 23, Appl	Sequence 23, Appl	45	1	US-08-250-858-10	Sequence 10, Appl
888	4	28.6	37	4	US-09-454-533-25	Sequence 25, Appl	Sequence 25, Appl	45	1	US-08-446-915-10	Sequence 10, Appl
889	4	28.6	37	4	US-09-454-533-26	Sequence 26, Appl	Sequence 26, Appl	45	2	US-08-744-139-10	Sequence 10, Appl
890	4	28.6	37	4	US-09-454-533-27	Sequence 27, Appl	Sequence 27, Appl	45	2	US-08-779-599-10	Sequence 10, Appl
891	4	28.6	37	4	US-09-454-533-34	Sequence 34, Appl	Sequence 34, Appl	45	5	PCT-US95-08639-10	Sequence 10, Appl
892	4	28.6	37	4	US-09-454-533-35	Sequence 35, Appl	Sequence 35, Appl	45	6	5424221-3	Patent No. 5424221
893	4	28.6	37	4	US-09-454-533-36	Sequence 36, Appl	Sequence 36, Appl	45	6	5424221-3	Patent No. 5424221
894	4	28.6	37	4	US-09-454-533-37	Sequence 37, Appl	Sequence 37, Appl	46	2	US-08-691-814B-16	Sequence 16, Appl
895	4	28.6	37	4	US-09-454-533-38	Sequence 38, Appl	Sequence 38, Appl	46	3	US-09-257-218-13	Sequence 13, Appl
896	4	28.6	37	4	US-09-454-533-41	Sequence 41, Appl	Sequence 41, Appl	46	3	US-09-311-760-13	Sequence 13, Appl
897	4	28.6	37	4	US-09-084-303B-265	Sequence 265, App	Sequence 265, App	46	4	US-08-865-579-13	Sequence 13, Appl
898	4	28.6	37	4	US-09-084-303B-281	Sequence 281, App	Sequence 281, App	46	4	US-10-059-749-13	Sequence 13, Appl
899	4	28.6	37	4	US-09-813-345C-3	Sequence 3, Appli	Sequence 3, Appli	46	6	5240847-24	Patent No. 5240847
900	4	28.6	37	4	US-09-813-345C-4	Sequence 4, Appli	Sequence 4, Appli	46	6	5240847-24	Patent No. 5240847
901	4	28.6	37	4	US-09-813-345C-5	Sequence 5, Appli	Sequence 5, Appli	47	3	US-09-052-089A-14	Sequence 14, Appl
902	4	28.6	37	4	US-09-813-345C-6	Sequence 6, Appli	Sequence 6, Appli	48	1	US-07-786-361A-15	Sequence 15, Appl
903	4	28.6	37	4	US-09-813-345C-7	Sequence 7, Appli	Sequence 7, Appli	48	3	US-09-227-357-241	Sequence 241, App

977 4 28.6 49 2 US-08-456-647B-26
978 4 28.6 49 3 US-08-237-401A-26
979 4 28.6 49 3 US-09-284-819-4
980 4 28.6 49 4 US-09-369-247-114
981 4 28.6 50 1 US-08-262-037-39
982 4 28.6 50 2 US-08-142-551B-119
983 4 28.6 51 1 US-08-421-661-2
984 4 28.6 51 3 US-09-044-536A-7
985 4 28.6 51 4 US-10-002-818-3
986 4 28.6 51 4 US-09-621-976-6219
987 4 28.6 51 4 US-09-270-767-39632
988 4 28.6 51 4 US-09-270-767-54849
989 4 28.6 51 4 US-09-344-639D-3
990 4 28.6 51 4 US-10-067-422-24
991 4 28.6 51 4 US-09-851-873-47
992 4 28.6 52 4 US-09-621-976-7370
993 4 28.6 53 2 US-08-456-647B-40
994 4 28.6 53 2 US-08-237-401A-40
995 4 28.6 53 2 US-08-799-173A-9
996 4 28.6 53 4 US-09-170-042A-9
997 4 28.6 54 2 US-08-456-647B-46
998 4 28.6 54 2 US-08-237-401A-46
999 4 28.6 55 1 US-08-446-692-94
1000 4 28.6 55 2 US-08-488-351A-94

ALIGNMENTS

RESULT 1
US-09-054-492B-5
; Sequence 5, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-5
Query Match 100.0%; Score 14; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 9.7e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 26, Appl
Sequence 26, Appl
Sequence 4, Appl
Sequence 114, Appl
Sequence 39, Appl
Sequence 119, Appl
Sequence 2, Appl
Sequence 7, Appl
Sequence 3, Appl
Sequence 6219, Ap
Sequence 39632, A
Sequence 54849, A
Sequence 3, Appl
Sequence 24, Appl
Sequence 47, Appl
Sequence 7370, Ap
Sequence 40, Appl
Sequence 40, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 94, Appl
Sequence 94, Appl

Qy 1 EDNVSENVGVCVT 14
| | | | | | | | | |
Db 1 EDNVSENVGVCVT 14

RESULT 2
US-08-969-106-6
; Sequence 6, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-969-106-6
Query Match 100.0%; Score 14; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENVGVCVT 14
| | | | | | | | | |
Db 343 EDNVSENVGVCVT 356

RESULT 3
US-09-054-492B-1
; Sequence 1, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-054-492B-1

Query Match      100.0%; Score 14; DB 3; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNVSENVGVCVT 14
      |||||||
Db      343 EDNVSENVGVCVT 356

RESULT 4
US-09-338-125-6
; Sequence 6, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leelle
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEX: 212-869-9741
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids
```

```
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-09-338-125-6

Query Match      100.0%; Score 14; DB 4; Length 377;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EDNVSENVGVCVT 14
      |||||||
Db      343 EDNVSENVGVCVT 356

RESULT 5
US-09-538-092-781
; Sequence 781, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 781
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number YPL133C
US-09-538-092-781

Query Match      50.0%; Score 7; DB 4; Length 446;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VSENVGS 10
      |||||||
Db      125 VSENVGS 131

RESULT 6
US-08-324-301-5
; Sequence 5, Application US/08324301
; Patent No. 5597569
; GENERAL INFORMATION:
; APPLICANT: Siegall, Clay B.
; APPLICANT: Gawlak, Susan L.
; APPLICANT: Marquardt, Hans
; TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
```

;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/324,301
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,891
;; FILING DATE: 25-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ONO109A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-728-4800
;; TELEFAX: 206-727-3601
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; ORGANISM: Bryonica dioica
;; TISSUE TYPE: root
US-08-324-301-5

Query Match 42.9%; Score 6; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 VSENVG 9
|||
Db 6 VSENVG 11

RESULT 7
US-08-324-301-15
;; Sequence 15, Application US/08324301
;; Patent No. 5597569
;; GENERAL INFORMATION:
;; APPLICANT: Siegall, Clay B.
;; APPLICANT: Gawlak, Susan L.
;; APPLICANT: Marquardt, Hans
;; TITLE OF INVENTION: A NEW RIBOSOME-INACTIVATING PROTEIN
;; TITLE OF INVENTION: ISOLATED FROM THE PLANT BRYONICA DIOICA
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Bristol-Myers Squibb Company
;; STREET: 3005 First Avenue
;; CITY: Seattle
;; STATE: Washington
;; COUNTRY: USA
;; ZIP: 98121
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/324,301
;; FILING DATE:
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/141,891
;; FILING DATE: 25-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Poor, Brian W.
;; REGISTRATION NUMBER: 32,928
;; REFERENCE/DOCKET NUMBER: ONO109A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 206-728-4800
;; TELEFAX: 206-727-3601

;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 282 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FRAGMENT TYPE: N-terminal
;; ORIGINAL SOURCE:
;; ORGANISM: Bryonia dioica
;; TISSUE TYPE: leaf
US-08-324-301-15

Query Match 42.9%; Score 6; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 VSENVG 9
|||
Db 194 VSENVG 199

RESULT 8
US-09-834-309-1
;; Sequence 1, Application US/09834309
;; Patent No. 6820011
;; GENERAL INFORMATION:
;; APPLICANT: Chen, Xiaojiang
;; APPLICANT: Holers, V. Michael
;; TITLE OF INVENTION: THREE-DIMENSIONAL STRUCTURE OF COMPLEMENT RECEPTOR TYPE 2 AND USE
;; TITLE OF INVENTION: THEREOF
;; FILE REFERENCE: 2848-43
;; CURRENT APPLICATION NUMBER: US/09/834,309
;; CURRENT FILING DATE: 2001-04-11
;; NUMBER OF SEQ ID NOS: 9
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 1
;; LENGTH: 1033
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-834-309-1

Query Match 42.9%; Score 6; DB 4; Length 1033;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 SENVGS 10
|||
Db 167 SENVGS 172

RESULT 9
US-09-541-782-8
;; Sequence 8, Application US/09541782
;; Patent No. 6284480
;; GENERAL INFORMATION:
;; APPLICANT: Nislow, Corey
;; APPLICANT: Sakowicz, Roman
;; APPLICANT: Beraud, Christophe
;; TITLE OF INVENTION: Antifungal Assay
;; FILE REFERENCE: 1015
;; CURRENT APPLICATION NUMBER: US/09/541,782
;; CURRENT FILING DATE: 2000-04-03
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8
;; LENGTH: 1066
;; TYPE: PRT
;; ORGANISM: Drosophila melanogaster
US-09-541-782-8

Query Match 42.9%; Score 6; DB 3; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 10
US-09-723-820-8
; Sequence 8, Application US/09723820
; Patent No. 6468760
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/09/723,820
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-723-820-8

Query Match      42.9%; Score 6; DB 4; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 11
US-10-270-085-8
; Sequence 8, Application US/10270085
; Patent No. 6627408
; GENERAL INFORMATION:
; APPLICANT: Nislow, Corey
; APPLICANT: Sakowicz, Roman
; APPLICANT: Beraud, Christophe
; TITLE OF INVENTION: Antifungal Assay
; FILE REFERENCE: 1015
; CURRENT APPLICATION NUMBER: US/10/270,085
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/09/723,820
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/541,782
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1066
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-270-085-8

Query Match      42.9%; Score 6; DB 4; Length 1066;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      828  ENVGSV 833

RESULT 12
US-09-252-991A-26438
; Sequence 26438, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26438
; LENGTH: 1415
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26438

Query Match      42.9%; Score 6; DB 4; Length 1415;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  ENVGSV 10
Db      616  ENVGSV 621

RESULT 13
US-09-949-016-8985
; Sequence 8985, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8985
; LENGTH: 2362
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8985

Query Match      42.9%; Score 6; DB 4; Length 2362;
Best Local Similarity 100.0%; Pred. No. 4.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6  ENVGSV 11
Db      2299  ENVGSV 2304

RESULT 14
US-08-469-486-52
; Sequence 52, Application US/08469486
; Patent No. 5739281
; GENERAL INFORMATION:
; APPLICANT: Thøgersen, Hans Christian
; APPLICANT: Holtet, Thor Las
; APPLICANT: Etzerodt, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; TITLE OF INVENTION: proteins
; NUMBER OF SEQUENCES: 58
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,486
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-486-52

Query Match 42.9%; Score 6; DB 1; Length 4544;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
Db 2280 ENVGSV 2285

Search completed: February 11, 2005, 03:18:39
Job time : 11.2174 secs

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995

Query Match 42.9%; Score 6; DB 2; Length 4544;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
Db 2280 ENVGSV 2285

Search completed: February 11, 2005, 03:18:39
Job time : 11.2174 secs

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version
; SOFTWARE: #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,658
; FILING DATE: June 5, 1995
```

```
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/192,060
; FILING DATE: February 4, 1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Paul T. Clark
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 06363/002002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 542 5070
; TELEFAX: 617 542 8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4544 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-469-658-52

Query Match 42.9%; Score 6; DB 2; Length 4544;
Best Local Similarity 100.0%; Pred. No. 7.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
Db 2280 ENVGSV 2285

Search completed: February 11, 2005, 03:18:39
Job time : 11.2174 secs
```


87	5	35.7	11	14	US-10-160-506-32	Sequence 32, Appl	160	5	35.7	107	16	US-10-449-379-68	Sequence 68, Appl
88	5	35.7	11	16	US-10-449-379-32	Sequence 32, Appl	161	5	35.7	107	16	US-10-688-015-48	Sequence 48, Appl
89	5	35.7	11	16	US-10-688-015-32	Sequence 32, Appl	162	5	35.7	107	16	US-10-688-015-50	Sequence 50, Appl
90	5	35.7	16	14	US-10-040-862-10457	Sequence 10457, A	163	5	35.7	107	16	US-10-688-015-62	Sequence 62, Appl
91	5	35.7	16	15	US-10-057-475B-10457	Sequence 10457, A	164	5	35.7	107	16	US-10-688-015-63	Sequence 63, Appl
92	5	35.7	16	15	US-10-154-884B-10457	Sequence 10457, A	165	5	35.7	107	16	US-10-688-015-64	Sequence 64, Appl
93	5	35.7	16	16	US-10-764-324-10457	Sequence 10457, A	166	5	35.7	107	16	US-10-688-015-65	Sequence 65, Appl
94	5	35.7	30	14	US-10-040-862-10451	Sequence 10451, A	167	5	35.7	107	16	US-10-688-015-66	Sequence 66, Appl
95	5	35.7	30	14	US-10-040-862-10451	Sequence 10451, A	168	5	35.7	107	16	US-10-688-015-68	Sequence 68, Appl
96	5	35.7	30	15	US-10-057-475B-10451	Sequence 10451, A	169	5	35.7	108	16	US-09-930-169-2	Sequence 2, Appl
97	5	35.7	30	15	US-10-057-475B-10452	Sequence 10452, A	170	5	35.7	108	16	US-10-823-730-2	Sequence 2, Appl
98	5	35.7	30	15	US-10-154-884B-10451	Sequence 10451, A	171	5	35.7	109	9	US-09-939-980-440	Sequence 440, App
99	5	35.7	30	15	US-10-154-884B-10452	Sequence 10452, A	172	5	35.7	109	9	US-10-424-599-246648	Sequence 246648, A
100	5	35.7	30	16	US-10-764-324-10451	Sequence 10451, A	173	5	35.7	109	16	US-10-437-963-145674	Sequence 145674, A
101	5	35.7	30	16	US-10-764-324-10452	Sequence 10452, A	174	5	35.7	111	11	US-09-864-408A-3776	Sequence 3776, Ap
102	5	35.7	38	15	US-10-424-599-172545	Sequence 172545, A	175	5	35.7	112	15	US-10-424-599-223522	Sequence 223522, A
103	5	35.7	42	14	US-10-217-584-11	Sequence 11, Appl	176	5	35.7	114	9	US-09-860-670-130	Sequence 130, App
104	5	35.7	47	9	US-09-864-761-37914	Sequence 37914, A	177	5	35.7	114	15	US-10-227-646-130	Sequence 130, App
105	5	35.7	51	15	US-10-424-599-204691	Sequence 204691, A	178	5	35.7	114	15	US-10-242-355-471	Sequence 471, App
106	5	35.7	56	10	US-09-764-872-390	Sequence 390, App	179	5	35.7	115	16	US-10-767-701-39276	Sequence 39276, A
107	5	35.7	56	15	US-10-424-599-210228	Sequence 210228, A	180	5	35.7	117	15	US-10-289-762-951	Sequence 951, App
108	5	35.7	58	15	US-10-424-599-185026	Sequence 185026, A	181	5	35.7	117	15	US-10-425-114-50550	Sequence 50550, A
109	5	35.7	59	16	US-10-437-963-145005	Sequence 145005, A	182	5	35.7	118	14	US-10-385-072-13	Sequence 13, Appl
110	5	35.7	62	15	US-10-424-599-213579	Sequence 213579, A	183	5	35.7	119	15	US-10-424-599-147520	Sequence 147520, A
111	5	35.7	63	16	US-10-767-701-46618	Sequence 46618, A	184	5	35.7	120	16	US-10-437-963-198266	Sequence 198266, A
112	5	35.7	65	9	US-09-864-761-39828	Sequence 39828, A	185	5	35.7	121	15	US-10-424-599-147400	Sequence 147400, A
113	5	35.7	68	9	US-09-864-761-40776	Sequence 40776, A	186	5	35.7	123	15	US-10-415-253-9	Sequence 9, Appl
114	5	35.7	68	14	US-10-211-962-131	Sequence 131, App	187	5	35.7	123	16	US-10-437-963-116512	Sequence 116512, A
115	5	35.7	70	16	US-10-437-963-166821	Sequence 166821, A	188	5	35.7	124	15	US-10-108-260A-2942	Sequence 2942, Ap
116	5	35.7	72	15	US-10-424-599-269038	Sequence 269038, A	189	5	35.7	125	15	US-10-424-599-186845	Sequence 186845, A
117	5	35.7	75	15	US-10-424-599-205429	Sequence 205429, A	190	5	35.7	128	15	US-10-282-122A-45210	Sequence 45210, A
118	5	35.7	77	15	US-10-424-599-246869	Sequence 246869, A	191	5	35.7	128	15	US-10-282-122A-56639	Sequence 56639, A
119	5	35.7	78	15	US-10-424-599-227220	Sequence 227220, A	192	5	35.7	128	15	US-10-282-122A-60151	Sequence 60151, A
120	5	35.7	80	15	US-10-424-599-221946	Sequence 221946, A	193	5	35.7	129	15	US-10-424-599-176693	Sequence 176693, A
121	5	35.7	81	9	US-09-864-761-38603	Sequence 38603, A	194	5	35.7	129	16	US-10-437-963-190293	Sequence 190293, A
122	5	35.7	81	15	US-10-424-599-257131	Sequence 257131, A	195	5	35.7	135	15	US-10-425-114-65328	Sequence 65328, A
123	5	35.7	85	14	US-10-029-386-30284	Sequence 30284, A	196	5	35.7	135	16	US-10-767-701-53143	Sequence 53143, A
124	5	35.7	86	15	US-10-424-599-256032	Sequence 256032, A	197	5	35.7	137	15	US-10-424-599-203171	Sequence 203171, A
125	5	35.7	87	16	US-10-437-963-144219	Sequence 144219, A	198	5	35.7	137	15	US-10-424-599-213271	Sequence 213271, A
126	5	35.7	89	15	US-10-424-599-164077	Sequence 164077, A	199	5	35.7	139	15	US-10-424-599-245760	Sequence 245760, A
127	5	35.7	89	16	US-10-437-963-158060	Sequence 158060, A	200	5	35.7	140	15	US-10-087-080-3	Sequence 3, Appl
128	5	35.7	92	14	US-10-238-075-1351	Sequence 1351, Ap	201	5	35.7	140	15	US-10-087-080-5	Sequence 5, Appl
129	5	35.7	92	16	US-10-767-701-45629	Sequence 45629, A	202	5	35.7	142	15	US-10-282-122A-71612	Sequence 71612, A
130	5	35.7	93	15	US-10-424-599-283837	Sequence 283837, A	203	5	35.7	146	16	US-10-767-701-54271	Sequence 54271, A
131	5	35.7	94	14	US-10-238-075-1349	Sequence 1349, Ap	204	5	35.7	147	10	US-09-930-169-1	Sequence 1, Appl
132	5	35.7	94	14	US-10-180-158-20	Sequence 20, Appl	205	5	35.7	147	15	US-10-424-599-280916	Sequence 280916, A
133	5	35.7	94	15	US-10-424-599-272645	Sequence 272645, A	206	5	35.7	147	16	US-10-823-730-1	Sequence 1, Appl
134	5	35.7	94	16	US-10-437-963-106428	Sequence 106428, A	207	5	35.7	152	15	US-10-424-599-254995	Sequence 254995, A
135	5	35.7	97	14	US-10-211-962-126	Sequence 126, App	208	5	35.7	153	15	US-10-424-599-154112	Sequence 154112, A
136	5	35.7	97	15	US-10-335-977-6253	Sequence 6253, Ap	209	5	35.7	154	15	US-10-424-599-274304	Sequence 274304, A
137	5	35.7	98	14	US-10-106-698-7296	Sequence 7296, Ap	210	5	35.7	156	9	US-09-925-298-644	Sequence 644, App
138	5	35.7	99	16	US-10-437-963-150194	Sequence 150194, A	211	5	35.7	156	14	US-10-102-806-644	Sequence 644, App
139	5	35.7	102	16	US-10-437-963-123629	Sequence 123629, A	212	5	35.7	160	15	US-10-369-493-5550	Sequence 5550, Ap
140	5	35.7	104	14	US-10-180-158-24	Sequence 24, Appl	213	5	35.7	163	13	US-10-114-893-18	Sequence 18, Appl
141	5	35.7	104	15	US-10-424-599-144161	Sequence 144161, A	214	5	35.7	163	15	US-10-424-599-280377	Sequence 280377, A
142	5	35.7	105	14	US-10-106-698-7605	Sequence 7605, Ap	215	5	35.7	164	15	US-10-104-047-3796	Sequence 3796, Ap
143	5	35.7	105	16	US-10-437-963-204843	Sequence 204843, A	216	5	35.7	166	9	US-09-764-864-1562	Sequence 1562, Ap
144	5	35.7	106	15	US-10-424-599-204929	Sequence 204929, A	217	5	35.7	166	10	US-09-930-169-3	Sequence 3, Appl
145	5	35.7	107	14	US-10-160-506-48	Sequence 48, Appl	218	5	35.7	166	16	US-10-823-730-3	Sequence 3, Appl
146	5	35.7	107	14	US-10-160-506-50	Sequence 50, Appl	219	5	35.7	167	16	US-10-767-701-62632	Sequence 62632, A
147	5	35.7	107	14	US-10-160-506-62	Sequence 62, Appl	220	5	35.7	170	16	US-10-437-963-164507	Sequence 164507, A
148	5	35.7	107	14	US-10-160-506-63	Sequence 63, Appl	221	5	35.7	171	15	US-10-424-599-217933	Sequence 217933, A
149	5	35.7	107	14	US-10-160-506-64	Sequence 64, Appl	222	5	35.7	171	15	US-10-296-115-1286	Sequence 1286, Ap
150	5	35.7	107	14	US-10-160-506-65	Sequence 65, Appl	223	5	35.7	174	9	US-09-738-626-4599	Sequence 4599, Ap
151	5	35.7	107	14	US-10-160-506-66	Sequence 66, Appl	224	5	35.7	174	17	US-10-494-541-16	Sequence 16, Appl
152	5	35.7	107	14	US-10-160-506-68	Sequence 68, Appl	225	5	35.7	175	9	US-09-839-479-64	Sequence 64, Appl
153	5	35.7	107	16	US-10-449-379-48	Sequence 48, Appl	226	5	35.7	175	15	US-10-376-537-65	Sequence 65, Appl
154	5	35.7	107	16	US-10-449-379-50	Sequence 50, Appl	227	5	35.7	175	15	US-10-702-148-64	Sequence 64, Appl
155	5	35.7	107	16	US-10-449-379-62	Sequence 62, Appl	228	5	35.7	176	9	US-09-839-479-65	Sequence 65, Appl
156	5	35.7	107	16	US-10-449-379-63	Sequence 63, Appl	229	5	35.7	176	15	US-10-376-537-66	Sequence 66, Appl
157	5	35.7	107	16	US-10-449-379-64	Sequence 64, Appl	230	5	35.7	176	15	US-10-702-148-65	Sequence 65, Appl
158	5	35.7	107	16	US-10-449-379-65	Sequence 65, Appl	231	5	35.7	177	15	US-10-424-599-210963	Sequence 210963, A
159	5	35.7	107	16	US-10-449-379-66	Sequence 66, Appl	232	5	35.7	179	16	US-10-767-701-31951	Sequence 31951, A

233	5	35.7	186	14	US-10-379-616-2	Sequence 2, Appli	306	5	35.7	292	15	US-10-424-599-262410	Sequence 262410,
234	5	35.7	186	16	US-10-767-701-59551	Sequence 59551, A	307	5	35.7	294	16	US-10-437-963-163248	Sequence 163248,
235	5	35.7	190	14	US-10-029-386-32464	Sequence 32464, A	308	5	35.7	295	15	US-10-424-599-191991	Sequence 191991,
236	5	35.7	191	15	US-10-108-260A-2677	Sequence 2677, Ap	309	5	35.7	296	15	US-10-424-599-157290	Sequence 157290,
237	5	35.7	194	15	US-10-424-599-142883	Sequence 142883,	310	5	35.7	297	14	US-10-180-158-56	Sequence 56, Appl
238	5	35.7	194	16	US-10-767-701-59997	Sequence 59997, A	311	5	35.7	299	14	US-10-156-761-12105	Sequence 12105, A
239	5	35.7	195	15	US-10-425-114-68513	Sequence 68513, A	312	5	35.7	301	15	US-10-425-114-68293	Sequence 68293, A
240	5	35.7	199	16	US-10-437-963-179485	Sequence 179485,	313	5	35.7	303	16	US-10-437-963-129511	Sequence 129511,
241	5	35.7	204	14	US-10-211-962-127	Sequence 127, App	314	5	35.7	305	15	US-10-437-963-122481	Sequence 122481,
242	5	35.7	204	15	US-10-424-599-260913	Sequence 260913,	315	5	35.7	309	15	US-10-424-599-246147	Sequence 246147,
243	5	35.7	206	15	US-10-424-599-2678056	Sequence 2678056,	316	5	35.7	309	15	US-10-424-599-262432	Sequence 262432,
244	5	35.7	208	16	US-10-437-963-166056	Sequence 166056,	317	5	35.7	311	15	US-10-310-154-716	Sequence 716, App
245	5	35.7	210	15	US-10-425-114-68348	Sequence 68348, A	318	5	35.7	312	9	US-09-851-026-36	Sequence 36, Appl
246	5	35.7	216	15	US-10-424-599-253265	Sequence 253265,	319	5	35.7	313	15	US-10-424-599-219585	Sequence 219585,
247	5	35.7	217	15	US-10-369-493-4145	Sequence 4145, Ap	320	5	35.7	333	16	US-10-474-776-406	Sequence 406, App
248	5	35.7	218	15	US-10-424-599-274301	Sequence 274301,	321	5	35.7	333	17	US-10-472-928-1113907	Sequence 1113907,
249	5	35.7	218	16	US-10-767-701-36133	Sequence 36133, A	322	5	35.7	316	16	US-10-437-963-4413907	Sequence 4413907,
250	5	35.7	220	15	US-10-424-599-161667	Sequence 161667,	323	5	35.7	318	14	US-10-156-761-8907	Sequence 8907, Ap
251	5	35.7	225	14	US-10-385-072-14	Sequence 14, Appl	324	5	35.7	318	15	US-10-721-692-2	Sequence 2, Appl
252	5	35.7	225	15	US-10-424-599-203671	Sequence 203671,	325	5	35.7	320	15	US-10-154-884B-11042	Sequence 11042, A
253	5	35.7	228	15	US-10-424-599-211967	Sequence 211967,	326	5	35.7	320	16	US-10-688-011-2	Sequence 1042, A
254	5	35.7	232	15	US-10-424-599-259889	Sequence 259889,	327	5	35.7	323	14	US-10-067-076-2	Sequence 2, Appl
255	5	35.7	234	15	US-10-282-122A-74167	Sequence 74167, A	328	5	35.7	323	15	US-10-389-566-547	Sequence 547, App
256	5	35.7	234	15	US-10-424-599-261438	Sequence 261438,	329	5	35.7	325	15	US-10-369-493-14625	Sequence 14625, A
257	5	35.7	234	17	US-10-472-928-4066	Sequence 4066, Ap	330	5	35.7	325	15	US-10-369-493-15076	Sequence 15076, A
258	5	35.7	235	15	US-10-369-493-16629	Sequence 16629, A	331	5	35.7	325	15	US-10-425-114-38918	Sequence 38918, A
259	5	35.7	235	15	US-10-369-493-19336	Sequence 19336, A	332	5	35.7	325	15	US-10-425-114-46017	Sequence 46017, A
260	5	35.7	239	14	US-10-180-158-58	Sequence 58, Appl	333	5	35.7	329	15	US-10-424-599-268338	Sequence 268338,
261	5	35.7	239	15	US-10-424-599-239717	Sequence 239717,	334	5	35.7	331	15	US-10-369-493-2706	Sequence 2706, Ap
262	5	35.7	242	15	US-10-369-493-8377	Sequence 8377, Ap	335	5	35.7	331	16	US-10-437-963-146325	Sequence 146325, A
263	5	35.7	244	16	US-10-437-963-145776	Sequence 145776,	336	5	35.7	332	15	US-10-369-493-18828	Sequence 18828, A
264	5	35.7	246	16	US-10-363-829-469	Sequence 469, App	337	5	35.7	335	15	US-10-282-122A-44291	Sequence 44291, A
265	5	35.7	248	15	US-10-282-122A-77374	Sequence 77374, A	338	5	35.7	337	9	US-09-815-242-5617	Sequence 5617, Ap
266	5	35.7	248	15	US-10-425-114-43770	Sequence 43770, A	339	5	35.7	337	9	US-09-815-242-12539	Sequence 12539, A
267	5	35.7	250	15	US-10-369-493-13580	Sequence 13580, A	340	5	35.7	337	14	US-09-815-242-12876	Sequence 12876, A
268	5	35.7	252	14	US-10-391-2538-9	Sequence 9, Appl	341	5	35.7	337	9	US-10-097-237-9	Sequence 9, Appl
269	5	35.7	252	15	US-10-369-493-16974	Sequence 16974, A	342	5	35.7	337	15	US-10-282-122A-43996	Sequence 43996, A
270	5	35.7	252	15	US-10-425-114-71061	Sequence 71061, A	343	5	35.7	337	15	US-10-282-122A-70889	Sequence 70889, A
271	5	35.7	254	15	US-10-369-493-15717	Sequence 15717, A	344	5	35.7	337	15	US-10-282-122A-71733	Sequence 71733, A
272	5	35.7	255	14	US-10-040-862-9612	Sequence 9612, Ap	345	5	35.7	340	15	US-10-264-213-225	Sequence 225, App
273	5	35.7	255	15	US-10-057-4758-9612	Sequence 9612, Ap	346	5	35.7	342	15	US-10-425-114-68594	Sequence 68594, A
274	5	35.7	255	15	US-10-154-884B-9612	Sequence 9612, Ap	347	5	35.7	343	15	US-10-282-122A-61435	Sequence 61435, A
275	5	35.7	255	15	US-10-154-884B-11057	Sequence 11057, A	348	5	35.7	345	15	US-10-424-599-167321	Sequence 167321,
276	5	35.7	255	15	US-10-424-599-161858	Sequence 161858,	349	5	35.7	346	15	US-10-424-599-262445	Sequence 262445,
277	5	35.7	255	16	US-10-764-324-9612	Sequence 9612, Ap	350	5	35.7	349	9	US-09-738-626-4437	Sequence 4437, Ap
278	5	35.7	257	15	US-10-369-493-14250	Sequence 14250, A	351	5	35.7	349	10	US-09-746-660A-70	Sequence 70, Appl
279	5	35.7	257	15	US-10-369-493-15350	Sequence 15350, A	352	5	35.7	350	10	US-09-906-179A-3	Sequence 3, Appl
280	5	35.7	258	15	US-10-369-493-22360	Sequence 22360, A	353	5	35.7	350	10	US-09-906-179A-213	Sequence 213, App
281	5	35.7	258	15	US-10-424-599-246340	Sequence 246340,	354	5	35.7	350	10	US-09-906-179A-226	Sequence 226, App
282	5	35.7	261	14	US-10-040-862-9611	Sequence 9611, Ap	355	5	35.7	350	15	US-10-671-403-124	Sequence 124, App
283	5	35.7	261	15	US-10-057-4758-9611	Sequence 9611, Ap	356	5	35.7	350	15	US-10-671-419-124	Sequence 124, App
284	5	35.7	261	15	US-10-154-884B-9611	Sequence 9611, Ap	357	5	35.7	350	15	US-10-670-844-124	Sequence 124, App
285	5	35.7	261	15	US-10-154-884B-11056	Sequence 11056, A	358	5	35.7	350	15	US-10-671-134-124	Sequence 124, App
286	5	35.7	261	15	US-10-424-599-156048	Sequence 156048,	359	5	35.7	350	15	US-10-673-098-124	Sequence 124, App
287	5	35.7	261	16	US-10-764-324-9611	Sequence 9611, Ap	360	5	35.7	350	15	US-10-673-127-124	Sequence 124, App
288	5	35.7	262	14	US-10-180-158-62	Sequence 62, Appl	361	5	35.7	350	15	US-10-673-127-124	Sequence 124, App
289	5	35.7	263	15	US-10-425-114-69724	Sequence 69724, A	362	5	35.7	350	16	US-10-670-817-124	Sequence 124, App
290	5	35.7	263	15	US-10-424-599-284438	Sequence 284438,	363	5	35.7	350	16	US-10-673-119-124	Sequence 124, App
291	5	35.7	267	16	US-10-767-701-44378	Sequence 44378, A	364	5	35.7	350	16	US-10-746-167-95	Sequence 95, Appl
292	5	35.7	271	15	US-10-369-493-18215	Sequence 18215, A	365	5	35.7	350	16	US-10-671-207-124	Sequence 124, App
293	5	35.7	272	15	US-10-154-884B-11049	Sequence 11049, A	366	5	35.7	352	15	US-10-369-493-20074	Sequence 20074, A
294	5	35.7	275	15	US-10-335-977-7679	Sequence 7679, Ap	367	5	35.7	359	14	US-10-029-386-32133	Sequence 32133, A
295	5	35.7	276	15	US-10-369-493-11582	Sequence 11582, A	368	5	35.7	359	14	US-10-361-460-11	Sequence 11, Appl
296	5	35.7	278	15	US-10-335-977-7680	Sequence 7680, Ap	369	5	35.7	360	14	US-10-087-714-22	Sequence 22, Appl
297	5	35.7	286	15	US-10-424-599-191038	Sequence 191038,	370	5	35.7	362	14	US-10-259-740-4	Sequence 4, Appl
298	5	35.7	287	15	US-10-425-114-67678	Sequence 67678, A	371	5	35.7	364	10	US-09-863-776-39	Sequence 39, Appl
299	5	35.7	288	9	US-09-895-913A-122	Sequence 122, App	372	5	35.7	365	15	US-10-154-884B-11047	Sequence 11047, A
300	5	35.7	288	15	US-10-320-797-3070	Sequence 3070, Ap	373	5	35.7	365	15	US-10-424-599-225609	Sequence 225609,
301	5	35.7	288	15	US-10-282-122A-58858	Sequence 58858, A	374	5	35.7	366	15	US-10-424-599-278238	Sequence 278238,
302	5	35.7	288	17	US-10-472-928-132	Sequence 132, App	375	5	35.7	367	15	US-10-154-884B-11050	Sequence 11050, A
303	5	35.7	290	15	US-10-369-493-20468	Sequence 20468, A	376	5	35.7	367	15	US-10-282-122A-63404	Sequence 63404, A
304	5	35.7	291	15	US-10-369-493-18158	Sequence 18158, A	377	5	35.7	367	16	US-10-437-963-156275	Sequence 156275,
305	5	35.7	291	16	US-10-767-701-42245	Sequence 42245, A	378	5	35.7	371	14	US-10-032-585-7445	Sequence 7445, Ap

379	5	35.7	371	15	US-10-369-493-3828	Sequence 3828, Ap	452	5	35.7	481	16	US-10-437-963-183222	Sequence 183222,
380	5	35.7	374	15	US-10-425-114-40569	Sequence 40569, A	453	5	35.7	482	15	US-10-282-122A-59920	Sequence 59920, A
381	5	35.7	377	9	US-09-881-752A-92	Sequence 92, Appl	454	5	35.7	483	15	US-10-369-493-22491	Sequence 22491, A
382	5	35.7	377	15	US-10-335-977-6255	Sequence 6255, Ap	455	5	35.7	485	15	US-10-282-122A-65246	Sequence 65246, A
383	5	35.7	379	15	US-10-225-066A-188	Sequence 188, App	456	5	35.7	485	15	US-10-282-122A-65246	Sequence 65246, A
384	5	35.7	379	15	US-10-225-067-104	Sequence 104, App	457	5	35.7	487	17	US-10-866-527-6	Sequence 6, Appli
385	5	35.7	379	15	US-10-374-780A-416	Sequence 416, App	458	5	35.7	490	16	US-10-648-593-196	Sequence 196, App
386	5	35.7	381	14	US-10-052-092-29	Sequence 29, Appl	459	5	35.7	490	16	US-10-755-889-256	Sequence 256, App
387	5	35.7	381	14	US-10-437-107-29	Sequence 29, Appl	460	5	35.7	493	15	US-10-417-476-5	Sequence 5, Appli
388	5	35.7	382	9	US-09-771-956-3	Sequence 3, Appli	461	5	35.7	494	16	US-10-767-701-0483	Sequence 4083, A
389	5	35.7	382	15	US-10-282-122A-73650	Sequence 73650, A	462	5	35.7	502	15	US-10-369-493-20870	Sequence 20870, A
390	5	35.7	382	17	US-10-424-599-185647	Sequence 185647, A	463	5	35.7	503	15	US-10-282-122A-56338	Sequence 56338, A
391	5	35.7	384	15	US-10-926-225-3	Sequence 3, Appli	464	5	35.7	503	16	US-10-739-096-25	Sequence 25, Appl
392	5	35.7	384	15	US-10-437-963-180472	Sequence 180472, A	465	5	35.7	503	16	US-10-739-096-35	Sequence 35, Appl
393	5	35.7	384	15	US-10-369-493-16754	Sequence 16754, A	466	5	35.7	505	14	US-10-156-761-14471	Sequence 14471, A
394	5	35.7	386	15	US-10-369-493-13152	Sequence 13152, A	467	5	35.7	505	16	US-10-739-096-30	Sequence 30, Appl
395	5	35.7	387	16	US-10-437-963-103157	Sequence 103157, A	468	5	35.7	506	14	US-10-205-823-168	Sequence 168, App
396	5	35.7	387	16	US-10-437-963-184671	Sequence 184671, A	469	5	35.7	506	15	US-10-369-493-13139	Sequence 13139, A
397	5	35.7	389	15	US-10-074-978A-219	Sequence 219, App	470	5	35.7	506	16	US-10-755-889-580	Sequence 580, App
398	5	35.7	389	15	US-10-425-114-65684	Sequence 65684, A	471	5	35.7	508	9	US-09-771-161A-102	Sequence 102, App
399	5	35.7	389	15	US-10-037-417-131	Sequence 131, App	472	5	35.7	508	14	US-10-040-862-10464	Sequence 10464, A
400	5	35.7	391	15	US-10-094-749-3102	Sequence 3102, Ap	473	5	35.7	508	15	US-10-057-475B-10464	Sequence 10464, A
401	5	35.7	391	15	US-10-369-493-22565	Sequence 22565, A	474	5	35.7	508	15	US-10-154-884B-10464	Sequence 10464, A
402	5	35.7	392	15	US-10-282-122A-73649	Sequence 73649, A	475	5	35.7	508	15	US-10-154-884B-11039	Sequence 11039, A
403	5	35.7	394	16	US-10-437-963-129071	Sequence 129071, A	476	5	35.7	508	16	US-10-764-324-10464	Sequence 10464, A
404	5	35.7	394	16	US-10-437-963-162156	Sequence 162156, A	477	5	35.7	509	13	US-10-072-152-6	Sequence 6, Appli
405	5	35.7	395	9	US-09-728-401A-2	Sequence 2, Appli	478	5	35.7	509	14	US-10-032-585-7717	Sequence 7717, Ap
406	5	35.7	395	10	US-09-771-023-8	Sequence 8, Appli	479	5	35.7	509	15	US-10-655-433-6	Sequence 6, Appli
407	5	35.7	395	17	US-10-741-849-7050	Sequence 7050, Ap	480	5	35.7	514	15	US-10-425-114-54818	Sequence 54818, A
408	5	35.7	396	15	US-10-425-114-56117	Sequence 56117, A	481	5	35.7	515	15	US-10-425-114-70123	Sequence 70123, A
409	5	35.7	396	15	US-10-425-114-63135	Sequence 63135, A	482	5	35.7	515	15	US-10-425-114-73028	Sequence 73028, A
410	5	35.7	399	15	US-10-424-599-254992	Sequence 254992, A	483	5	35.7	516	14	US-10-156-761-10628	Sequence 10628, A
411	5	35.7	400	16	US-10-437-963-141040	Sequence 141040, A	484	5	35.7	527	15	US-10-425-114-39205	Sequence 39205, A
412	5	35.7	406	15	US-10-437-963-197136	Sequence 197136, A	485	5	35.7	528	16	US-10-739-096-6	Sequence 6, Appli
413	5	35.7	406	15	US-10-425-114-56149	Sequence 56149, A	486	5	35.7	530	16	US-10-739-096-2	Sequence 2, Appli
414	5	35.7	407	15	US-10-601-309-78	Sequence 78, Appl	487	5	35.7	531	16	US-10-477-527-12	Sequence 12, Appl
415	5	35.7	413	15	US-10-154-884B-11040	Sequence 11040, A	488	5	35.7	534	16	US-10-739-096-10	Sequence 10, Appl
416	5	35.7	415	15	US-10-154-884B-11041	Sequence 11041, A	489	5	35.7	535	15	US-10-424-599-199751	Sequence 199751, A
417	5	35.7	415	15	US-10-424-599-254998	Sequence 254998, A	490	5	35.7	535	15	US-10-120-801-12	Sequence 12, Appl
418	5	35.7	416	14	US-10-067-076-1	Sequence 1, Appli	491	5	35.7	539	9	US-09-738-626-6722	Sequence 6722, Ap
419	5	35.7	416	14	US-10-067-076-20	Sequence 20, Appl	492	5	35.7	540	15	US-10-424-599-227611	Sequence 227611, A
420	5	35.7	416	14	US-10-067-076-22	Sequence 22, Appl	493	5	35.7	541	16	US-10-437-963-133506	Sequence 133506, A
421	5	35.7	416	15	US-10-369-493-18612	Sequence 18612, A	494	5	35.7	542	15	US-10-424-599-146181	Sequence 146181, A
422	5	35.7	424	9	US-09-853-450-16	Sequence 16, Appl	495	5	35.7	545	15	US-10-424-599-219246	Sequence 219246, A
423	5	35.7	424	10	US-09-849-772-2	Sequence 2, Appli	496	5	35.7	548	15	US-10-424-599-229536	Sequence 229536, A
424	5	35.7	425	16	US-10-767-701-44784	Sequence 44784, A	497	5	35.7	555	9	US-09-801-368-350	Sequence 350, App
425	5	35.7	426	15	US-10-369-493-21051	Sequence 21051, A	498	5	35.7	555	15	US-10-369-493-22500	Sequence 22500, A
426	5	35.7	432	14	US-10-205-219-48	Sequence 48, Appl	499	5	35.7	560	15	US-10-425-114-45686	Sequence 45686, A
427	5	35.7	433	14	US-10-205-219-48	Sequence 48, Appl	500	5	35.7	569	15	US-10-369-493-22322	Sequence 22322, A
428	5	35.7	437	15	US-10-369-493-6987	Sequence 6987, Ap	501	5	35.7	575	15	US-10-120-801-60	Sequence 60, Appli
429	5	35.7	440	15	US-10-425-114-59337	Sequence 59337, A	502	5	35.7	575	15	US-10-312-352-8	Sequence 8, Appli
430	5	35.7	444	16	US-10-437-963-113732	Sequence 113732, A	503	5	35.7	575	16	US-10-408-765A-1901	Sequence 1901, Ap
431	5	35.7	445	15	US-10-282-122A-57306	Sequence 57306, A	504	5	35.7	578	15	US-10-403-337-68	Sequence 68, Appl
432	5	35.7	448	15	US-10-369-493-12738	Sequence 12738, A	505	5	35.7	578	15	US-10-351-890-68	Sequence 68, Appl
433	5	35.7	451	15	US-10-282-122A-68682	Sequence 68682, A	506	5	35.7	583	16	US-10-437-963-180545	Sequence 180545, A
434	5	35.7	456	9	US-09-815-242-10870	Sequence 10870, A	507	5	35.7	583	16	US-10-437-963-160820	Sequence 160820, A
435	5	35.7	459	15	US-10-074-978A-246	Sequence 246, App	508	5	35.7	589	16	US-10-425-114-65930	Sequence 65930, A
436	5	35.7	460	15	US-10-154-884B-11048	Sequence 11048, A	509	5	35.7	592	15	US-10-425-114-70054	Sequence 70054, A
437	5	35.7	460	15	US-10-425-114-46265	Sequence 46265, A	510	5	35.7	592	15	US-10-425-114-58837	Sequence 58837, A
438	5	35.7	464	15	US-10-369-493-17155	Sequence 17155, A	511	5	35.7	604	15	US-10-425-114-58837	Sequence 58837, A
439	5	35.7	464	15	US-10-282-122A-48492	Sequence 48492, A	512	5	35.7	607	15	US-10-369-493-10287	Sequence 10287, A
440	5	35.7	465	14	US-10-097-340-151	Sequence 151, App	513	5	35.7	614	15	US-10-282-122A-67017	Sequence 67017, A
441	5	35.7	467	14	US-10-097-340-151	Sequence 151, App	514	5	35.7	617	16	US-10-437-963-107860	Sequence 107860, A
442	5	35.7	467	14	US-10-097-340-151	Sequence 151, App	515	5	35.7	619	15	US-10-369-493-481	Sequence 481, App
443	5	35.7	468	15	US-10-120-801-61	Sequence 61, Appl	516	5	35.7	620	9	US-09-815-242-10068	Sequence 10068, A
444	5	35.7	468	15	US-10-282-122A-78354	Sequence 78354, A	517	5	35.7	620	9	US-09-815-242-14083	Sequence 14083, A
445	5	35.7	469	16	US-10-437-963-186909	Sequence 186909, A	518	5	35.7	620	15	US-10-381-779-31	Sequence 31, Appl
446	5	35.7	471	15	US-10-369-493-4578	Sequence 4578, Ap	519	5	35.7	620	15	US-10-369-493-731	Sequence 731, App
447	5	35.7	473	15	US-10-369-493-3972	Sequence 3972, Ap	520	5	35.7	620	15	US-10-369-493-21174	Sequence 21174, A
448	5	35.7	474	9	US-09-752-639-148	Sequence 148, App	521	5	35.7	620	15	US-10-282-122A-55979	Sequence 55979, A
449	5	35.7	474	9	US-09-984-198-148	Sequence 148, App	522	5	35.7	620	15	US-10-282-122A-56450	Sequence 56450, A
450	5	35.7	475	15	US-10-282-122A-71103	Sequence 71103, A	523	5	35.7	620	15	US-10-282-122A-75419	Sequence 75419, A
451	5	35.7	479	14	US-10-238-075-1407	Sequence 1407, Ap	524	5	35.7	623	16	US-10-408-765A-1812	Sequence 1812, Ap
			479	15	US-10-369-493-7335	Sequence 7335, Ap						US-10-437-963-144350	Sequence 144350, A

525	5	35.7	624	15	US-10-282-122A-69045	Sequence 69045, A	598	943	16	US-10-467-534-79	Sequence 79, Appl
526	5	35.7	625	15	US-10-381-779-33	Sequence 33, Appl	599	946	16	US-10-437-963-180520	Sequence 180520, A
527	5	35.7	626	15	US-10-282-122A-58516	Sequence 58516, A	600	957	15	US-10-267-502-385	Sequence 385, App
528	5	35.7	627	15	US-10-282-122A-77171	Sequence 77171, A	601	957	15	US-09-840-746-19	Sequence 19, Appl
529	5	35.7	628	15	US-10-369-493-598	Sequence 598, App	602	957	16	US-10-437-963-122331	Sequence 122331, A
530	5	35.7	630	9	US-09-742-096-5	Sequence 5, Appl	603	1012	15	US-10-389-566-1458	Sequence 1458, Ap
531	5	35.7	630	16	US-10-474-776-706	Sequence 706, App	604	1024	14	US-10-211-963-43	Sequence 43, Appl
532	5	35.7	631	14	US-10-273-051-8	Sequence 8, Appl	605	1029	15	US-10-389-566-1945	Sequence 1945, Ap
533	5	35.7	631	15	US-10-129-518-8	Sequence 8, Appl	606	1037	15	US-10-389-566-1238	Sequence 1238, Ap
534	5	35.7	638	15	US-10-369-493-1991	Sequence 1991, Ap	607	1037	9	US-09-815-242-5573	Sequence 5573, Ap
535	5	35.7	641	14	US-10-156-761-8643	Sequence 8643, Ap	608	1045	14	US-10-389-566-1237	Sequence 1237, Ap
536	5	35.7	646	16	US-10-437-963-147390	Sequence 147390, A	609	1045	14	US-10-317-835-16	Sequence 16, Appl
537	5	35.7	650	17	US-10-472-928-3386	Sequence 3386, Ap	610	1049	15	US-10-168-583-7	Sequence 7, Appl
538	5	35.7	655	16	US-10-437-963-158260	Sequence 158260, A	611	1055	14	US-10-032-585-7652	Sequence 7652, Ap
539	5	35.7	657	15	US-10-282-122A-52022	Sequence 52022, A	612	1065	9	US-09-815-242-12617	Sequence 12617, A
540	5	35.7	659	16	US-10-437-963-165912	Sequence 165912, A	613	1065	15	US-10-282-122A-44343	Sequence 44343, A
541	5	35.7	662	16	US-10-437-963-197260	Sequence 197260, A	614	1065	17	US-10-857-625-704	Sequence 704, App
542	5	35.7	666	15	US-10-369-493-5126	Sequence 5126, Ap	615	1066	14	US-09-966-521-110	Sequence 110, App
543	5	35.7	667	10	US-09-358-635-2	Sequence 2, Appl	616	1066	14	US-10-429-094-110	Sequence 110, App
544	5	35.7	672	16	US-10-408-765A-2828	Sequence 2828, Ap	617	1066	16	US-10-437-963-157156	Sequence 157156, A
545	5	35.7	683	14	US-10-295-403-98	Sequence 98, Appl	618	1078	16	US-10-437-963-191478	Sequence 191478, A
546	5	35.7	684	14	US-10-286-264-44	Sequence 44, Appl	619	1094	16	US-10-437-963-181712	Sequence 181712, A
547	5	35.7	684	15	US-10-412-699B-564	Sequence 564, App	620	1133	15	US-10-282-122A-71757	Sequence 71757, A
548	5	35.7	686	9	US-09-815-242-11365	Sequence 11365, A	621	1147	11	US-09-921-157-5	Sequence 5, Appl
549	5	35.7	686	16	US-10-437-963-204806	Sequence 204806, A	622	1148	16	US-10-437-963-120457	Sequence 120457, A
550	5	35.7	699	15	US-10-369-493-4524	Sequence 4524, Ap	623	1172	16	US-10-437-963-149114	Sequence 149114, A
551	5	35.7	704	15	US-10-369-493-21102	Sequence 21102, A	624	1183	14	US-10-017-161-720	Sequence 720, App
552	5	35.7	705	15	US-10-369-493-7283	Sequence 7283, Ap	625	1194	15	US-10-282-122A-46577	Sequence 46577, A
553	5	35.7	714	15	US-10-282-122A-56827	Sequence 56827, A	626	1201	16	US-10-437-963-129457	Sequence 129457, A
554	5	35.7	715	16	US-10-437-963-155290	Sequence 155290, A	627	1217	16	US-10-734-564-122	Sequence 122, App
555	5	35.7	721	15	US-10-424-599-156721	Sequence 156721, A	628	1222	14	US-10-193-764-37	Sequence 37, Appl
556	5	35.7	727	15	US-10-369-493-5645	Sequence 5645, Ap	629	1228	14	US-10-193-764-34	Sequence 34, Appl
557	5	35.7	739	15	US-10-425-114-50080	Sequence 50080, A	630	1249	15	US-10-282-122A-76279	Sequence 76279, A
558	5	35.7	744	9	US-09-862-179A-1	Sequence 1, Appl	631	1262	14	US-10-032-585-7858	Sequence 7858, Ap
559	5	35.7	747	16	US-10-437-963-135565	Sequence 135565, A	632	1262	16	US-10-437-963-118488	Sequence 118488, A
560	5	35.7	756	9	US-09-771-161A-101	Sequence 101, App	633	1292	16	US-10-437-963-189422	Sequence 189422, A
561	5	35.7	762	15	US-10-282-122A-73465	Sequence 73465, A	634	1292	16	US-10-437-963-189422	Sequence 189422, A
562	5	35.7	765	15	US-10-282-122A-72723	Sequence 72723, A	635	1302	16	US-10-282-122A-69692	Sequence 69692, A
563	5	35.7	769	14	US-10-032-585-7117	Sequence 7117, Ap	636	1311	8	US-10-437-963-142101	Sequence 142101, A
564	5	35.7	771	16	US-10-437-963-108295	Sequence 108295, A	637	1311	10	US-09-754-032-4	Sequence 4, Appl
565	5	35.7	776	15	US-10-369-493-5483	Sequence 5483, Ap	638	1311	14	US-10-421-446-4	Sequence 4, Appl
566	5	35.7	793	15	US-10-369-493-22456	Sequence 22456, A	639	1338	9	US-09-402-100-4	Sequence 4, Appl
567	5	35.7	793	15	US-10-425-114-57786	Sequence 57786, A	640	1396	15	US-10-282-122A-55213	Sequence 55213, A
568	5	35.7	795	9	US-09-815-242-5499	Sequence 5499, Ap	641	1402	14	US-10-379-616-12	Sequence 12, Appl
569	5	35.7	797	14	US-10-267-989-6	Sequence 6, Appl	642	1402	14	US-10-408-765A-2282	Sequence 2282, Ap
570	5	35.7	818	15	US-10-114-270-172	Sequence 172, App	643	1415	16	US-10-282-122A-66678	Sequence 66678, A
571	5	35.7	819	15	US-10-282-122A-46349	Sequence 46349, A	644	1415	16	US-10-379-616-4	Sequence 4, Appl
572	5	35.7	834	16	US-10-436-715-34	Sequence 115995, A	645	1420	14	US-10-418-027-1	Sequence 1, Appl
573	5	35.7	848	15	US-10-436-715-78	Sequence 10, Appl	646	1424	14	US-10-170-682-3	Sequence 3, Appl
574	5	35.7	848	15	US-10-389-566-1944	Sequence 78, Appl	647	1441	15	US-10-355-218-2	Sequence 2, Appl
575	5	35.7	858	15	US-10-389-566-1944	Sequence 1944, Ap	648	1441	15	US-10-369-493-22554	Sequence 22554, A
576	5	35.7	878	14	US-10-457-031-171	Sequence 171, App	649	1445	16	US-10-437-963-131952	Sequence 131952, A
577	5	35.7	884	15	US-10-424-599-214353	Sequence 214353, A	650	1445	16	US-10-497-692-13	Sequence 13, Appl
578	5	35.7	887	15	US-10-282-122A-68895	Sequence 68895, A	651	1464	9	US-09-842-256-2	Sequence 2, Appl
579	5	35.7	887	15	US-10-114-270-170	Sequence 170, App	652	1475	9	US-09-832-292-37	Sequence 37, Appl
580	5	35.7	888	10	US-09-893-519A-73	Sequence 73, Appl	653	1478	16	US-10-437-963-140834	Sequence 140834, A
581	5	35.7	889	15	US-10-389-566-2238	Sequence 2238, Ap	654	1493	16	US-10-753-901-18	Sequence 18, Appl
582	5	35.7	891	9	US-09-815-242-10147	Sequence 10147, A	655	1507	14	US-10-080-608A-37	Sequence 37, Appl
583	5	35.7	891	14	US-10-267-989-10	Sequence 10, Appl	656	1507	15	US-10-370-685-126	Sequence 126, App
584	5	35.7	891	15	US-10-282-122A-56533	Sequence 56533, A	657	1507	15	US-10-282-122A-68175	Sequence 68175, A
585	5	35.7	891	15	US-10-282-122A-77868	Sequence 77868, A	658	1530	13	US-10-087-192-663	Sequence 663, App
586	5	35.7	892	9	US-09-815-242-13843	Sequence 13843, A	659	1586	13	US-10-437-963-188419	Sequence 188419, A
587	5	35.7	892	15	US-10-282-122A-75020	Sequence 75020, A	660	1592	16	US-09-820-843A-16	Sequence 16, Appl
588	5	35.7	892	15	US-10-282-122A-75981	Sequence 75981, A	661	1616	15	US-10-282-122A-63593	Sequence 63593, A
589	5	35.7	892	16	US-10-437-963-201319	Sequence 201319, A	662	1733	15	US-10-369-493-1564	Sequence 1564, Ap
590	5	35.7	894	15	US-10-282-122A-77378	Sequence 77378, A	663	1783	15	US-10-188-832-86	Sequence 86, Appl
591	5	35.7	896	16	US-10-014-156-13	Sequence 13, Appl	664	1786	9	US-09-742-096-3	Sequence 3, Appl
592	5	35.7	901	15	US-10-282-122A-43767	Sequence 43767, A	665	1787	15	US-10-415-253-2	Sequence 2, Appl
593	5	35.7	904	9	US-09-815-242-12407	Sequence 12407, A	666	1830	15	US-10-424-599-147146	Sequence 147146, A
594	5	35.7	910	15	US-10-259-194A-322	Sequence 322, App	667	1873	13	US-10-087-192-666	Sequence 666, App
595	5	35.7	910	16	US-10-437-963-111792	Sequence 111792, A	668	1876	9	US-09-839-479-70	Sequence 70, Appl
596	5	35.7	913	15	US-10-114-270-168	Sequence 168, App	669	1876	15	US-10-376-537-71	Sequence 71, Appl
597	5	35.7	928	15	US-10-425-114-39886	Sequence 39886, A	670	1876	15	US-10-702-148-70	Sequence 70, Appl

671	5	35.7	1878	9	US-09-839-479-13	Sequence 13, Appl	744	4	28.6	9	15	US-10-057-475B-10084	Sequence 10084, A
672	5	35.7	1878	15	US-10-376-537-13	Sequence 13, Appl	745	4	28.6	9	15	US-10-057-475B-10109	Sequence 10109, A
673	5	35.7	1878	15	US-10-702-148-13	Sequence 13, Appl	746	4	28.6	9	15	US-10-057-475B-10114	Sequence 10114, A
674	5	35.7	1946	15	US-10-282-122A-62947	Sequence 62947, A	747	4	28.6	9	15	US-10-057-475B-10122	Sequence 10122, A
675	5	35.7	1969	9	US-09-839-479-71	Sequence 71, Appl	748	4	28.6	9	15	US-10-057-475B-10138	Sequence 10138, A
676	5	35.7	1969	15	US-10-376-537-72	Sequence 72, Appl	749	4	28.6	9	15	US-10-057-475B-10306	Sequence 10306, A
677	5	35.7	1969	15	US-10-702-148-71	Sequence 71, Appl	750	4	28.6	9	15	US-10-154-884B-10084	Sequence 10084, A
678	5	35.7	1972	9	US-09-839-479-21	Sequence 21, Appl	751	4	28.6	9	15	US-10-154-884B-10109	Sequence 10109, A
679	5	35.7	1972	15	US-10-376-537-21	Sequence 21, Appl	752	4	28.6	9	15	US-10-154-884B-10114	Sequence 10114, A
680	5	35.7	1972	15	US-10-702-148-21	Sequence 21, Appl	753	4	28.6	9	15	US-10-154-884B-10122	Sequence 10122, A
681	5	35.7	1975	16	US-10-437-563-188418	Sequence 188418, A	754	4	28.6	9	15	US-10-154-884B-10138	Sequence 10138, A
682	5	35.7	2062	15	US-10-389-566-1082	Sequence 1082, Ap	755	4	28.6	9	15	US-10-154-884B-10306	Sequence 10306, A
683	5	35.7	2139	17	US-10-480-456-1	Sequence 1, Appli	756	4	28.6	9	15	US-10-398-104-95	Sequence 95, Appl
684	5	35.7	2192	16	US-10-437-563-201156	Sequence 201156, A	757	4	28.6	9	16	US-10-764-324-10084	Sequence 10084, A
685	5	35.7	2364	15	US-10-205-331-66	Sequence 66, Appl	758	4	28.6	9	16	US-10-764-324-10109	Sequence 10109, A
686	5	35.7	2697	15	US-10-144-198-12	Sequence 12, Appl	759	4	28.6	9	16	US-10-764-324-10114	Sequence 10114, A
687	5	35.7	4080	15	US-10-307-817-138	Sequence 138, App	760	4	28.6	9	16	US-10-764-324-10122	Sequence 10122, A
688	5	35.7	4264	15	US-10-187-975-112	Sequence 112, App	761	4	28.6	9	16	US-10-764-324-10138	Sequence 10138, A
689	5	35.7	4349	10	US-09-970-944-4	Sequence 4, Appli	762	4	28.6	9	16	US-10-764-324-10138	Sequence 10138, A
690	5	35.7	4349	10	US-09-970-944-18	Sequence 18, Appl	763	4	28.6	9	16	US-10-764-324-10306	Sequence 10306, A
691	5	35.7	4349	10	US-09-970-944-19	Sequence 19, Appl	764	4	28.6	10	10	US-09-778-026-20	Sequence 20, Appl
692	5	35.7	4349	14	US-10-160-758-15	Sequence 15, Appl	765	4	28.6	10	10	US-09-998-350-4	Sequence 4, Appli
693	5	35.7	4349	14	US-10-174-677-76	Sequence 76, Appl	766	4	28.6	10	10	US-09-998-350-5	Sequence 5, Appli
694	5	35.7	4349	15	US-10-187-975-112	Sequence 112, App	767	4	28.6	10	10	US-09-998-350-6	Sequence 6, Appli
695	5	35.7	4349	16	US-10-408-765A-1739	Sequence 1739, Ap	768	4	28.6	10	10	US-09-998-350-8	Sequence 8, Appli
696	5	35.7	4624	16	US-10-408-765A-2991	Sequence 2991, Ap	769	4	28.6	10	10	US-09-998-350-11	Sequence 11, Appl
697	5	35.7	4640	16	US-10-408-765A-2103	Sequence 2103, Ap	770	4	28.6	10	10	US-09-998-350-12	Sequence 12, Appl
698	5	35.7	4655	16	US-10-741-601-314	Sequence 314, App	771	4	28.6	10	10	US-09-998-350-13	Sequence 13, Appl
699	5	35.7	4655	16	US-10-479-875-3	Sequence 3, Appli	772	4	28.6	10	10	US-09-998-350-14	Sequence 14, Appl
700	5	35.7	4655	17	US-10-741-600-897	Sequence 897, App	773	4	28.6	10	10	US-09-572-404B-2021	Sequence 2021, Ap
701	4	28.6	6	9	US-09-956-625-17	Sequence 17, Appl	774	4	28.6	10	10	US-09-572-404B-4044	Sequence 4044, Ap
702	4	28.6	6	14	US-10-195-970-2	Sequence 2, Appli	775	4	28.6	10	10	US-09-572-404B-4045	Sequence 4045, Ap
703	4	28.6	6	15	US-10-453-420-2	Sequence 2, Appli	776	4	28.6	10	10	US-09-573-822C-43	Sequence 43, Appl
704	4	28.6	7	9	US-09-956-625-3	Sequence 3, Appli	777	4	28.6	10	14	US-10-062-109A-436	Sequence 436, App
705	4	28.6	7	14	US-10-145-415-79	Sequence 79, Appl	778	4	28.6	10	14	US-10-062-109A-537	Sequence 537, App
706	4	28.6	8	9	US-09-765-086-157	Sequence 157, App	779	4	28.6	10	14	US-10-062-109A-634	Sequence 634, App
707	4	28.6	8	9	US-09-904-117-5	Sequence 5, Appli	780	4	28.6	10	14	US-10-005-480A-436	Sequence 436, App
708	4	28.6	8	13	US-10-041-030-29	Sequence 29, Appl	781	4	28.6	10	14	US-10-005-480A-537	Sequence 537, App
709	4	28.6	8	13	US-10-101-812-5	Sequence 5, Appli	782	4	28.6	10	14	US-10-005-480A-634	Sequence 634, App
710	4	28.6	8	14	US-10-101-662A-5	Sequence 5, Appli	783	4	28.6	10	15	US-10-432-236-3	Sequence 3, Appli
711	4	28.6	8	14	US-10-040-862-10407	Sequence 10407, A	784	4	28.6	10	16	US-10-648-854-20	Sequence 20, Appl
712	4	28.6	8	14	US-10-264-374-157	Sequence 157, App	785	4	28.6	10	17	US-10-901-243-85	Sequence 85, Appl
713	4	28.6	8	14	US-10-287-670-5	Sequence 5, Appli	786	4	28.6	10	17	US-10-901-243-86	Sequence 86, Appl
714	4	28.6	8	14	US-10-375-992-157	Sequence 157, App	787	4	28.6	10	17	US-10-901-243-87	Sequence 87, Appl
715	4	28.6	8	15	US-10-057-475B-10407	Sequence 10407, A	788	4	28.6	10	17	US-10-901-243-88	Sequence 88, Appl
716	4	28.6	8	15	US-10-154-884B-10407	Sequence 10407, A	789	4	28.6	11	9	US-09-826-290-206	Sequence 206, App
717	4	28.6	8	15	US-10-464-302-53	Sequence 53, Appl	790	4	28.6	11	10	US-09-852-910-46	Sequence 46, Appl
718	4	28.6	8	15	US-10-257-384A-19	Sequence 19, Appl	791	4	28.6	11	10	US-09-852-910-94	Sequence 94, Appl
719	4	28.6	8	15	US-10-264-374-157	Sequence 157, App	792	4	28.6	11	11	US-09-979-275A-1	Sequence 1, Appli
720	4	28.6	8	16	US-10-375-992-157	Sequence 157, App	793	4	28.6	11	14	US-10-013-815-32	Sequence 32, Appl
721	4	28.6	8	16	US-10-764-324-10407	Sequence 10407, A	794	4	28.6	11	14	US-10-160-506-102	Sequence 102, App
722	4	28.6	9	9	US-09-803-126-22	Sequence 22, Appl	795	4	28.6	11	14	US-10-286-457-327	Sequence 327, App
723	4	28.6	9	9	US-09-894-018-42	Sequence 242, App	796	4	28.6	11	15	US-10-411-336A-46	Sequence 46, Appl
724	4	28.6	9	10	US-09-998-350-1	Sequence 1, Appli	797	4	28.6	11	15	US-10-411-336A-94	Sequence 94, Appl
725	4	28.6	9	10	US-09-998-350-3	Sequence 3, Appli	798	4	28.6	11	11	US-09-979-275A-1	Sequence 1, Appli
726	4	28.6	9	10	US-09-998-350-7	Sequence 7, Appli	799	4	28.6	11	15	US-10-264-309-130	Sequence 130, App
727	4	28.6	9	14	US-10-040-862-10084	Sequence 10084, A	800	4	28.6	11	15	US-10-398-104-235	Sequence 235, App
728	4	28.6	9	14	US-10-040-862-10109	Sequence 10109, A	801	4	28.6	11	16	US-10-449-379-102	Sequence 102, App
729	4	28.6	9	14	US-10-040-862-10114	Sequence 10114, A	802	4	28.6	11	16	US-10-688-015-102	Sequence 102, App
730	4	28.6	9	14	US-10-040-862-10122	Sequence 10122, A	803	4	28.6	12	10	US-09-988-493-197	Sequence 197, App
731	4	28.6	9	14	US-10-040-862-10138	Sequence 10138, A	804	4	28.6	12	16	US-10-601-837-27	Sequence 27, Appl
732	4	28.6	9	14	US-10-040-862-10306	Sequence 10306, A	805	4	28.6	13	10	US-10-128-520-92	Sequence 92, Appl
733	4	28.6	9	14	US-10-062-109A-137	Sequence 137, App	806	4	28.6	13	10	US-09-899-046-249	Sequence 249, App
734	4	28.6	9	14	US-10-062-109A-466	Sequence 466, App	807	4	28.6	13	10	US-09-878-281-249	Sequence 249, App
735	4	28.6	9	14	US-10-062-109A-567	Sequence 567, App	808	4	28.6	13	14	US-09-873-224-249	Sequence 249, App
736	4	28.6	9	14	US-10-360-836-32	Sequence 32, Appl	809	4	28.6	13	14	US-10-104-943-13	Sequence 13, Appl
737	4	28.6	9	14	US-10-005-480A-137	Sequence 137, App	810	4	28.6	13	14	US-10-104-943-58	Sequence 58, Appl
738	4	28.6	9	14	US-10-005-480A-466	Sequence 466, App	811	4	28.6	13	14	US-10-105-232-309	Sequence 309, App
739	4	28.6	9	14	US-10-005-480A-567	Sequence 567, App	812	4	28.6	13	14	US-10-105-232-330	Sequence 330, App
740	4	28.6	9	15	US-10-371-525-440	Sequence 440, App	813	4	28.6	13	14	US-10-189-437-296	Sequence 296, App
741	4	28.6	9	15	US-10-371-069-440	Sequence 440, App	814	4	28.6	13	14	US-10-189-437-317	Sequence 317, App
742	4	28.6	9	15	US-10-371-645-440	Sequence 440, App	815	4	28.6	13	16	US-10-601-837-74	Sequence 74, Appl
743	4	28.6	9	15	US-10-371-260-440	Sequence 440, App	816	4	28.6	13	16	US-10-468-496-682	Sequence 682, App

817	4	28.6	13	15	US-10-468-496-683	Sequence 583, App	890	20	14	US-10-189-437-294	Sequence 294, App
818	4	28.6	13	16	US-10-468-496-684	Sequence 584, App	891	20	15	US-10-238-960-7	Sequence 7, Appli
819	4	28.6	13	16	US-10-468-496-685	Sequence 585, App	892	20	15	US-10-238-960-8	Sequence 8, Appli
820	4	28.6	13	16	US-10-468-496-686	Sequence 586, App	893	20	15	US-10-651-165-35	Sequence 35, Appl
821	4	28.6	13	16	US-10-468-496-687	Sequence 587, App	894	20	15	US-10-651-165-36	Sequence 36, Appl
822	4	28.6	14	14	US-10-104-344-49	Sequence 49, Appl	895	20	15	US-10-239-103-5	Sequence 5, Appli
823	4	28.6	14	14	US-10-104-344-49	Sequence 49, Appl	896	20	15	US-10-239-103-5	Sequence 5, Appli
824	4	28.6	14	14	US-10-104-343-48	Sequence 48, Appl	897	20	15	US-10-432-465-63	Sequence 63, Appl
825	4	28.6	14	14	US-10-104-343-48	Sequence 48, Appl	898	20	15	US-10-432-465-64	Sequence 64, Appl
826	4	28.6	14	16	US-10-104-343-68	Sequence 68, Appl	899	20	15	US-10-432-465-65	Sequence 65, Appl
827	4	28.6	15	8	US-08-865-579-59	Sequence 59, Appl	900	20	16	US-10-433-091-32	Sequence 32, Appl
828	4	28.6	15	8	US-08-736-019-49	Sequence 49, Appl	901	20	16	US-10-433-091-33	Sequence 33, Appl
829	4	28.6	15	9	US-09-746-731-59	Sequence 59, Appl	902	20	16	US-10-321-798-79	Sequence 79, Appl
830	4	28.6	15	9	US-09-952-768-11	Sequence 41, Appl	903	20	16	US-10-321-798-80	Sequence 80, Appl
831	4	28.6	15	9	US-09-952-768-46	Sequence 46, Appl	904	20	16	US-10-794-929-69	Sequence 69, Appl
832	4	28.6	15	9	US-09-954-697-97	Sequence 97, Appl	905	20	11	US-09-833-245-1066	Sequence 1066, Ap
833	4	28.6	15	13	US-10-103-395-67	Sequence 67, Appl	906	21	14	US-10-174-410-45	Sequence 45, Appl
834	4	28.6	15	13	US-10-029-413A-26	Sequence 26, Appl	907	21	14	US-10-057-789-159	Sequence 159, App
835	4	28.6	15	13	US-10-059-749-59	Sequence 59, Appl	908	21	14	US-10-212-628-159	Sequence 159, App
836	4	28.6	15	14	US-10-174-105A-115	Sequence 115, App	909	21	14	US-10-105-232-306	Sequence 306, App
837	4	28.6	15	14	US-10-174-105A-116	Sequence 116, App	910	21	14	US-10-189-437-293	Sequence 293, App
838	4	28.6	15	15	US-10-378-707-3	Sequence 3, Appli	911	21	15	US-10-651-563-43	Sequence 43, Appl
839	4	28.6	15	15	US-10-668-955-46	Sequence 46, Appl	912	23	14	US-10-097-065-356	Sequence 356, App
840	4	28.6	16	8	US-08-736-019-37	Sequence 37, Appl	913	23	15	US-10-372-876-356	Sequence 356, App
841	4	28.6	16	9	US-09-776-430-47	Sequence 47, Appl	914	24	9	US-09-867-852-70	Sequence 70, Appl
842	4	28.6	16	9	US-09-776-431-47	Sequence 47, Appl	915	24	14	US-10-193-764-4	Sequence 4, Appli
843	4	28.6	16	14	US-10-006-760-58	Sequence 58, Appl	916	24	15	US-10-613-472-70	Sequence 70, Appl
844	4	28.6	16	15	US-10-378-173-139	Sequence 139, App	917	24	16	US-10-613-765-70	Sequence 70, Appl
845	4	28.6	16	15	US-10-436-715-244	Sequence 244, App	918	24	16	US-09-813-345-22	Sequence 22, Appl
846	4	28.6	16	15	US-10-436-715-283	Sequence 283, App	919	25	10	US-09-197-945-252	Sequence 252, App
847	4	28.6	16	15	US-10-182-936A-179	Sequence 179, App	920	25	10	US-09-924-447C-3	Sequence 3, Appli
848	4	28.6	16	16	US-10-128-520-93	Sequence 93, Appl	921	25	10	US-09-924-447C-4	Sequence 4, Appli
849	4	28.6	17	9	US-09-864-761-37350	Sequence 37350, A	922	25	14	US-10-239-423-29	Sequence 29, Appl
850	4	28.6	17	14	US-10-225-567A-1107	Sequence 1107, Ap	923	25	15	US-10-653-595-252	Sequence 252, App
851	4	28.6	17	16	US-10-258-637-40	Sequence 40, Appl	924	25	16	US-10-416-249-330	Sequence 330, App
852	4	28.6	17	16	US-10-258-637-43	Sequence 43, Appl	925	26	9	US-09-864-761-4151	Sequence 4151, A
853	4	28.6	18	10	US-09-776-724A-244	Sequence 244, App	926	26	9	US-09-864-761-46880	Sequence 46880, A
854	4	28.6	18	14	US-10-084-813-16	Sequence 16, Appl	927	26	9	US-09-921-397-7	Sequence 7, Appli
855	4	28.6	18	14	US-10-084-813-157	Sequence 157, App	928	26	9	US-09-921-397-35	Sequence 35, Appl
856	4	28.6	18	14	US-10-084-813-158	Sequence 158, App	929	26	10	US-09-983-802-579	Sequence 579, App
857	4	28.6	18	14	US-10-084-813-159	Sequence 159, App	930	26	10	US-09-984-490-579	Sequence 490, App
858	4	28.6	18	14	US-10-225-567A-1440	Sequence 1440, Ap	931	26	10	US-09-998-350-18	Sequence 18, Appl
859	4	28.6	18	15	US-10-419-462-39	Sequence 39, Appl	932	26	10	US-09-998-350-19	Sequence 19, Appl
860	4	28.6	19	8	US-08-841-636A-29	Sequence 29, Appl	933	26	11	US-09-973-278-607	Sequence 607, App
861	4	28.6	19	14	US-10-105-232-308	Sequence 308, App	934	26	11	US-10-029-386-30581	Sequence 30581, A
862	4	28.6	19	14	US-10-189-437-295	Sequence 295, App	935	27	9	US-09-864-761-34056	Sequence 34056, A
863	4	28.6	19	16	US-10-412-964-69	Sequence 69, Appl	936	27	10	US-09-933-767-702	Sequence 702, App
864	4	28.6	19	16	US-10-782-002-29	Sequence 29, Appl	937	27	14	US-10-004-860-702	Sequence 702, App
865	4	28.6	19	16	US-10-825-378-29	Sequence 29, Appl	938	27	14	US-10-057-789-275	Sequence 275, App
866	4	28.6	20	9	US-09-884-441-407	Sequence 407, App	939	27	14	US-10-212-628-275	Sequence 275, App
867	4	28.6	20	9	US-09-813-333-5	Sequence 5, Appli	940	27	14	US-10-023-282-702	Sequence 702, App
868	4	28.6	20	9	US-09-973-025-79	Sequence 79, Appl	941	27	14	US-10-339-740-293	Sequence 293, App
869	4	28.6	20	9	US-09-973-025-80	Sequence 80, Appl	942	28	8	US-08-424-550B-456	Sequence 456, App
870	4	28.6	20	10	US-09-991-433-49	Sequence 49, Appl	943	28	8	US-10-105-232-329	Sequence 329, App
871	4	28.6	20	10	US-09-991-433-50	Sequence 50, Appl	944	28	8	US-10-189-437-316	Sequence 316, App
872	4	28.6	20	10	US-09-899-303-79	Sequence 79, Appl	945	28	15	US-10-424-599-251229	Sequence 251229, App
873	4	28.6	20	10	US-09-899-303-80	Sequence 80, Appl	946	28	16	US-10-695-499-156	Sequence 156, App
874	4	28.6	20	10	US-09-907-969-407	Sequence 407, App	947	28	6	US-09-864-761-43902	Sequence 43902, A
875	4	28.6	20	10	US-09-995-808-79	Sequence 79, Appl	948	29	9	US-09-813-345-1	Sequence 1, Appli
876	4	28.6	20	10	US-09-995-808-80	Sequence 80, Appl	949	29	9	US-09-813-345-2	Sequence 2, Appli
877	4	28.6	20	10	US-09-995-860-79	Sequence 79, Appl	950	29	9	US-09-921-397-24	Sequence 24, Appl
878	4	28.6	20	10	US-09-995-860-80	Sequence 80, Appl	951	29	14	US-09-071-838-189	Sequence 189, App
879	4	28.6	20	10	US-09-995-791-79	Sequence 79, Appl	952	30	9	US-10-213-512-189	Sequence 189, App
880	4	28.6	20	10	US-09-995-791-80	Sequence 80, Appl	953	30	9	US-09-864-761-48497	Sequence 48497, A
881	4	28.6	20	10	US-09-995-791-80	Sequence 80, Appl	954	30	9	US-09-813-345-19	Sequence 19, Appl
882	4	28.6	20	13	US-10-044-703-5	Sequence 5, Appli	955	30	10	US-09-983-802-662	Sequence 662, App
883	4	28.6	20	14	US-10-053-485-48	Sequence 48, Appl	956	30	10	US-09-984-490-662	Sequence 662, App
884	4	28.6	20	14	US-10-013-815-3	Sequence 3, Appli	957	30	11	US-09-973-278-443	Sequence 443, App
885	4	28.6	20	14	US-10-198-053-407	Sequence 407, App	958	30	14	US-10-162-538-15	Sequence 15, Appl
886	4	28.6	20	14	US-10-198-053-613	Sequence 613, App	959	30	14	US-10-299-043-11	Sequence 11, Appl
887	4	28.6	20	14	US-10-371-634-42	Sequence 42, Appl	960	30	15	US-10-411-544-52	Sequence 52, Appl
888	4	28.6	20	14	US-10-105-232-307	Sequence 307, App	961	30	15	US-10-105-232-307	Sequence 307, App
889	4	28.6	20	14	US-10-280-066-32	Sequence 32, App	962	30	15	US-10-296-734-472	Sequence 472, App
										US-10-296-734-474	Sequence 474, App


```
RESULT 4
US-10-369-493-18546
; Sequence 18546, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 18546
; LENGTH: 1190
; TYPE: PRT
; ORGANISM: Halobacterium sp. NRC-1
US-10-369-493-18546
Query Match 50.0%; Score 7; DB 15; Length 1190;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGSV 11
Db 106 SENVGSV 112
|||||

RESULT 5
US-10-424-599-154932
; Sequence 154932, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 154932
; LENGTH: 74
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_110925C.1.pep
US-10-424-599-154932
Query Match 42.9%; Score 6; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 2 VGSVCG 7
|||||

RESULT 6
US-10-264-049-3886
; Sequence 3886, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
```

```
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3886
; LENGTH: 81
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (10)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (28)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-3886
Query Match 42.9%; Score 6; DB 15; Length 81;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
Db 71 ENVGSV 76
|||||

RESULT 7
US-10-437-963-179908
; Sequence 179908, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 179908
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77324C.1.pep
US-10-437-963-179908
Query Match 42.9%; Score 6; DB 16; Length 95;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 48 VGSVCG 53
|||||
```


RESULT 8

US-10-424-599-244020
; Sequence 244020, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 244020
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_62378C.1.pep
US-10-424-599-244020

Query Match 42.9%; Score 6; DB 15; Length 98;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NVSENV 8
|||||
Db 52 NVSENV 57

RESULT 9

US-10-437-963-119862
; Sequence 119862, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 119862
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(100)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23037C.1.pep
US-10-437-963-119862

Query Match 42.9%; Score 6; DB 16; Length 100;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSVCGT 14
|||||
Db 93 GSVCGT 98

RESULT 10

US-10-369-493-17361
; Sequence 17361, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17361
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Bacillus halodurans
US-10-369-493-17361

Query Match 42.9%; Score 6; DB 15; Length 169;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DNVSSEN 7
|||||
Db 117 DNVSSEN 122

RESULT 11

US-10-437-963-180011
; Sequence 180011, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 180011
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77417C.1.pep
US-10-437-963-180011

Query Match 42.9%; Score 6; DB 16; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
|||||
Db 138 VGSVCG 143

RESULT 12

US-10-094-749-2381
; Sequence 2381, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:

APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUOI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YURI
APPLICANT: OTSUKA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: IRIE, KYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHICO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOTOKYUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: MASUHO, YASUHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 084335/0160 US/10/094,749
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT FILING DATE: 2002-03-12
PRIOR APPLICATION NUMBER: 60/350,435
PRIOR FILING DATE: 2002-01-24
PRIOR APPLICATION NUMBER: JP 2001-328381
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2381
LENGTH: 219
TYPE: PRT
ORGANISM: Homo sapiens
US-10-094-749-2381

Query Match 42.9%; Score 6; DB 15; Length 219;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
Db 37 VGSVCG 42

RESULT 13
US-10-437-963-197887
; Sequence 197887, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 197887
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_93601C.1.pcp
US-10-437-963-197887

Query Match 42.9%; Score 6; DB 16; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GSVCGT 14
Db 182 GSVCGT 187

RESULT 14
US-10-080-170-315
; Sequence 315, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 315
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-315

Query Match 42.9%; Score 6; DB 14; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 189 VSENVG 194

RESULT 15
US-10-080-170-315
; Sequence 315, Application US/10080170
; Publication No. US20040121322A9
; GENERAL INFORMATION:
; APPLICANT: COLE, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR
; TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
; TITLE OF INVENTION: TREATMENT OF MYCOBACTERIOSES
; FILE REFERENCE: 03495.0218
; CURRENT APPLICATION NUMBER: US/10/080,170
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: 60/270,123
; PRIOR FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 652
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 315
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Mycobacterium leprae
US-10-080-170-315

Query Match 42.9%; Score 6; DB 16; Length 224;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVG 9
Db 189 VSENVG 194

Search completed: February 11, 2005, 03:25:36
Job time : 19.2225 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:06:34 ; Search time 1.07417 Seconds
(without alignments)
1254.025 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSNVSGVCGT 14

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR.79.*
1: Piri.*
2: Piri2.*
3: Piri3.*
4: Piri4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	50.0	446	2 S69051	hypothetical prote
2	7	50.0	1069	2 D81826	exodeoxyribonuclea
3	7	50.0	1190	2 B84193	chromosome segrega
4	6	42.9	106	2 C86086	hypothetical prote
5	6	42.9	109	2 G82929	ATP synthase C cha
6	6	42.9	118	2 AE1214	hypothetical prote
7	6	42.9	169	2 D83998	acetyl-CoA carboxy
8	6	42.9	224	2 D87236	conserved membrane
9	6	42.9	231	2 T20304	hypothetical prote
10	6	42.9	233	2 A1367	16S pseudouridylat
11	6	42.9	269	1 WZB241	gene 24 protein -
12	6	42.9	291	2 D82491	hypothetical prote
13	6	42.9	296	2 B75555	probable lipase/es
14	6	42.9	345	2 S51548	killer toxin K28 -
15	6	42.9	359	2 H65201	pts system, fructo
16	6	42.9	381	2 AC1432	DNA polymerase III
17	6	42.9	381	2 AC1433	DNA polymerase III
18	6	42.9	389	2 D64333	pyruvate synthase
19	6	42.9	396	2 A13554	xylose transport s
20	6	42.9	457	2 S39079	puff C-8 protein -
21	6	42.9	759	2 A46188	CAMP-activated Na+
22	6	42.9	862	1 A49346	aldehyde dehydroge
23	6	42.9	935	2 E36806	hypothetical prote
24	6	42.9	1066	1 A48669	kinesin-related pr
25	6	42.9	1091	1 P10009	complement C3d/Eps
26	6	42.9	1131	2 T14517	hypothetical prote
27	6	42.9	1776	2 G86280	protein T5E21.13 (
28	6	42.9	1844	2 T51890	related to Nup98-N
29	6	42.9	4543	1 A53102	alpha-2-macroglobu

30	6	42.9	4544	1 S02392	alpha-2-macroglobu
31	6	42.9	4545	1 S25111	hypothetical prote
32	6	42.9	5170	2 T15348	26K kidney and gal
33	5	35.7	16	2 D58501	gene GFAP gamma pr
34	5	35.7	43	2 I52659	hypothetical prote
35	5	35.7	50	2 T20498	hypothetical prote
36	5	35.7	72	2 E84462	hypothetical prote
37	5	35.7	74	2 S26001	conserved hypotnet
38	5	35.7	84	2 D75545	interleukin-beta
39	5	35.7	88	2 E56084	Ig light chain v r
40	5	35.7	91	2 PH1071	Ig light chain v r
41	5	35.7	96	2 A69007	ribosomal protein
42	5	35.7	98	2 T39208	very hypothetical
43	5	35.7	103	2 D64034	hypothetical prote
44	5	35.7	107	2 PL0268	Ig kappa chain v r
45	5	35.7	107	2 AE1605	B. subtilis comg o
46	5	35.7	108	2 C64455	hypothetical prote
47	5	35.7	121	2 T44408	ribosomal protein
48	5	35.7	122	2 G95504	hypothetical prote
49	5	35.7	123	2 T26709	hypothetical prote
50	5	35.7	128	2 C91053	Nifu-like protein
51	5	35.7	128	2 H65029	iron-sulfur cofact
52	5	35.7	128	2 G85897	Nifu-like protein
53	5	35.7	131	2 S45059	AC1 protein (clone
54	5	35.7	140	2 I38232	gene SMA3 protein
55	5	35.7	140	2 I38233	gene SMA4 protein
56	5	35.7	140	2 T38234	gene SMA5 protein
57	5	35.7	143	2 T04524	photosystem I chai
58	5	35.7	145	2 A84587	hypothetical prote
59	5	35.7	149	2 A71074	probable methylal
60	5	35.7	154	2 A11231	hypothetical prote
61	5	35.7	154	2 AH1585	hypothetical prote
62	5	35.7	156	2 E90508	conserved hypotnet
63	5	35.7	160	2 A48975	Thy-1 glycoprotein
64	5	35.7	160	2 T27963	hypothetical prote
65	5	35.7	163	2 JC5045	epithelial membran
66	5	35.7	166	2 T46231	hypothetical prote
67	5	35.7	179	2 D84773	hypothetical prote
68	5	35.7	184	2 T00277	conserved hypotnet
69	5	35.7	185	2 T31939	hypothetical prote
70	5	35.7	186	2 T25346	hypothetical prote
71	5	35.7	193	2 T26581	hypothetical prote
72	5	35.7	194	2 H90912	hypothetical prote
73	5	35.7	200	2 G84066	hypothetical prote
74	5	35.7	201	2 C96634	hypothetical prote
75	5	35.7	203	2 E97022	hypothetical prote
76	5	35.7	205	2 S34919	ribosomal protein
77	5	35.7	209	2 F64416	polyferredoxin - M
78	5	35.7	217	2 J50492	adenylate kinase (
79	5	35.7	220	2 F90065	hypothetical prote
80	5	35.7	221	2 JC4722	toxin co-regulated
81	5	35.7	222	2 H89763	hypothetical prote
82	5	35.7	225	2 T44105	hypothetical prote
83	5	35.7	226	2 T22445	hypothetical prote
84	5	35.7	227	2 G69762	two-component resp
85	5	35.7	228	2 AC1263	two-component resp
86	5	35.7	228	2 AE1625	two-component resp
87	5	35.7	229	2 A81169	hypothetical prote
88	5	35.7	231	2 A60468	venombin A (EC 3.4
89	5	35.7	231	2 G81936	hypothetical prote
90	5	35.7	232	1 A54361	venombin A (EC 3.4
91	5	35.7	233	1 JG0169	venombin A (EC 3.4
92	5	35.7	234	2 B95228	conserved hypotnet
93	5	35.7	234	2 F98092	conserved hypotnet
94	5	35.7	235	1 S65621	venombin AB (EC 3.
95	5	35.7	235	1 A41456	venombin A (EC 3.4
96	5	35.7	236	1 A41456	sulfate transport
97	5	35.7	236	2 T07260	probable membrane
98	5	35.7	239	2 G81369	hypothetical prote
99	5	35.7	240	2 E70115	hypothetical prote
100	5	35.7	241	2 F81218	competence protein
101	5	35.7	242	1 LNRTMC	mannose-binding le
102	5	35.7	244	2 T12051	3-oxoacyl-l-acyl-ca

103	5	35.7	244	2	T30120	hypothetical prote	176	5	35.7	344	2	D69420	hydrogenase expres
104	5	35.7	247	2	S73076	hypothetical prote	177	5	35.7	344	2	S22796	probable portal pr
105	5	35.7	248	1	Q0BE4L	probable glycoprot	178	5	35.7	346	2	T01123	hypothetical prote
106	5	35.7	248	2	F82128	3-oxoacyl-(acyl-ca	179	5	35.7	349	2	S12863	G protein-coupled
107	5	35.7	252	2	A87535	probable short cha	180	5	35.7	350	2	B70395	hypothetical prote
108	5	35.7	252	2	T14964	phage lambda-relat	181	5	35.7	355	2	G84651	biotin holocarboxy
109	5	35.7	252	2	B70602	hypothetical prote	182	5	35.7	356	2	AG0370	probable ABC-trans
110	5	35.7	253	2	T04059	hypothetical prote	183	5	35.7	359	2	S39235	gene C1 protein -
111	5	35.7	255	1	A28169	venombin A (BC 3.4	184	5	35.7	359	2	S39211	gene C1 protein -
112	5	35.7	255	2	JC7593	SH2 domain-contain	185	5	35.7	359	2	S22593	hypothetical prote
113	5	35.7	256	1	WMI02	28.5K transport pr	186	5	35.7	360	2	S57777	cysteine proteinas
114	5	35.7	257	1	JC2479	venombin B (BC 3.4	187	5	35.7	367	2	G97649	glutamine syntheta
115	5	35.7	257	2	T52298	squamosa promoter	188	5	35.7	367	2	F64202	probable GTP-bind
116	5	35.7	258	1	S36783	venombin A (BC 3.4	189	5	35.7	371	2	D84186	hypothetical prote
117	5	35.7	258	2	A57290	venom plasminogen	190	5	35.7	373	2	G83574	hypothetical prote
118	5	35.7	258	2	A54907	casein kinase II (191	5	35.7	374	2	T44945	hypothetical prote
119	5	35.7	259	2	S28998	hypothetical prote	192	5	35.7	377	2	B64703	conserved hypothet
120	5	35.7	260	2	A21158	hypothetical prote	193	5	35.7	377	2	A71818	hypothetical prote
121	5	35.7	262	1	JC4803	venombin A (BC 3.4	194	5	35.7	379	2	T46002	hypothetical prote
122	5	35.7	267	2	B55850	hypothetical prote	195	5	35.7	380	1	G64509	conserved hypothet
123	5	35.7	270	2	AC1956	phosphoserine-re	196	5	35.7	380	2	T48953	hypothetical prote
124	5	35.7	270	2	C97772	diaminopimelate ep	197	5	35.7	382	2	B46133	neuropeptide Y/pep
125	5	35.7	275	2	T28738	hypothetical prote	198	5	35.7	383	2	T26902	hypothetical prote
126	5	35.7	276	2	B83161	probable short-cha	199	5	35.7	385	2	C87250	dnaj protein limpo
127	5	35.7	276	2	A30392	conserved hypothet	200	5	35.7	387	2	F96798	hypothetical prote
128	5	35.7	276	2	A82668	molybdopterin bios	201	5	35.7	388	2	H84079	L-arabinose ABC tr
129	5	35.7	282	2	B81161	phosphoribosylamin	202	5	35.7	391	2	T39992	ribonucleoside-dip
130	5	35.7	287	2	G81943	probable phosphori	203	5	35.7	391	2	S34808	conserved hypothet
131	5	35.7	288	2	C71936	probable co-chaper	204	5	35.7	397	2	A80148	cell division prot
132	5	35.7	288	2	H64647	co-chaperone-curve	205	5	35.7	399	2	B84955	probable ribose/ga
133	5	35.7	288	2	H95018	transcription regu	206	5	35.7	400	2	E71338	hypothetical prote
134	5	35.7	289	1	A37209	thiosulfate sulfur	207	5	35.7	402	2	B90519	hypothetical prote
135	5	35.7	289	2	D70440	DNA polymerase I 3	208	5	35.7	408	2	T44859	glycosyltransferas
136	5	35.7	289	2	E30397	dihydrodipicolinat	209	5	35.7	412	2	C38104	LFY floral meriste
137	5	35.7	290	2	A57394	hypothetical prote	210	5	35.7	415	2	S37340	f1o protein nomolo
138	5	35.7	290	2	AC2612	conserved hypothet	211	5	35.7	416	2	B84276	glutamate dehydrog
139	5	35.7	292	2	AD2133	ferric aerobactin	212	5	35.7	419	2	T24820	hypothetical prote
140	5	35.7	292	2	E95130	hypothetical prote	213	5	35.7	420	2	AF1239	B. subtilis Yluc p
141	5	35.7	292	2	E85975	hypothetical prote	214	5	35.7	420	2	B38104	LFY floral meriste
142	5	35.7	292	2	T16085	hypothetical prote	215	5	35.7	422	1	A69853	hexuronate transpo
143	5	35.7	292	2	A40993	H+/K+-exchanging A	216	5	35.7	424	2	AG1804	LFY floral meriste
144	5	35.7	296	2	AH3343	serine O-acetyltra	217	5	35.7	427	2	AG1855	hypothetical prote
145	5	35.7	298	2	AB3190	hypothetical prote	218	5	35.7	429	2	JC4986	site-specific DNA-
146	5	35.7	298	2	S69523	hypothetical prote	219	5	35.7	431	2	H70302	conserved hypothet
147	5	35.7	305	2	A96593	unknown protein [i	220	5	35.7	432	2	T51020	chorismate synthas
148	5	35.7	310	2	B55053	endothelial monocy	221	5	35.7	432	2	T46725	chorismate synthas
149	5	35.7	310	2	G86490	probable biotin ho	222	5	35.7	433	2	S63447	hypothetical prote
150	5	35.7	313	2	C95247	conserved hypothet	223	5	35.7	433	2	H84826	hypothetical prote
151	5	35.7	313	2	H98111	conserved hypothet	224	5	35.7	437	2	T21518	kynurenine-oxoglut
152	5	35.7	316	1	A38743	loricrin - human	225	5	35.7	439	2	D86297	hypothetical prote
153	5	35.7	317	2	T10813	1-aminocyclopropan	226	5	35.7	451	2	C81059	conserved hypothet
154	5	35.7	317	2	C82450	1-phosphofructokin	227	5	35.7	451	2	B81818	conserved hypothet
155	5	35.7	317	2	A97684	hypothetical prote	228	5	35.7	453	2	T21528	hypothetical prote
156	5	35.7	317	2	AB2909	rhizobioicin [impor	229	5	35.7	456	2	T22347	hypothetical prote
157	5	35.7	318	2	C84212	immunogenic protei	230	5	35.7	459	2	G89980	aldehyde dehydrog
158	5	35.7	319	2	A53502	follicstatin - Afri	231	5	35.7	460	2	G81327	probable glycolate
159	5	35.7	320	2	G96714	hypothetical prote	232	5	35.7	464	2	H83752	glutamate dehydrog
160	5	35.7	322	2	JN0265	genome polypoteine	233	5	35.7	465	2	D84427	hypothetical prote
161	5	35.7	322	2	E30457	rieske iron-sulfur	234	5	35.7	466	2	H96591	secreted protein c
162	5	35.7	322	2	B84635	hypothetical prote	235	5	35.7	468	2	AB0040	replicative DNA he
163	5	35.7	322	2	T50494	hypothetical prote	236	5	35.7	470	2	T31049	hypothetical prote
164	5	35.7	329	2	E69054	cobalamin biosynth	237	5	35.7	471	2	T27856	hypothetical prote
165	5	35.7	331	2	S74810	probable succinate	238	5	35.7	473	2	T40368	H+-transporting tw
166	5	35.7	333	2	AF1924	succinate dehydrog	239	5	35.7	473	2	AI1390	H+-transporting AT
167	5	35.7	335	2	E90014	hypothetical prote	240	5	35.7	475	2	AC1766	H+-transporting AT
168	5	35.7	336	2	B96020	probable sugar upt	241	5	35.7	475	2	AF0687	bacteriophage tail
169	5	35.7	337	2	D89850	glycolytic operon	242	5	35.7	481	2	S49778	hypothetical prote
170	5	35.7	337	2	T18431	hypothetical prote	243	5	35.7	483	2	S61975	glutathione-disulf
171	5	35.7	339	2	A95937	hypothetical adeny	244	5	35.7	485	2	B81871	probable GTP-bind
172	5	35.7	340	2	T13781	NADH2 dehydrogenas	245	5	35.7	485	2	G81149	essential Gnpase N
173	5	35.7	341	2	T51897	related to sorbito	246	5	35.7	488	2	T32149	hypothetical prote
174	5	35.7	341	2	A53057	retinal-binding pr	247	5	35.7	490	2	AF0156	probable D-mannosa
175	5	35.7	344	2	AF2873	glutamine syntheta	248	5	35.7	491	2	T50346	hypothetical prote

249 5 35.7 492 2 AD3047 copper tolerance p
250 5 35.7 492 2 H98238 hypothetical prote
251 5 35.7 493 2 T05161 hypothetical prote
252 5 35.7 497 1 T41397 DNA damage inducib
253 5 35.7 493 2 S33938 penton protein (II
254 5 35.7 497 2 S57073 probable membrane
255 5 35.7 499 2 T03877 hypothetical prote
256 5 35.7 504 2 D71615 hypothetical prote
257 5 35.7 504 2 T34411 hypothetical prote
258 5 35.7 505 2 H85361 leucyl aminopeptid
259 5 35.7 506 2 T38915 histidyl-tRNA synt
260 5 35.7 507 2 D75029 protein-export mem
261 5 35.7 507 2 A71215 hypothetical prote
262 5 35.7 518 2 G70174 hypothetical prote
263 5 35.7 520 2 H64510 hypothetical prote
264 5 35.7 520 2 S54151 cvl B protein - Az
265 5 35.7 521 2 F86418 61.6K hypothetical
266 5 35.7 526 2 E71423 hypothetical prote
267 5 35.7 527 2 T04659 hypothetical prote
268 5 35.7 528 1 WNEVB8 58K protein - barl
269 5 35.7 528 2 F70331 2-isopropylmalate
270 5 35.7 529 2 T03879 hypothetical prote
271 5 35.7 532 2 AD2420 hypothetical prote
272 5 35.7 535 2 E96730 hypothetical prote
273 5 35.7 537 2 T19764 hypothetical prote
274 5 35.7 541 2 T37945 conserved hypothet
275 5 35.7 544 1 S41389 penton protein (II
276 5 35.7 549 2 T50295 hypothetical prote
277 5 35.7 550 2 T34220 hypothetical prote
278 5 35.7 553 2 B55514 dihydrolipoamide S
279 5 35.7 555 2 S50157 cyclin-dependent k
280 5 35.7 560 2 S41808 glucose-6-phosphat
281 5 35.7 560 2 C84632 hypothetical prote
282 5 35.7 564 2 T11548 probable zinc meta
283 5 35.7 566 2 S38399 glutamate/aspartat
284 5 35.7 566 2 S19063 hypothetical prote
285 5 35.7 569 2 S64957 aspergillopepsin I
286 5 35.7 570 2 A11828 flavoprotein [impo
287 5 35.7 571 1 XZAD32 penton protein (II
288 5 35.7 571 1 XZADH5 penton protein (II
289 5 35.7 586 2 T39769 trp-asp repeats co
290 5 35.7 591 2 B87361 flagellar hook pro
291 5 35.7 593 1 S52984 catechol oxidase (
292 5 35.7 599 2 T10798 phenophorin-S - Vo
293 5 35.7 601 2 T38258 coronin-like prote
294 5 35.7 603 2 AG2070 hypothetical prote
295 5 35.7 619 2 A10385 1-deoxy-D-xylulose
296 5 35.7 620 2 A70554 1-deoxyxylulose-5-
297 5 35.7 620 2 D84771 dxs protein - Esch
298 5 35.7 620 2 B95538 1-deoxy-D-xylulose
299 5 35.7 620 2 B90688 1-deoxy-D-xylulose
300 5 35.7 620 2 T50150 yeast nrd1-like pr
301 5 35.7 625 2 B64172 dxs protein - Haem
302 5 35.7 626 2 H82266 1-deoxyxylulose-5-
303 5 35.7 627 2 D84494 probable Tail-like
304 5 35.7 629 2 G75390 1-deoxy-D-xylulose
305 5 35.7 630 2 B95191 endopeptidase O [i
306 5 35.7 630 2 B98058 endopeptidase O (E
307 5 35.7 632 2 E81684 1-deoxyxylulose-5-
308 5 35.7 633 2 A25473 chorion E2 protein
309 5 35.7 634 2 C96541 10-formyltetrahydr
310 5 35.7 634 2 T27881 hypothetical prote
311 5 35.7 635 2 H81793 hypothetical prote
312 5 35.7 638 1 S62932 hypothetical prote
313 5 35.7 640 2 F71527 probable transketo
314 5 35.7 646 2 S38819 plasma protein S -
315 5 35.7 656 2 T38741 major facilitator
316 5 35.7 657 2 C97113 serine/threonine p
317 5 35.7 659 2 C85057 probable receptor-
318 5 35.7 663 2 T24881 hypothetical prote
319 5 35.7 666 2 A47650 STE12 protein - ye
320 5 35.7 666 2 T24170 hypothetical prote
321 5 35.7 667 2 T15710 hypothetical prote

322 5 35.7 673 2 C86278
323 5 35.7 675 1 KXMS
324 5 35.7 675 1 KXMS
325 5 35.7 682 2 T10319 envelope protein S p
326 5 35.7 686 2 G64618 envelope-transporti
327 5 35.7 688 2 D72418 DNA ligase - Therm
328 5 35.7 701 2 T15235 hypothetical prote
329 5 35.7 702 2 T41792 OGV-B56 orf46 - Bo
330 5 35.7 702 2 D90886 VgrE protein [impo
331 5 35.7 704 2 F72855 occlusion-derived
332 5 35.7 708 2 C86404 probable protein A
333 5 35.7 714 2 B85732 Rbe element associ
334 5 35.7 718 2 S74509 polyribonucleotide
335 5 35.7 719 2 AD2355 polyribonucleotide
336 5 35.7 720 2 T02154 protein kinase hom
337 5 35.7 722 2 F85572 probable outer mem
338 5 35.7 722 2 T19772 hypothetical prote
339 5 35.7 727 2 G90721 probable outer mem
340 5 35.7 727 2 T26096 hypothetical prote
341 5 35.7 728 2 S76968 hypothetical prote
342 5 35.7 733 2 A45301 microtubule-associ
343 5 35.7 735 2 T35778 probable fusidic a
344 5 35.7 736 2 T41629 hypothetical prote
345 5 35.7 738 2 I49295 IL-12 receptor bet
346 5 35.7 739 2 F86337 F4O10.2 protein -
347 5 35.7 747 2 T39879 hypothetical prote
348 5 35.7 756 2 S47656 TMDC II protein -
349 5 35.7 758 2 T38811 Na+/H+-exchanging
350 5 35.7 759 2 T11631 Na+/H+-exchanging
351 5 35.7 776 2 T20896 hypothetical prote
352 5 35.7 778 2 T16111 hypothetical prote
353 5 35.7 783 2 T30413 viral enhancing fa
354 5 35.7 793 2 S65240 F-cadherin - Afric
355 5 35.7 793 2 S65240 probable membrane
356 5 35.7 801 2 A33630 zinc finger protei
357 5 35.7 807 2 T32463 hypothetical prote
358 5 35.7 827 2 S48455 6-phosphofructo-2-
359 5 35.7 829 2 B96640 hypothetical prote
360 5 35.7 852 2 S41886 DNA repair protein
361 5 35.7 856 2 D87515 TonB-dependent rec
362 5 35.7 858 2 E96602 hypothetical prote
363 5 35.7 863 2 C90482 ABC transporter, A
364 5 35.7 891 1 DEEC acetaldehyde dehyd
365 5 35.7 891 2 D85704 hypothetical prote
366 5 35.7 891 2 E90846 acetaldehyde dehyd
367 5 35.7 891 2 AG0265 acetaldehyde dehyd
368 5 35.7 892 2 AE0650 alcohol dehydrogen
369 5 35.7 894 2 D82127 alcohol dehydrogen
370 5 35.7 901 2 C89810 conserved hypothet
371 5 35.7 906 2 T47340 hypothetical prote
372 5 35.7 940 2 S49087 lactoferrin bindin
373 5 35.7 943 2 C81070 lactoferrin-bindin
374 5 35.7 944 2 C81798 lactoferrin bindin
375 5 35.7 950 2 T44422 oxoglutarate dehyd
376 5 35.7 966 2 T30017 hypothetical prote
377 5 35.7 970 2 S01352 type III site-spec
378 5 35.7 971 2 T03181 hypothetical prote
379 5 35.7 972 2 H84903 hypothetical prote
380 5 35.7 991 2 A99604 hypothetical prote
381 5 35.7 1007 2 F80156 glutamate receptor
382 5 35.7 1008 2 S28858 glutamate receptor
383 5 35.7 1008 2 T12532 hypothetical prote
384 5 35.7 1009 2 T16604 hypothetical prote
385 5 35.7 1017 2 T48452 hypothetical prote
386 5 35.7 1024 2 T05234 hypothetical prote
387 5 35.7 1029 2 F96602 hypothetical prote
388 5 35.7 1042 2 S43904 hyaluronidase - Cl
389 5 35.7 1051 2 A39712 kinase-like protei
390 5 35.7 1065 2 C89954 DNA polymerase III
391 5 35.7 1085 2 S66149 gene pipsqueak pro
392 5 35.7 1093 2 H84126 cation efflux syst
393 5 35.7 1111 2 T23047 hypothetical prote
394 5 35.7 1132 2 S37206 phytochrome - moss

F14L17.15 protein
plasma protein S p
plasma protein S p
envelope protein E
cadmium-transporti
DNA ligase - Therm
hypothetical prote
Ogv-B56 orf46 - Bo
VgrE protein [impo
occlusion-derived
probable protein A
Rbe element associ
polyribonucleotide
polyribonucleotide
protein kinase hom
probable outer mem
hypothetical prote
probable outer mem
hypothetical prote
microtubule-associ
probable fusidic a
hypothetical prote
IL-12 receptor bet
F4O10.2 protein -
hypothetical prote
TMDC II protein -
Na+/H+-exchanging
Na+/H+-exchanging
hypothetical prote
hypothetical prote
viral enhancing fa
F-cadherin - Afric
probable membrane
zinc finger protei
hypothetical prote
6-phosphofructo-2-
hypothetical prote
DNA repair protein
TonB-dependent rec
hypothetical prote
ABC transporter, A
acetaldehyde dehyd
hypothetical prote
acetaldehyde dehyd
alcohol dehydrogen
alcohol dehydrogen
alcohol dehydrogen
conserved hypothet
hypothetical prote
lactoferrin bindin
lactoferrin-bindin
lactoferrin bindin
oxoglutarate dehyd
hypothetical prote
type III site-spec
hypothetical prote
hypothetical prote
hypothetical prote
glutamate receptor
glutamate receptor
hypothetical prote
hypothetical prote
hypothetical prote
hyaluronidase - Cl
kinase-like protei
DNA polymerase III
gene pipsqueak pro
cation efflux syst
hypothetical prote
phytochrome - moss

395	5	35.7	1151	2	S03722	DNA-directed DNA p	468	4	28.6	2	C71343	hypothetical prote
396	5	35.7	1185	2	T19212	hypothetical prote	469	4	28.6	44	F82837	hypothetical prote
397	5	35.7	1186	2	C64588	cag pathogenicity	470	4	28.6	45	A35752	caltrin-like prote
398	5	35.7	1215	2	B48281	cytotoxin-associat	471	4	28.6	45	H83936	hypothetical prote
399	5	35.7	1249	2	AC1065	helicase related p	472	4	28.6	49	S72213	beta-fructofuranos
400	5	35.7	1261	2	T50065	hypothetical prote	473	4	28.6	50	I38970	fibroblast growth
401	5	35.7	1271	2	A45555	glutamate rich pro	474	4	28.6	50	G82540	hypothetical prote
402	5	35.7	1275	2	T38397	probable GTPase ac	475	4	28.6	51	C88470	protein C28H8.2 [i
403	5	35.7	1319	2	S49951	SNM4 protein - yea	476	4	28.6	53	A27537	rubredoxin - Chlor
404	5	35.7	1326	2	AC3372	kinesin-like prote	477	4	28.6	53	RUPF	rubredoxin - Pepto
405	5	35.7	1338	2	T18416	hypothetical prote	478	4	28.6	54	S36814	fibroblast growth
406	5	35.7	1351	2	S44665	ZK370.4 protein -	479	4	28.6	54	S23360	SNAP receptor - bo
407	5	35.7	1396	2	F81686	DNA-directed RNA p	480	4	28.6	55	G43256	hypothetical prote
408	5	35.7	1397	2	T51292	Dna2p - fission ye	481	4	28.6	55	T03370	gene m4 protein -
409	5	35.7	1398	2	T39568	hypothetical helic	482	4	28.6	56	T1BOA	pancreatic secreto
410	5	35.7	1405	1	DJZPA	DNA-directed DNA p	483	4	28.6	56	TIPG	pancreatic secreto
411	5	35.7	1417	2	A83080	hypothetical prote	484	4	28.6	56	T1SHA	pancreatic secreto
412	5	35.7	1424	2	T03851	thyroid hormone re	485	4	28.6	56	I37977	zinc finger protei
413	5	35.7	1429	2	T41699	C2-domain family p	486	4	28.6	56	H82667	hypothetical prote
414	5	35.7	1433	1	A36734	bacillopeptidase F	487	4	28.6	57	C84213	30S ribosomal prot
415	5	35.7	1447	2	S63669	unpGlucose-glycopr	488	4	28.6	57	S74693	hypothetical prote
416	5	35.7	1462	2	T42639	glucocorticoid rec	489	4	28.6	59	T01278	hypothetical prote
417	5	35.7	1505	2	UC4851	hypoxia-inducible	490	4	28.6	60	B86682	prophage pil prote
418	5	35.7	1509	2	T19486	hypothetical prote	491	4	28.6	60	C69169	hypothetical prote
419	5	35.7	1522	2	H88380	protein T22F7.3 [i	492	4	28.6	61	T1EEH	proteinase inhibit
420	5	35.7	1557	2	D41214	protein-tyrosine-p	493	4	28.6	61	A90343	carboxy-end of fer
421	5	35.7	1558	2	B71603	RBSA-H3 antigen pF	494	4	28.6	61	S57815	antimicrobial pept
422	5	35.7	1616	2	G64242	cytadherence-acces	495	4	28.6	62	AB1042	hypothetical prote
423	5	35.7	1630	2	C41214	protein-tyrosine-p	496	4	28.6	62	A36891	transfer complex p
424	5	35.7	1630	2	T40217	hypothetical prote	497	4	28.6	62	S30239	hypothetical prote
425	5	35.7	1733	1	RNB52L	DNA-directed RNA p	498	4	28.6	63	B69333	4-oxalocrotonate t
426	5	35.7	1829	2	T24583	hypothetical prote	499	4	28.6	63	D86673	hypothetical prote
427	5	35.7	1848	2	A44140	cellulose-binding	500	4	28.6	63	S57816	antimicrobial pept
428	5	35.7	1854	2	T13576	hypothetical prote	501	4	28.6	64	B86800	phage pi3 prote
429	5	35.7	1964	2	A59282	nonmuscle myosin I	502	4	28.6	65	I79540	dnak-type molecula
430	5	35.7	2023	2	T13154	polycomb protein e	503	4	28.6	67	D83719	mercuric transport
431	5	35.7	2044	2	AB1180	probable peptidogl	504	4	28.6	67	T17537	hypothetical prote
432	5	35.7	2062	2	G96602	probable receptor	505	4	28.6	67	A12190	hypothetical prote
433	5	35.7	2090	2	T30075	hypothetical prote	506	4	28.6	68	D82027	hypothetical prote
434	5	35.7	2153	2	T30074	hypothetical prote	507	4	28.6	70	T14969	hypothetical prote
435	5	35.7	2163	2	T51397	hypothetical prote	508	4	28.6	70	S25190	pilin precursor -
436	5	35.7	2185	1	GNNYB3	genome polyprotein	509	4	28.6	70	S07731	hypothetical prote
437	5	35.7	2252	2	S06188	genome polyprotein	510	4	28.6	70	AD1995	hypothetical prote
438	5	35.7	2364	2	A56577	microtubule-associ	511	4	28.6	71	T50483	glucose-repressibl
439	5	35.7	2396	2	T13714	kakapo gene protei	512	4	28.6	72	I37232	calcitonin gene-re
440	5	35.7	2478	2	AH2140	polyketide synthas	513	4	28.6	72	B35523	hypothetical prote
441	5	35.7	2523	2	F70846	probable PPG prote	514	4	28.6	72	T07370	ubiquinol-cytochro
442	5	35.7	2664	2	T28626	variant-specific s	515	4	28.6	72	D98143	hypothetical prote
443	5	35.7	2802	2	F97686	cyclic beta-(1-2)	516	4	28.6	73	S61830	subtilisin/chymotr
444	5	35.7	2831	2	A12911	beta (1->2) glucan	517	4	28.6	73	A12727	hypothetical prote
445	5	35.7	2833	2	A43360	inositol 1,4,5-tri	518	4	28.6	74	S33831	hypothetical prote
446	5	35.7	2895	2	H85362	hypothetical prote	519	4	28.6	75	AD3131	hypothetical prote
447	5	35.7	2946	2	T15840	hypothetical prote	520	4	28.6	75	AG1917	hypothetical prote
448	5	35.7	3014	1	UC5620	genome polyprotein	521	4	28.6	76	B64700	carbon storage reg
449	5	35.7	3135	2	A48584	transmission block	522	4	28.6	76	I52570	glycophorin - huma
450	5	35.7	3259	1	A56539	giantin - human	523	4	28.6	76	E71820	probable carbon st
451	5	35.7	4767	2	T31345	hypothetical prote	524	4	28.6	76	T48276	hypothetical prote
452	5	35.7	4868	2	B54161	ryanodine-binding	525	4	28.6	76	S43590	M04D8.3 protein (C
453	4	28.6	14	2	B28018	very late antigen-	526	4	28.6	77	C69359	snRNP homolog - Ar
454	4	28.6	21	2	PC7043	ubiquitin carboxyl	527	4	28.6	77	A75048	hypothetical prote
455	4	28.6	23	2	A33105	dihydrofolate redu	528	4	28.6	77	E82612	hypothetical prote
456	4	28.6	31	2	D95212	hypothetical prote	529	4	28.6	77	AF1091	E. coli yjdi prote
457	4	28.6	32	2	S32971	dodecandrin - endo	530	4	28.6	77	AB1958	hypothetical prote
458	4	28.6	32	2	C26393	calelectrin - marb	531	4	28.6	78	A47243	T-cell receptor be
459	4	28.6	34	2	A43564	neurogenic protein	532	4	28.6	78	F72807	gp63 protein - Myc
460	4	28.6	35	2	I52325	P2x purinoceptor s	533	4	28.6	78	S31008	gene 63 protein -
461	4	28.6	36	2	E84416	hypothetical prote	534	4	28.6	79	T1HUA	pancreatic secreto
462	4	28.6	37	2	JH0709	calcitonin gene-re	535	4	28.6	79	T1RT1	pancreatic secreto
463	4	28.6	37	2	S05037	insulinoma amyloid	536	4	28.6	79	T1RT2	pancreatic secreto
464	4	28.6	37	2	T11815	hypothetical prote	537	4	28.6	79	T17014	metallothionein-li
465	4	28.6	40	2	C82780	hypothetical prote	538	4	28.6	79	T06381	proteinase inhibit
466	4	28.6	41	2	D82458	hypothetical prote	539	4	28.6	79	AG1062	bacteriophage gene
467	4	28.6	42	2	T09597	probable LFY flora	540	4	28.6	79	D86945	hypothetical prote

541 4 28.6 79 2 S57905 hypothetical prote
542 4 28.6 79 2 T37512 hypothetical prote
543 4 28.6 79 2 G82863 conserved hypothet
544 4 28.6 79 2 B83671 hypothetical prote
545 4 28.6 80 1 S01498 pancreatic secreto
546 4 28.6 80 1 EGVZSF growth factor - ra
547 4 28.6 80 2 AG0150 probable stress re
548 4 28.6 81 1 S29820 acrosin/trypsin in
549 4 28.6 81 2 C86710 hypothetical prote
550 4 28.6 81 2 B82705 hypothetical prote
551 4 28.6 82 2 S77795 H+ transporting tw
552 4 28.6 82 2 S28655 hypothetical prote
553 4 28.6 82 2 T17685 hypothetical prote
554 4 28.6 82 2 AC2753 conserved hypothet
555 4 28.6 82 2 AC2804 hypothetical prote
556 4 28.6 82 2 C97583 hypothetical prote
557 4 28.6 83 1 G5BPSV gene 5 protein - s
558 4 28.6 83 2 JN0400 hypothetical 8.8K
559 4 28.6 83 2 C84274 hypothetical prote
560 4 28.6 83 2 T19790 hypothetical prote
561 4 28.6 83 2 AG2771 hypothetical prote
562 4 28.6 84 2 B82599 hypothetical prote
563 4 28.6 85 2 S60856 M protein precurs
564 4 28.6 85 2 D70488 cytochrome-c oxida
565 4 28.6 86 1 A34427 peptide PEC-60 pre
566 4 28.6 86 2 S39579 DNA-directed RNA p
567 4 28.6 86 2 H64246 ribosomal protein
568 4 28.6 87 2 T471286 probable ribosomal
569 4 28.6 87 2 T47413 hypothetical prote
570 4 28.6 88 2 A37262 Ig kappa chain V r
571 4 28.6 88 2 B90584 30S ribosomal prot
572 4 28.6 88 2 D37914 homeotic protein C
573 4 28.6 89 1 TCHUIA islet amyloid poly
574 4 28.6 89 2 S22344 islet amyloid poly
575 4 28.6 89 2 A33542 islet amyloid poly
576 4 28.6 89 2 S32551 thionin variant Th
577 4 28.6 89 2 S55648 hypothetical prote
578 4 28.6 89 2 T26222 hypothetical prote
579 4 28.6 89 2 JQ1822 Salfa protein - va
580 4 28.6 89 2 AF0312 probable exported
581 4 28.6 89 2 T03072 probable zinc fing
582 4 28.6 90 2 A81313 probable membrane
583 4 28.6 90 2 A86968 hypothetical prote
584 4 28.6 90 2 T17562 hypothetical prote
585 4 28.6 90 2 T42196 transposase tras -
586 4 28.6 90 2 S23259 iro protein - Thio
587 4 28.6 91 2 G72088 ferredoxin [2Fe-2S
588 4 28.6 91 2 B86536 ferredoxin IV [imp
589 4 28.6 91 2 E81715 ferredoxin [2Fe-2S
590 4 28.6 91 2 G71562 ferredoxin [2Fe-2S
591 4 28.6 91 2 A71654 ribosomal protein
592 4 28.6 91 2 AG1980 hypothetical prote
593 4 28.6 92 2 T48895 glyA protein [imp
594 4 28.6 92 2 S13116 islet amyloid prot
595 4 28.6 92 2 T5688 seminal vesicle pr
596 4 28.6 92 2 T16884 hypothetical prote
597 4 28.6 93 1 C33542 islet amyloid poly
598 4 28.6 93 1 TCR7IA islet amyloid poly
599 4 28.6 93 2 T47252 conidiation protei
600 4 28.6 94 1 C21895 ribosomal protein
601 4 28.6 94 1 RBP222 abci protein - pha
602 4 28.6 94 2 D89947 50S ribosomal prot
603 4 28.6 94 2 S62084 M-like protein enn
604 4 28.6 95 1 BORT3 prostatic steroid-
605 4 28.6 95 2 B82793 hypothetical prote
606 4 28.6 95 2 B37857 hypothetical prote
607 4 28.6 96 2 T11096 NADH2 dehydrogenas
608 4 28.6 96 2 S42410 protein translocat
609 4 28.6 96 2 S42409 protein translocat
610 4 28.6 96 2 E69790 hypothetical prote
611 4 28.6 96 2 T08761 hypothetical prote
612 4 28.6 97 2 S60846 M protein precurs
613 4 28.6 97 2 D64344 hypothetical prote

614 4 28.6 98 2 I50101
615 4 28.6 98 2 C84323
616 4 28.6 98 2 E81205 hypothetical prote
617 4 28.6 99 2 A42196 preprotein translo
618 4 28.6 99 2 AE1422 PTS, cellobiose-sp
619 4 28.6 99 2 G70931 probable PE protei
620 4 28.6 99 2 B90329 conserved hypothet
621 4 28.6 99 2 S22957 hypothetical prote
622 4 28.6 99 2 T02626 hypothetical prote
623 4 28.6 99 2 AD1454 hypothetical prote
624 4 28.6 99 2 AE1090 hypothetical prote
625 4 28.6 99 2 AC3260 hypothetical prote
626 4 28.6 100 2 F71725 glutamyl-tRNA amid
627 4 28.6 100 2 T40494 probable guanine n
628 4 28.6 100 2 G98295 hypothetical prote
629 4 28.6 101 2 T28661 hypothetical prote
630 4 28.6 101 2 AF0223 hypothetical prote
631 4 28.6 102 2 A23620 ribonuclease T1 (E
632 4 28.6 102 2 G69007 ribosomal protein
633 4 28.6 102 2 T17738 hypothetical prote
634 4 28.6 102 2 S09892 hypothetical prote
635 4 28.6 102 2 F82517 conserved hypothet
636 4 28.6 102 2 A97534 hypothetical prote
637 4 28.6 102 2 A82829 colicin V precurs
638 4 28.6 102 2 F81377 flagellar motor sw
639 4 28.6 103 1 W1BP22 gene 17 protein -
640 4 28.6 103 2 T34790 hypothetical prote
641 4 28.6 104 1 NRNCT1 ribonuclease T1 (E
642 4 28.6 104 2 S55728 chitin synthase T1
643 4 28.6 104 2 B72491 hypothetical prote
644 4 28.6 104 2 A75016 hypothetical prote
645 4 28.6 104 2 T39020 hypothetical prote
646 4 28.6 104 2 AD0289 probable lipoprote
647 4 28.6 105 2 H81136 hypothetical prote
648 4 28.6 105 2 A71249 hypothetical prote
649 4 28.6 105 2 C72631 hypothetical prote
650 4 28.6 106 1 R6D0P2 acidic ribosomal p
651 4 28.6 106 2 JC7175 Arpase inhibitor p
652 4 28.6 106 2 C69436 LSU ribosomal prot
653 4 28.6 106 2 AF1181 E. coli SugE prote
654 4 28.6 106 2 AG1538 E. coli SugE prote
655 4 28.6 106 2 AC0177 hypothetical prote
656 4 28.6 106 2 AI2219 hypothetical prote
657 4 28.6 106 2 G95152 v-type sodium ATP
658 4 28.6 107 2 S38713 Ig kappa chain V r
659 4 28.6 107 2 S33132 Ig kappa chain V r
660 4 28.6 107 2 AI1242 B. subtilis comG o
661 4 28.6 108 2 E72426 transposase - Ther
662 4 28.6 108 2 T14951 hypothetical prote
663 4 28.6 108 2 T33901 hypothetical prote
664 4 28.6 108 2 G72624 hypothetical prote
665 4 28.6 108 2 T49731 hypothetical prote
666 4 28.6 108 2 S43582 insulin homolog 2
667 4 28.6 108 2 AD0715 conserved hypothet
668 4 28.6 108 2 AF1043 hypothetical prote
669 4 28.6 108 2 AG0853 hypothetical prote
670 4 28.6 109 1 A44275 nonstructural prot
671 4 28.6 109 1 MNIBH2 nonstructural prot
672 4 28.6 109 2 S58182 nonstructural prot
673 4 28.6 109 2 S29387 nif0 protein - Azo
674 4 28.6 109 2 S64313 probable membrane
675 4 28.6 109 2 F81953 hypothetical prote
676 4 28.6 109 2 D81012 hypothetical prote
677 4 28.6 109 2 A86104 probable regulator
678 4 28.6 110 1 B6SSP2 acidic ribosomal p
679 4 28.6 110 2 B72496 hypothetical prote
680 4 28.6 110 2 S50991 hypothetical prote
681 4 28.6 110 2 G81192 hypothetical prote
682 4 28.6 110 2 E82781 hypothetical prote
683 4 28.6 111 1 QQSABE hypothetical prote
684 4 28.6 111 2 JX0085 pancreatic ribonuc
685 4 28.6 111 2 D37286 Ig kappa chain V r
686 4 28.6 111 2 A53221 acidic ribosomal p

neuromedin B recep
30S ribosomal prot
hypothetical prote
preprotein translo
PTS, cellobiose-sp
probable PE protei
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
glutamyl-tRNA amid
probable guanine n
hypothetical prote
hypothetical prote
hypothetical prote
ribonuclease T1 (E
ribosomal protein
hypothetical prote
hypothetical prote
conserved hypothet
hypothetical prote
colicin V precurs
flagellar motor sw
gene 17 protein -
hypothetical prote
ribonuclease T1 (E
chitin synthase T1
hypothetical prote
hypothetical prote
probable lipoprote
hypothetical prote
hypothetical prote
acidic ribosomal p
Arpase inhibitor p
LSU ribosomal prot
E. coli SugE prote
E. coli SugE prote
hypothetical prote
hypothetical prote
v-type sodium ATP
Ig kappa chain V r
Ig kappa chain V r
B. subtilis comG o
transposase - Ther
hypothetical prote
hypothetical prote
hypothetical prote
nonstructural prot
nonstructural prot
nonstructural prot
nif0 protein - Azo
probable membrane
hypothetical prote
hypothetical prote
probable regulator
acidic ribosomal p
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
pancreatic ribonuc
Ig kappa chain V r
acidic ribosomal p

687 4 28.6 111 2 S11128 genome polypeptide
688 4 28.6 111 2 A30918 hypothetetical prote
689 4 28.6 111 2 A64917 probable membrane
690 4 28.6 111 2 F85766 hypothetetical prote
691 4 28.6 111 2 C72514 hypothetetical prote
692 4 28.6 111 2 S19475 hypothetetical prote
693 4 28.6 111 2 C95414 hypothetetical prote
694 4 28.6 112 1 L1HUMM Ig lambda chain V-
695 4 28.6 112 2 T44986 probable sulfate/t
696 4 28.6 112 2 A69451 conserved hypoteth
697 4 28.6 112 2 A69451 omega-agatoxin IA
698 4 28.6 112 2 A45069 hypothetetical prote
699 4 28.6 112 2 F49338 conserved hypoteth
700 4 28.6 113 2 AD1039 conserved hypoteth
701 4 28.6 113 2 D84389 hypothetetical prote
702 4 28.6 114 2 G91112 hypothetetical prote
703 4 28.6 114 2 T41969 hypothetetical prote
704 4 28.6 114 2 S11952 hypothetetical prote
705 4 28.6 115 1 PTHU parathyroid hormon
706 4 28.6 115 1 PTHG parathyroid hormon
707 4 28.6 115 1 PTHG parathyroid hormon
708 4 28.6 115 2 J42402 parathyroid hormon
709 4 28.6 115 2 A29156 seminal fluid prot
710 4 28.6 115 2 T44712 acyl carrier prote
711 4 28.6 115 2 A33376 arsenate reductase
712 4 28.6 115 2 T40456 very hypothetetical
713 4 28.6 116 2 S41118 lipid transfer pro
714 4 28.6 116 2 H86042 hypothetetical prote
715 4 28.6 116 2 G91195 hypothetetical prote
716 4 28.6 116 2 E72786 hypothetetical prote
717 4 28.6 116 2 H97213 reductase/isomeras
718 4 28.6 117 2 B84604 probable glycine-r
719 4 28.6 117 2 A72310 hypothetetical prote
720 4 28.6 117 2 S73025 hypothetetical prote
721 4 28.6 117 2 T13210 minor capsid prote
722 4 28.6 117 2 T47990 hypothetetical prote
723 4 28.6 117 2 A95381 hypothetetical prote
724 4 28.6 117 2 AC3421 hypothetetical expor
725 4 28.6 118 2 C96746 thionin, 63255-627
726 4 28.6 118 2 S25249 thionin variant Th
727 4 28.6 118 2 I33932 Ig kappa chain pre
728 4 28.6 118 2 A17139 PPS system, cellob
729 4 28.6 118 2 S55185 hypothetetical prote
730 4 28.6 118 2 T15655 hypothetetical prote
731 4 28.6 118 2 C81005 hypothetetical prote
732 4 28.6 118 2 B82026 hypothetetical prote
733 4 28.6 118 2 A81007 purine nucleoside
734 4 28.6 118 2 C82887 hypothetetical prote
735 4 28.6 118 2 B1207 early chorion prot
736 4 28.6 119 2 B45937 chorion protein -
737 4 28.6 119 2 S24292 chorion protein -
738 4 28.6 119 2 S24294 chorion protein -
739 4 28.6 119 2 S24294 hypothetetical prote
740 4 28.6 119 2 F49804 hypothetetical prote
741 4 28.6 119 2 B72633 hypothetetical prote
742 4 28.6 119 2 G86755 prophage p12 prote
743 4 28.6 119 2 E83106 hypothetetical prote
744 4 28.6 119 2 T03071 transposase tras-
745 4 28.6 120 2 A50844 protein-Npi-phosph
746 4 28.6 120 2 H75483 aspartate 1-decarb
747 4 28.6 120 2 J01740 hypothetetical 12.7K
748 4 28.6 120 2 I40821 regA protein - Clo
749 4 28.6 120 2 T03071 hypothetical prote
750 4 28.6 120 2 A11446 Protein gp9 (Bacte
751 4 28.6 120 2 F71005 hypothetical prote
752 4 28.6 121 1 LAKGAW alpha-lactalbumin
753 4 28.6 121 2 T51726 phosphotransferase
754 4 28.6 121 2 S24293 chorion class CA p
755 4 28.6 121 2 C75127 hypothetical prote
756 4 28.6 121 2 S27145 gene 30.7 protein
757 4 28.6 121 2 A39407 succinate dehydrog
758 4 28.6 121 2 A17130 hypothetical prote

760 4 28.6 121 2 AG2065 hypothetical prote
761 4 28.6 122 2 E71834 ribosomal protein
762 4 28.6 122 2 E64683 ribosomal protein
763 4 28.6 122 2 S29540 seminal vesicle se
764 4 28.6 122 2 T42844 endonuclease homol
765 4 28.6 122 2 S72337 hypothetetical prote
766 4 28.6 122 2 T44906 hypothetetical prote
767 4 28.6 122 2 B82271 hypothetetical prote
768 4 28.6 122 2 E82519 hypothetical prote
769 4 28.6 122 2 A05304 hemoglobin beta-1
770 4 28.6 122 2 A11214 hypothetical prote
771 4 28.6 122 2 A12992 conserved hypoteth
772 4 28.6 123 1 WQEC3S phosphotransferase
773 4 28.6 123 2 G85918 hypothetical prote
774 4 28.6 123 2 H91073 hypothetical prote
775 4 28.6 123 2 E90066 aspartate 1-decarb
776 4 28.6 123 2 S49906 HAE (highly acidic
777 4 28.6 123 2 S49907 HAE (highly acidic
778 4 28.6 123 2 S29714 guanine-nucleotide
779 4 28.6 123 2 S29714 guanine-nucleotide
780 4 28.6 123 2 A97333 fMN-binding protei
781 4 28.6 123 2 T38821 hypothetical prote
782 4 28.6 123 2 T33456 hypothetical prote
783 4 28.6 123 2 F45891 hypothetical prote
784 4 28.6 124 2 H97720 hypothetical prote
785 4 28.6 124 2 C72206 conserved hypoteth
786 4 28.6 124 2 D81810 hypothetical prote
787 4 28.6 124 2 S33081 G4L protein - vari
788 4 28.6 124 2 H72158 I4L protein - vari
789 4 28.6 124 2 T28504 hypothetical prote
790 4 28.6 124 2 T09126 protein CP12 precu
791 4 28.6 124 2 T48833 hypothetical prote
792 4 28.6 124 2 A95136 conserved hypoteth
793 4 28.6 124 2 AG2789 hypothetical prote
794 4 28.6 124 2 S71888 S phase inhibitor
795 4 28.6 124 2 A11754 bacteriophage prot
796 4 28.6 125 1 TCCHRP calcitonin gene-re
797 4 28.6 125 1 F1SP4 photosystem I chai
798 4 28.6 125 2 T02490 hypothetical prote
799 4 28.6 125 2 T51037 hypothetical prote
800 4 28.6 125 2 T34595 hypothetical prote
801 4 28.6 125 2 AB1595 hypothetical prote
802 4 28.6 125 2 A97202 desulfoferrodoxin
803 4 28.6 125 2 A69354 rubredoxin-NAD+ re
804 4 28.6 125 2 S68837 rubredoxin-NAD+ re
805 4 28.6 125 2 A53627 fibroblast growth
806 4 28.6 126 1 RDDVBX rubredoxin-NAD+ re
807 4 28.6 126 2 I46489 cysteine-rich hair
808 4 28.6 126 2 T34033 hypothetical prote
809 4 28.6 126 2 C72650 hypothetical prote
810 4 28.6 126 2 F91065 hypothetical prote
811 4 28.6 126 2 F90906 hypothetical prote
812 4 28.6 126 2 B90836 hypothetical prote
813 4 28.6 126 2 D90856 hypothetical prote
814 4 28.6 126 2 F90766 conserved hypoteth
815 4 28.6 126 2 G90350 conserved hypoteth
816 4 28.6 126 2 AH1334 hypothetical prote
817 4 28.6 126 2 AC1833 hypothetical prote
818 4 28.6 127 1 VCBP77 coat protein - pha
819 4 28.6 127 2 G84999 iron-sulfur cofact
820 4 28.6 127 2 H82285 calcitonin gene-re
821 4 28.6 127 2 A25864 crCB protein (impo
822 4 28.6 127 2 H87494 hypothetical prote
823 4 28.6 127 2 S76684 killer toxin KP4 p
824 4 28.6 127 2 S40034 hypothetical prote
825 4 28.6 127 2 E90038 calcitonin gene-re
826 4 28.6 128 1 TCCHUR calcitonin gene-re
827 4 28.6 128 1 TCCHUR Nifu-like protein
828 4 28.6 128 2 AG0824 Nifu family protei
829 4 28.6 128 2 AG0352 lysozyme (EC 3.2.1
830 4 28.6 128 2 S10046 calcitonin gene-re
831 4 28.6 128 2 B44173 repressor (penicil
832 4 28.6 128 2 AE1106

833	4	28.6	128	2	S33949	early E3B 14.7K pr	906	4	28.6	135	2	S52555	thionin variant Th
834	4	28.6	128	2	S46976	coat protein - pha	907	4	28.6	135	2	S52552	thionin variant Th
835	4	28.6	128	2	AH1816	hypothetical prote	908	4	28.6	135	2	JQ0472	T-cell receptor be
836	4	28.6	128	2	C48552	hypothetical prote	909	4	28.6	135	2	C64453	translation initia
837	4	28.6	128	2	T29978	hypothetical prote	910	4	28.6	135	2	S67160	hypothetical prote
838	4	28.6	128	2	T32502	hypothetical prote	911	4	28.6	135	2	C72315	hypothetical prote
839	4	28.6	128	2	S31009	gene 64 protein -	912	4	28.6	135	2	F72494	hypothetical prote
840	4	28.6	128	2	A1276	probable desulfof	913	4	28.6	135	2	S55647	hypothetical prote
841	4	28.6	128	2	T25200	hypothetical prote	914	4	28.6	135	2	C98128	hypothetical prote
842	4	28.6	129	2	C70022	3-oxoacyl- acyl-ca	915	4	28.6	135	2	AC3159	hypothetical prote
843	4	28.6	129	2	T08993	urease (EC 3.5.1.5	916	4	28.6	135	2	AF0734	probable bacteriop
844	4	28.6	129	2	T10175	acyl carrier prote	917	4	28.6	135	2	AF0734	probable bacteriop
845	4	28.6	129	2	A37798	mor protein - Esch	918	4	28.6	135	2	D82468	hypothetical prote
846	4	28.6	129	2	J72205	transposase - ther	919	4	28.6	135	2	S76237	hypothetical prote
847	4	28.6	129	2	JU0394	allergen Der f II	920	4	28.6	135	2	S67924	spore-wall fungal
848	4	28.6	129	2	A61501	allergen Der f II	921	4	28.6	135	2	T21733	hypothetical prote
849	4	28.6	129	2	T17710	hypothetical prote	922	4	28.6	136	1	KVMS21	thionin variant Th
850	4	28.6	129	2	T21290	hypothetical prote	923	4	28.6	136	2	S52545	thymic shared anti
851	4	28.6	129	2	A81933	hypothetical prote	924	4	28.6	136	2	T49013	hypothetical prote
852	4	28.6	129	2	E72777	hypothetical prote	925	4	28.6	136	2	H84485	hypothetical prote
853	4	28.6	130	2	H70010	polyribonucleotide	926	4	28.6	136	2	S46102	hypothetical prote
854	4	28.6	130	2	B34302	hypothetical prote	927	4	28.6	136	2	H70838	hypothetical prote
855	4	28.6	130	2	G70799	hypothetical prote	928	4	28.6	136	2	G95224	hypothetical prote
856	4	28.6	130	2	AH2876	conserved hypotet	929	4	28.6	136	2	B99089	hypothetical prote
857	4	28.6	130	2	B37653	hypothetical prote	930	4	28.6	136	2	T53300	interleukin-1-beta
858	4	28.6	131	2	H82909	DNA-binding protei	931	4	28.6	136	2	F87461	hypothetical prote
859	4	28.6	131	2	A97791	nifu protein [limp	932	4	28.6	137	1	S38484	urease (EC 3.5.1.5
860	4	28.6	131	2	H71651	iron-sulfur cofact	933	4	28.6	137	2	S22515	thionin precursor,
861	4	28.6	131	2	S14390	tap2 protein - gar	934	4	28.6	137	2	B27586	hypothetical prote
862	4	28.6	131	2	C75117	hypothetical prote	935	4	28.6	137	2	D75148	hypothetical prote
863	4	28.6	131	2	T32405	hypothetical prote	936	4	28.6	137	2	T38500	hypothetical prote
864	4	28.6	131	2	T29455	hypothetical prote	937	4	28.6	137	2	D83882	hypothetical prote
865	4	28.6	131	2	B82451	hypothetical prote	938	4	28.6	137	2	AF3056	conserved hypotet
866	4	28.6	131	2	B83787	hypothetical prote	939	4	28.6	137	2	H98229	hypothetical prote
867	4	28.6	131	2	AH0348	probable membrane	940	4	28.6	137	2	H84345	inosine-5'-monopho
868	4	28.6	131	2	AG1361	protein gp8 (Bacte	941	4	28.6	137	2	H71348	conserved hypotet
869	4	28.6	131	2	AH1446	protein gp8 (Bacte	942	4	28.6	137	2	D72776	hypothetical prote
870	4	28.6	131	2	T28863	hypothetical prote	943	4	28.6	137	2	AB3085	conserved hypotet
871	4	28.6	131	2	E84540	hypothetical prote	944	4	28.6	137	2	G98201	hypothetical prote
872	4	28.6	131	2	H83156	hypothetical prote	945	4	28.6	138	1	C64005	hypothetical prote
873	4	28.6	131	2	S54573	hypothetical prote	946	4	28.6	138	2	D90164	hypothetical prote
874	4	28.6	132	1	MTONLK	melanin-concentrat	947	4	28.6	138	2	JC5742	membrane-bound pro
875	4	28.6	132	2	S34653	melanin-concentrat	948	4	28.6	138	2	G82915	ribosomal protein
876	4	28.6	132	2	B32910	melanin-concentrat	949	4	28.6	138	2	I51285	xCRABP - African c
877	4	28.6	132	2	F82916	ribosomal protein	950	4	28.6	138	2	S24081	envelope protein -
878	4	28.6	132	2	E90583	30S ribosomal prot	951	4	28.6	138	2	S24080	envelope protein -
879	4	28.6	132	2	S17928	acyl carrier prote	952	4	28.6	138	2	A87126	NrdI-family protei
880	4	28.6	132	2	T44951	flagella-related p	953	4	28.6	138	2	B61241	allergen Der f II
881	4	28.6	132	2	A0244	probable rhodanese	954	4	28.6	138	2	A61241	allergen Der f II
882	4	28.6	133	2	S52547	thionin variant Th	955	4	28.6	138	2	D83824	transcription regu
883	4	28.6	133	2	S52554	thionin variant Th	956	4	28.6	138	2	JC4597	signal transductio
884	4	28.6	133	2	C48776	polyprotein (E2/NS	957	4	28.6	138	2	T40987	hypothetical prote
885	4	28.6	133	2	E48776	polyprotein (E2/NS	958	4	28.6	138	2	A11156	hypothetical prote
886	4	28.6	133	2	G75061	hypothetical prote	959	4	28.6	138	2	A84482	hypothetical prote
887	4	28.6	133	2	S10038	hypothetical prote	960	4	28.6	138	2	S18587	hypothetical prote
888	4	28.6	133	2	E90792	hypothetical prote	961	4	28.6	139	1	S03579	probable transcrip
889	4	28.6	133	2	A38197	hypothetical prote	962	4	28.6	139	1	B70955	aspartate 1-decarb
890	4	28.6	133	2	C85824	unknown protein en	963	4	28.6	139	2	E97426	flagellar basal-bo
891	4	28.6	133	2	H30669	hypothetical prote	964	4	28.6	139	2	A52644	flagellar basal-bo
892	4	28.6	133	2	E90977	hypothetical prote	965	4	28.6	139	2	F84415	hypothetical prote
893	4	28.6	133	2	B90260	conserved hypotet	966	4	28.6	139	2	A12536	hypothetical prote
894	4	28.6	133	2	T17609	hypothetical prote	967	4	28.6	140	2	A60394	alpha-lactalbumin
895	4	28.6	133	2	A12987	hypothetical prote	968	4	28.6	140	2	T10059	cycokinin-induced
896	4	28.6	134	2	A44173	calcitonin gene-re	969	4	28.6	140	2	B81431	hypothetical prote
897	4	28.6	134	2	F96685	probable thionin F	970	4	28.6	140	2	F75335	probable transpos
898	4	28.6	134	2	S2546	thionin variant Th	971	4	28.6	140	2	S35275	probable flagellar
899	4	28.6	134	2	S2553	thionin variant Th	972	4	28.6	140	2	A11360	protein gp14 (Bact
900	4	28.6	134	2	A43589	mtp40 protein - My	973	4	28.6	140	2	AF1447	protein gp14 (Bact
901	4	28.6	134	2	B83762	hypothetical prote	974	4	28.6	140	2	A13155	hypothetical prote
902	4	28.6	134	2	H69544	conserved hypotet	975	4	28.6	140	2	H98131	probable transcrip
903	4	28.6	134	2	T20928	hypothetical prote	976	4	28.6	140	2	T29914	hypothetical prote
904	4	28.6	134	2	D71188	hypothetical prote	977	4	28.6	140	2	AG3645	flagellar basal-bo
905	4	28.6	135	2	A56855	islet amyloid poly	978	4	28.6	141	1	HASNv	hemoglobin alpha c

979 28.6 141 1 HZFG
 980 28.6 141 2 C86845
 981 28.6 141 2 S78354
 982 28.6 141 2 B70816
 983 28.6 141 2 D91263
 984 28.6 141 2 T39554
 985 28.6 141 2 E97811
 986 28.6 141 2 S15788
 987 28.6 141 2 PC1294
 988 28.6 141 2 F95986
 989 28.6 141 2 AF0368
 990 28.6 142 2 S71361
 991 28.6 142 2 C48175
 992 28.6 142 2 G86937
 993 28.6 142 2 D71663
 994 28.6 142 2 C39610
 995 28.6 142 2 AII521
 996 28.6 142 2 JC7636
 997 28.6 142 2 T34136
 998 28.6 142 2 E84069
 999 28.6 142 2 D96983
 1000 28.6 143 1 F64466

hemoglobin zeta ch
 H+-transporting tw
 ribosomal protein
 probable molybdopt
 probable phn opero
 very hypothetical
 hypothetical prote
 intermediate early
 trophozoite surfac
 conserved hypothet
 probable acetyltra
 actin-binding prot
 hypothetical plasm
 probable aspartate
 hypothetical prote
 BEF1 protein - yea
 hypothetical prote
 cystatin 1 - wheat
 hypothetical prote
 CBS domains [impor
 phosphopeptose iso

ALIGNMENTS

RESULT 1
 E89051
 hypothetical protein YPL133c - Yeast (Saccharomyces cerevisiae)
 C:Species: Saccharomyces cerevisiae
 C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 16-Aug-2004
 C:Accession: S69051; S12795
 R:Hall, J.; DePaulo, T.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.;
 submitted to the EMBL Data Library, December 1995
 A:Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.
 A:Reference number: S69040
 A:Accession: S69051
 A:Molecule type: DNA
 A:Residues: 1-446 <HAL>
 A:Cross-references: UNIPROT:P19541; EMBL:U43703; NID:gl244769; PIDN:AAB68226.1; PID:gl24
 R:Rizgolooff, A.; Capitanio, N.; Nobrega, M.P.; Gattli, D.
 EMBL J. 9, 2759-2764, 1990
 A:Title: Cytochrome oxidase assembly in yeast requires the product of COX11, a homolog o
 A:Reference number: S12795; MUID:90360986; PMID:2167832
 A:Accession: S12795
 A:Molecule type: DNA
 A:Residues: 1-95 <TZA>
 A:Cross-references: EMBL:X55731; NID:G3565; PIDN:CAA39262.1; PID:G3566
 A:Note: the authors translated the codon GAT for residue 84 as Gln
 C:Genetics:
 A:Cross-references: SGD:S0006054
 A:Map position: 16L
 A:Note: YPL133c
 C:Superfamily: GAL4 zinc binuclear cluster homology
 F:12-50/Domain: GAL4 zinc binuclear cluster homology <GAL4>

Query Match 50.0%; Score 7; DB 2; Length 446;
 Best Local Similarity 100.0%; Pred. No. 2.9; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 VSENVGS 10
 Db 125 VSENVGS 131
 |||||

RESULT 2
 D81826
 exodeoxyribonuclease V (EC 3.1.11.15) NMA1974 [imported] - Neisseria meningitidis (strain
 C:Species: Neisseria meningitidis
 C>Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
 C:Accession: D81826
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
 Nature 404, 502-506, 2000
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
 A:Reference number: A81775; MUID:20222556; PMID:10761919
 A:Accession: D81826
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1069 <PAR>
 A:Cross-references: UNIPROT:Q9JT46; GB:AL162757; GB:AL157959; NID:g7380371; PIDN:CAB8519
 A:Experimental source: serogroup A, strain Z2491
 C:Genetics:
 A:Gene: recC; NMA1974
 C:Superfamily: exodeoxyribonuclease V 125K chain
 C:Keywords: hydrolase

Query Match 50.0%; Score 7; DB 2; Length 1069;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SENVGSV 11
 Db 317 SENVGSV 323
 |||||

RESULT 3
 E84193
 chromosome segregation [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
 C:Accession: E84193
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
 Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablo
 Jung, K.H.; Alam, M.; Freitas, T.
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li;
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: A84160; MUID:20504483; PMID:11016950
 A:Accession: E84193
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1190 <STO>
 A:Cross-references: UNIPROT:Q9HS95; GB:AE004437; NID:gl0579965; PIDN:AAG18913.1; GSPDB:G
 C:Genetics:
 A:Gene: smc1

Query Match 50.0%; Score 7; DB 2; Length 1190;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 5 SENVGSV 11
 Db 106 SENVGSV 112
 |||||

RESULT 4
 C86086
 hypothetical protein frwC 2 [imported] - Escherichia coli (strain O157:H7, substrain EDL
 C:Species: Escherichia coli
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
 C:Accession: C86086
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimailanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: C86086
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-106 <STO>
 A:Cross-references: UNIPROT:Q8X3P5; GB:AE005174; NID:gl2518668; PIDN:AAG59151.1; GSPDB:G
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: frwC_2

```

Query Match      42.9%; Score 6; DB 2; Length 106;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 VGSVCG 13
      |||||
Db      28 VGSVCG 33

RESULT 5
G82929
ATP synthase C chain UUI36 [imported] - Ureaplasma urealyticum
C;Species: Ureaplasma urealyticum
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: G82929
R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
A;Reference number: A82870
A;Accession: G82929
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-109 <GLA>
A;Cross-references: GB:AF002114; GB:AF222894; NID:96899086; PIDN:AAF30542.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
C;Genetics:
A;Gene: atpB; UUI36
A;Genetic code: SGC3

Query Match      42.9%; Score 6; DB 2; Length 109;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 SENVGS 10
      |||||
Db      24 SENVGS 29

RESULT 6
AE1214
hypothetical protein lmo117 [imported] - Listeria monocytogenes (strain EGD-e)
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AE1214
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Feihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative Genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AE1214
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-118 <GLA>
A;Cross-references: UNIPROT:Q8Y802; GB:NC_003210; PIDN:CAC99195.1; PID:g16410519; GSPDB:
C;Genetics:
A;Experimental source: strain EGD-e
A;Gene: lmo117

Query Match      42.9%; Score 6; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 NVSENV 8
      |||||
Db      58 NVSENV 63

RESULT 7
D83998
acetyl-CoA carboxylase biotin carboxyl carrier subunit accB [imported] - Bacillus halodu
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: D83998
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: D83998
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-169 <STO>
A;Cross-references: UNIPROT:Q9K962; GB:AF001516; GB:BA000004; NID:g10175192; PIDN:BA8065
A;Experimental source: strain C-125
C;Genetics:
A;Gene: accB
C;Superfamily: biotin carboxyl carrier protein; lipoyl/biotin-binding homology

Query Match      42.9%; Score 6; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DNVSSE 7
      |||||
Db      117 DNVSSE 122

RESULT 8
D87236
conserved membrane protein ML2614 [imported] - Mycobacterium leprae
C;Species: Mycobacterium leprae
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87236
R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
eam, M.A.; Rutherford, K.M.
Nature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
A;Title: Massive gene decay in the leprosy bacillus.
A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: D87236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: UNIPROT:O06076; GB:AL450380; NID:g13093840; PIDN:CAC32146.1; GSPDB:G
C;Genetics:
A;Gene: ML2614

Query Match      42.9%; Score 6; DB 2; Length 224;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 VSENVG 9
      |||||
Db      189 VSENVG 194

RESULT 9
T20304
hypothetical protein D1054.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20304
R;Matthews, P.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19255
A;Accession: T20304
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-231 <WIL>
A;Cross-references: UNIPROT:Q27488; EMBL:Z74030; PIDN:CAA98441.1; GSPDB:GN00023; CESP:DI
A;Experimental source: clone D1054
C;Genetics:

```

A;Gene: CESP:D1054.2
 A;Map position: 5
 A;Introns: 13/2; 39/1; 121/2
 C;Superfamily: multicatalytic endopeptidase complex chain C9

Query Match 42.9%; Score 6; DB 2; Length 231;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ENVGSV 11
 |||||
 Db 48 ENVGSV 53

RESULT 10

AF1367
 16S pseudouridylylate synthase homolog lmo2342 [imported] - Listeria monocytogenes (strain
 C;Species: Listeria monocytogenes
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AF1367

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
 D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karet, U.
 Science 294, 849-852, 2001
 A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A;Title: Comparative genomics of Listeria species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1367
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-233 <GLA>

A;Cross-references: UNIPROT:Q8V4U0; GB:NC_003210; PIDN:CAD00420.1; PID:G16411830; GSPDB:
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Superfamily: conserved hypothetical protein HI1243

Query Match 42.9%; Score 6; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSE 6
 |||||
 Db 76 EDNVSE 81

RESULT 11

WZBE24
 gene 24 protein - human herpesvirus 3
 C;Species: human herpesvirus 3, varicella-zoster virus
 C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 09-Jul-2004
 C;Accession: F27343

R;Davison, A.J.; Scott, J.E.
 J. Gen. Virol. 67, 1759-1816, 1986
 A;Title: The complete DNA sequence of varicella-zoster virus.
 A;Reference number: A27345; MUID:86306657; PMID:3018124

A;Accession: F27343
 A;Molecule type: DNA
 A;Residues: 1-269 <DAV>

A;Cross-references: UNIPROT:P09280; EMBL:X04370; NID:G59989; PIDN:CAA27907.1; PID:G60013
 C;Genetics:
 A;Gene: 24
 C;Superfamily: varicella-zoster virus gene 24 protein

Query Match 42.9%; Score 6; DB 1; Length 269;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSE 6
 |||||
 Db 57 EDNVSE 62

RESULT 12

D82491
 hypothetical protein VCA0181 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C;Species: Vibrio cholerae
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C;Accession: D82491
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82491
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-291 <HEI>
 A;Cross-references: UNIPROT:Q9RMV5; GB:AE004358; GB:AE003853; NID:G9657566; PIDN:AAF9609
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VCA0181
 A;Map position: 2

Query Match 42.9%; Score 6; DB 2; Length 291;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
 |||||
 Db 120 VGSVCG 125

RESULT 13

B75555
 Probable lipase/esterase - Deinococcus radiodurans (strain R1)
 C;Species: Deinococcus radiodurans
 C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C;Accession: B75555
 R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: B75555
 A;Status: preliminary
 A;Molecule type: DNA

A;Residues: 1-296 <WHI>
 A;Cross-references: UNIPROT:Q9RY19; GB:AE001876; GB:AE000513; NID:G6457800; PIDN:AAF0972;
 A;Experimental source: strain R1
 C;Genetics:

A;Gene: DR0133
 A;Map position: 1
 C;Superfamily: probable lipolytic protein ybaC

Query Match 42.9%; Score 6; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13
 |||||
 Db 173 VGSVCG 178

RESULT 14

S51548
 killer toxin K28 - Saccharomyces cerevisiae killer particle M28
 C;Species: Saccharomyces cerevisiae killer particle M28
 C;Date: 15-Jul-1995 #sequence_revision 19-Jul-1996 #text_change 09-Jul-2004

C;Accession: S51548
 R;Schmitt, M.J.

Mol. Gen. Genet. 246, 236-246, 1995
 A;Title: Cloning and expression of a cDNA copy of the viral K(28) killer toxin gene in y;

A;Reference number: S51548; MUID:95166181; PMID:7862095

A;Accession: S51548

A;Molecule type: mRNA

A;Residues: 1-345 <SCH>

A;Cross-references: UNIPROT:Q7LZU3

C;Superfamily: Saccharomyces cerevisiae killer particle M28 killer toxin K28

Query Match 42.9%; Score 6; DB 2; Length 345;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SENVGS 10

|||||

Db 268 SENVGS 273

RESULT 15

H65201

Dts system, fructose-like-2 IIC component - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: H65201

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: H65201

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-359 <BLAT>

A;Cross-references: UNIPROT:P32672; GB:AE000469; GB:U000096; NID:gl790385; PIDN:AAC76931.

A;Experimental source: strain K-12, substrain MG1655

C;Genetics:

A;Gene: frwC

Query Match

Best Local Similarity 42.9%; Score 6; DB 2; Length 359;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCG 13

|||||

Db 281 VGSVCG 286

Search completed: February 11, 2005, 03:16:22

Job time : 12.0742 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 11, 2005, 03:11:19 ; Search time 3.72379 Seconds
(without alignments)
1925.221 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDVNSVNGVCGT 14

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	377	1	CYCI_HUMAN
2	14	100.0	377	2	Q6FHHO
3	9	64.3	377	1	CYCI_MOUSE
4	9	64.3	377	2	Q8C7E2
5	9	64.3	377	2	Q99LF2
6	8	57.1	600	2	Q8BXL7
7	7	50.0	310	2	Q8SYJ3
8	7	50.0	423	2	Q8GP73
9	7	50.0	446	1	YP33_YEAST
10	7	50.0	462	2	Q8FJY2
11	7	50.0	556	2	Q9VFG2
12	7	50.0	1006	2	Q9U360
13	7	50.0	1069	2	Q9JT46
14	7	50.0	1190	2	Q9HS95
15	7	50.0	2153	2	Q6LFD0
16	7	50.0	106	2	Q8X3P5
17	6	42.9	109	1	APPL_UREPA
18	6	42.9	118	2	Q8Y802
19	6	42.9	118	2	Q8Y802
20	6	42.9	118	2	Q720W6
21	6	42.9	129	2	Q96ZRI
22	6	42.9	154	2	Q6M0U3
23	6	42.9	156	2	Q8BE81
24	6	42.9	157	2	Q6LS75
25	6	42.9	161	2	Q92229
26	6	42.9	165	2	Q87Y87
27	6	42.9	169	2	Q9K962
28	6	42.9	181	2	Q8TNH7
29	6	42.9	191	2	Q8JPH9
30	6	42.9	194	2	Q9VC16
31	6	42.9	199	2	Q7F0B3

32	6	42.9	200	2	Q8S290
33	6	42.9	200	2	Q86BN8
34	6	42.9	205	2	Q6SHG0
35	6	42.9	211	2	Q9SH05
36	6	42.9	224	2	Q06076
37	6	42.9	231	1	PSA2_CAEEL
38	6	42.9	233	2	Q8Y4U0
39	6	42.9	233	2	Q71X87
40	6	42.9	248	2	Q8LEE9
41	6	42.9	249	2	Q7R9T7
42	6	42.9	249	2	Q9FKJ8
43	6	42.9	269	1	UL34_VZVD
44	6	42.9	269	2	Q6QCN1
45	6	42.9	282	1	RIP2_BRIDI
46	6	42.9	291	2	Q9KMY5
47	6	42.9	296	2	Q9RY19
48	6	42.9	304	2	Q9N120
49	6	42.9	306	2	Q6J2C5
50	6	42.9	313	1	RBN_VIBVU
51	6	42.9	313	1	RBN_VIBVY
52	6	42.9	323	2	Q91XQ8
53	6	42.9	337	2	Q8PZT1
54	6	42.9	344	2	Q75E08
55	6	42.9	345	2	Q7LZU3
56	6	42.9	359	1	PTWC_ECOLI
57	6	42.9	359	2	Q7UB89
58	6	42.9	359	2	Q8FBA5
59	6	42.9	366	2	Q6C8N4
60	6	42.9	366	2	Q83PD2
61	6	42.9	373	2	Q52987
62	6	42.9	373	2	Q6NYZ5
63	6	42.9	381	2	Q8YAW1
64	6	42.9	381	2	Q92FV1
65	6	42.9	381	2	Q725G9
66	6	42.9	383	2	Q8T257
67	6	42.9	389	1	PORA_METJA
68	6	42.9	396	2	Q8YDI5
69	6	42.9	396	2	Q937U1
70	6	42.9	401	2	Q6ACCO
71	6	42.9	413	2	Q7RIT0
72	6	42.9	425	2	Q8LQ73
73	6	42.9	448	2	Q8VUK5
74	6	42.9	450	2	Q27920
75	6	42.9	456	2	Q75BN2
76	6	42.9	457	2	Q26227
77	6	42.9	462	2	Q977P2
78	6	42.9	462	2	Q8L7L2
79	6	42.9	489	2	Q6BWU8
80	6	42.9	490	2	Q8MPG5
81	6	42.9	490	2	Q8MPG7
82	6	42.9	490	2	Q8MPG8
83	6	42.9	492	2	Q6LXX3
84	6	42.9	492	2	Q6QTA3
85	6	42.9	494	2	Q7RRV9
86	6	42.9	496	2	Q8BMR0
87	6	42.9	501	2	Q9N425
88	6	42.9	530	2	Q6FT30
89	6	42.9	530	2	Q8ES70
90	6	42.9	599	2	Q7QXX4
91	6	42.9	604	2	Q6L4X6
92	6	42.9	605	2	Q7R9G1
93	6	42.9	622	1	DXS_THETN
94	6	42.9	634	2	Q64S11
95	6	42.9	634	2	Q64VM9
96	6	42.9	643	2	Q8KGZ8
97	6	42.9	701	2	Q8CB43
98	6	42.9	733	2	Q9Y6A6
99	6	42.9	758	2	Q7RRC8
100	6	42.9	759	1	NAHB_ONCMY
101	6	42.9	760	2	Q7QUX6
102	6	42.9	762	2	Q95W15
103	6	42.9	778	2	Q9NEW7
104	6	42.9	779	2	Q8NEM7

Q8ez90	drosophila
Q86bn8	drosophila
Q6shg0	uncultured
Q9sh05	arabidopsis
Q06076	mycobacteri
Q27488	caenorhabdi
Q8Y4U0	listeria mo
Q71x87	listeria mo
Q8lee9	arabidopsis
Q7r9t7	plasmodium
Q9fkj8	arabidopsis
P09280	varicella-z
Q6qcn1	human herpe
P96184	bryonia dio
Q98185	vibrio chol
Q9ry19	deinococcus
Q9n120	oryctolagus
Q6j2c5	pseudomonas
Q8dd82	vibrio vuln
Q7mq07	vibrio vuln
Q9ixq8	mus musculus
Q9pzt1	methanosarc
Q75e08	ashbya gos
Q7lzu3	m28 virus
P32672	escherichia
Q7ub89	shigella fl
Q8fba5	escherichia
Q6c8n4	yarrowia li
Q83pd2	shigella fl
Q52987	escherichia
Q8ny25	brachydanio
Q8yawi	listeria mo
Q92fv1	listeria in
Q725g9	listeria mo
Q8tz57	methanopyru
Q57715	methanococc
Q8ydl5	brucella me
Q937u1	brucella su
Q6acc0	leifsonia x
Q7rit0	plasmodium
Q8lqt3	oryza sativ
Q8vuk5	paracoccus
Q27920	bradyzia hy
Q75bn2	ashbya gos
Q26227	rhynchosia
Q977p2	uncultured
Q8l7l2	arabidopsis
Q6bwu8	debaromyce
Q8mpg5	trypanosoma
Q8mpg7	trypanosoma
Q8mpg8	trypanosoma
Q6lxx3	methanococc
Q6qta3	trypanosoma
Q7rrv9	plasmodium
Q8bmr0	m mus muscu
Q9n425	caenorhabdi
Q6ft30	candida gla
Q8es70	oceanobacil
Q7gkx4	giardia lam
Q6l4x6	oryza sativ
Q7r9g1	plasmodium
Q8rac5	thermoanaer
Q64s11	bacteroides
Q64vm9	bacteroides
Q8kgz8	rhizobium l
Q8cb43	mus musculus
Q9y6a6	homo sapien
Q7rrc8	plasmodium
Q01345	oncorhynch
Q7qux6	giardia lam
Q95w15	trypanosoma
Q9new7	caenorhabdi
Q8nem7	homo sapien

105	6	42.9	779	2	Q80417	Q80417 pseudopleur	178	5	35.7	88	2	Q909Y4	Q909Y4 human immun
106	6	42.9	785	1	Q8RXF1	Q8rxfl arabidopsis	179	5	35.7	89	2	Q7RXU8	Q7rxu8 neurospora
107	6	42.9	794	1	Z148_HUMAN	Q9uqr1 homo sapien	180	5	35.7	92	2	Q8TM63	Q8tm63 methanosarc
108	6	42.9	794	1	Z148_MOUSE	Q61f24 mus musculus	181	5	35.7	92	2	Q8GWV2	Q8gwv2 arabidopsis
109	6	42.9	794	1	Z148_RAT	Q82806 rattus norv	182	5	35.7	92	2	Q8G9V7	Q8g9v7 escherichia
110	6	42.9	794	1	Q8TDH4	Q8tdh4 homo sapien	183	5	35.7	93	2	Q8E1W6	Q8e1w6 streptococc
111	6	42.9	794	2	Q7UP50	Q7up50 rhodospirell	184	5	35.7	94	2	Q8G9V6	Q8g9v6 escherichia
112	6	42.9	803	2	Q7RKX6	Q7rkx6 plasmodium	185	5	35.7	96	2	Q6DT49	Q6dt49 arabidopsis
113	6	42.9	862	1	ADHE_CLOAB	P33744 clostridium	186	5	35.7	98	1	RL3E_METTH	Q27127 methanobact
114	6	42.9	865	2	Q8XHFA	Q8xhf4 clostridium	187	5	35.7	98	2	Q8A076	Q8a076 bacteroides
115	6	42.9	867	2	Q8IKI7	Q8iki7 plasmodium	188	5	35.7	99	2	Q14287	Q14287 schizosacch
116	6	42.9	869	2	Q9C744	Q9c744 arabidopsis	189	5	35.7	100	2	Q8TF32	Q8tf32 methanosarc
117	6	42.9	876	2	Q895B4	Q895b4 clostridium	190	5	35.7	100	2	Q8BN15	Q8bn15 mus musculu
118	6	42.9	888	2	Q09435	Q09435 giardia lam	191	5	35.7	100	2	Q9CVP1	Q9cvp1 mus musculu
119	6	42.9	889	2	Q9FHH9	Q9fhh9 arabidopsis	192	5	35.7	100	2	Q66099	Q66099 carnation r
120	6	42.9	935	2	Q9CA26	Q9ca26 arabidopsis	193	5	35.7	101	2	Q6S3H0	Q6s3h0 brassica ju
121	6	42.9	960	2	Q8BXD5	Q8bxds debaryomyce	194	5	35.7	101	2	Q6S3H1	Q6s3h1 brassica ju
122	6	42.9	1026	2	Q9SS79	Q9ss79 arabidopsis	195	5	35.7	102	2	Q9DQD5	Q9dqds microplitis
123	6	42.9	1033	1	CR2_HUMAN	P20023 homo sapien	196	5	35.7	103	2	Q6BZB6	Q6bzbb debaryomyce
124	6	42.9	1066	1	KL61_DROME	P46863 drosophila	197	5	35.7	104	1	VATF_THEAC	Q9hm66 thermoplas
125	6	42.9	1131	2	Q23741	Q23741 brassica ol	198	5	35.7	107	2	Q6EVD9	Q6evd9 avena barba
126	6	42.9	1147	2	Q8X0V3	Q8x0v3 neurospora	199	5	35.7	107	2	Q92C09	Q92c09 listeria in
127	6	42.9	1154	2	Q7XPW1	Q7xpw1 oryza sativ	200	5	35.7	107	2	Q6SXN0	Q6sxn0 ctenopharyn
128	6	42.9	1296	2	Q6UJG6	Q6ujg6 sorghum bic	201	5	35.7	108	1	YC44_METJA	Q8s641 methanococ
129	6	42.9	1731	2	Q8WY30	Q8wy30 homo sapien	202	5	35.7	108	2	Q8RTC9	Q8rtc9 escherichia
130	6	42.9	1776	2	Q9MA20	Q9ma20 arabidopsis	203	5	35.7	109	2	Q7YUX8	Q7yux8 trypanosoma
131	6	42.9	1844	2	Q7S601	Q7s6q1 neurospora	204	5	35.7	109	2	Q7XK05	Q7xk05 oryza sativ
132	6	42.9	1980	2	Q7RF56	Q7rf56 plasmodium	205	5	35.7	110	2	Q7FY22	Q7fy22 arabidopsis
133	6	42.9	3207	2	Q8IHQ0	Q8ihq0 plasmodium	206	5	35.7	110	2	Q7MI06	Q7mio6 vibrio vuln
134	6	42.9	3366	2	Q6QCE1	Q6qce1 brachydanio	207	5	35.7	110	2	Q8DBW3	Q8dbw3 vibrio vuln
135	6	42.9	4513	1	DY1B_CHLRE	Q9mbf8 chlamydomon	208	5	35.7	110	2	Q80GN5	Q80gn5 human herpe
136	6	42.9	4543	1	LRP1_CHICK	P98157 gallus gall	209	5	35.7	111	2	Q81CN9	Q81cn9 bacillus ce
137	6	42.9	4544	1	LRP1_HUMAN	Q07954 homo sapien	210	5	35.7	115	2	Q9FDY5	Q9fdy5 arabidopsis
138	6	42.9	4545	2	Q91ZX7	Q91zx7 mus musculu	211	5	35.7	116	2	Q7RMD5	Q7rmd5 plasmodium
139	6	42.9	4545	2	Q920Y4	Q920y4 mus musculu	212	5	35.7	116	2	Q7VLE1	Q7vle1 haemophilus
140	6	42.9	4545	2	Q61291	Q61291 mus musculu	213	5	35.7	117	2	Q7RBE5	Q7rbe5 plasmodium
141	6	42.9	4599	1	LR1B_HUMAN	Q9nzzr2 homo sapien	214	5	35.7	117	2	Q6JIG7	Q6jig7 bacterioph
142	6	42.9	4599	1	LR1B_MOUSE	Q9jil18 mus musculu	215	5	35.7	117	2	Q665Q9	Q665q9 yersinia ps
143	6	42.9	6994	2	Q17343	Q17343 caenorhabdi	216	5	35.7	117	2	Q80KV1	Q80kv1 hepatitis c
144	6	42.9	6994	2	Q17490	Q17490 caenorhabdi	217	5	35.7	119	2	Q6UVP6	Q6uvp6 pseudodocl
145	5	35.7	16	2	Q7M1D3	Q7m1d3 unidentified	218	5	35.7	121	1	RS13_BACHD	Q50632 bacillus ha
146	5	35.7	28	1	COXB_SOLTU	P80499 solanum tub	219	5	35.7	122	1	Q92W42	Q92w42 rhizobium m
147	5	35.7	39	2	Q7RKY0	Q7rky0 plasmodium	220	5	35.7	122	2	Q6LSG5	Q6lsg5 photobacter
148	5	35.7	40	2	Q6GAQ3	Q6gaq3 staphylococ	221	5	35.7	123	2	Q7S2F8	Q7s2f8 neurospora
149	5	35.7	40	2	Q6GGLO	Q6gglo staphylococ	222	5	35.7	123	2	Q9XX40	Q9xx40 caenorhabdi
150	5	35.7	43	2	Q7M055	Q7m055 mus sp. gen	223	5	35.7	126	2	Q63AN2	Q63an2 bacillus ce
151	5	35.7	50	2	Q19112	Q19112 caenorhabdi	224	5	35.7	126	2	Q737B6	Q737b6 bacillus ce
152	5	35.7	51	2	Q6YH83	Q6ynb3 ambystoma t	225	5	35.7	126	2	Q81PUI	Q81pul bacillus an
153	5	35.7	55	2	Q6S465	Q6s465 burkholderi	226	5	35.7	126	2	Q6H1I9	Q6h1i9 bacillus th
154	5	35.7	61	2	Q8S4V1	Q8s4v1 arabidopsis	227	5	35.7	127	2	Q8ZXY7	Q8zxy7 pyrobaculum
155	5	35.7	64	2	Q8IBX4	Q8ibx4 plasmodium	228	5	35.7	127	2	Q61JTI	Q61jt1 drosophila
156	5	35.7	64	2	Q8JFG5	Q8jfg5 brachydanio	229	5	35.7	127	2	Q953C4	Q953c4 cuculotogast
157	5	35.7	68	2	Q85WS9	Q85ws9 pinus korai	230	5	35.7	127	2	Q74BC7	Q74bc7 geobacter s
158	5	35.7	70	2	Q8KEZ8	Q8kez8 tetradon n	231	5	35.7	127	2	Q91L80	Q91l80 white spot
159	5	35.7	72	2	Q9S5J72	Q9s5j72 arabidopsis	232	5	35.7	127	2	Q7TCM4	Q7tcm4 white spot
160	5	35.7	73	2	Q6VXZ6	Q6vxz6 echinococcu	233	5	35.7	128	1	NIFU_ECOLI	P77310 escherichia
161	5	35.7	73	2	Q74EW1	Q74ew1 geobacter s	234	5	35.7	130	2	Q6EVD8	Q6evd8 rhodopseudo
162	5	35.7	74	1	YM34_MARPO	P39476 marchantia	235	5	35.7	130	2	Q6EVD8	Q6evd8 avena longi
163	5	35.7	74	2	Q63H11	Q63h11 bacillus ce	236	5	35.7	131	2	Q7NGV4	Q7ngv4 gloeobacter
164	5	35.7	74	2	Q73FF6	Q73ff6 bacillus ce	237	5	35.7	131	2	Q66MD1	Q66mdi hepatitis c
165	5	35.7	74	2	Q81VY8	Q81vy8 bacillus an	238	5	35.7	131	2	Q88946	Q88946 tomato yell
166	5	35.7	74	2	Q6HPW5	Q6hpw5 bacillus th	239	5	35.7	133	2	Q8PW94	Q8pw94 methanosarc
167	5	35.7	74	2	Q83940	Q83940 olive laten	240	5	35.7	133	2	Q7X9D0	Q7x9d0 pyrus pyrif
168	5	35.7	75	2	Q6VXZ5	Q6vxz5 echinococcu	241	5	35.7	135	2	Q84XX2	Q84xx2 brassica ra
169	5	35.7	76	2	Q8PSU2	Q8psu2 methanosarc	242	5	35.7	135	2	Q62PQ0	Q62pq0 bacillus li
170	5	35.7	76	2	Q8H810	Q8h810 oryza sativ	243	5	35.7	136	2	Q8W601	Q8w601 bacterioph
171	5	35.7	77	2	Q8CJU0	Q8cj0 streptomyce	244	5	35.7	136	2	Q84RQ4	Q84rq4 chlamydomon
172	5	35.7	79	2	Q8FAZ7	Q8faz7 escherichia	245	5	35.7	137	2	Q9SVZ4	Q9svz4 arabidopsis
173	5	35.7	80	2	Q6LWW8	Q6lww8 methanococc	246	5	35.7	137	2	Q991Y9	Q99iy9 uncultured
174	5	35.7	84	2	Q6K6X5	Q6k6x5 oryza sativ	247	5	35.7	138	2	Q9CZF7	Q9czf7 mus musculu
175	5	35.7	84	2	Q9RXT2	Q9rxt2 deinococcus	248	5	35.7	140	1	SMP3_HUMAN	Q15486 homo sapien
176	5	35.7	84	2	Q919H0	Q919h0 culex nigri	249	5	35.7	140	1	SMP4_HUMAN	Q15487 homo sapien
177	5	35.7	86	2	Q8LDR2	Q8ldr2 arabidopsis	250	5	35.7	140	1	SMP5_HUMAN	Q15488 homo sapien

251	5	35.7	140	1	SMPL_HUMAN	Q9nqg0	homo sapien	324	5	35.7	177	2	Q7PLC9	Q7plc9	drosophila
252	5	35.7	141	2	Q6FW3	Q6fw3	candida gla	325	5	35.7	178	2	Q7UT14	Q7uti14	rhodospirella
253	5	35.7	142	2	Q8H127	Q8h127	arabidopsis	326	5	35.7	179	2	Q8SX75	Q8sx75	drosophila
254	5	35.7	143	2	Q9PV16	Q9pv16	dicentrarch	327	5	35.7	179	2	Q7Q705	Q7q705	anopheles g
255	5	35.7	143	1	PSE1_ARATH	Q9831	arabidopsis	328	5	35.7	180	2	Q84HR5	Q84hr5	rhizobium g
256	5	35.7	143	2	Q96ZM6	Q96zm6	sulfolobus	329	5	35.7	180	2	Q84HR6	Q84hr6	rhizobium g
257	5	35.7	143	2	Q8LC58	Q8lc58	arabidopsis	330	5	35.7	180	2	Q84HR8	Q84hr8	rhizobium g
258	5	35.7	143	2	Q8LG63	Q8lg63	arabidopsis	331	5	35.7	180	2	Q9X9T2	Q9x9t2	synechococ
259	5	35.7	144	2	Q7RK64	Q7rk64	plasmodium	332	5	35.7	181	2	Q9XEX7	Q9xex7	listeria mo
260	5	35.7	144	2	Q9S4X0	Q9s4x0	escherichia	333	5	35.7	182	2	Q6XLZ1	Q6xlz1	feldmannia
261	5	35.7	144	2	Q81346	Q81346	hepatitis c	334	5	35.7	183	2	Q6BNF9	Q6bnf9	debaromyce
262	5	35.7	145	1	PSE2_ARATH	Q98714	arabidopsis	335	5	35.7	184	2	Q8KP48	Q8kp48	peptostrept
263	5	35.7	145	2	Q9V8Y6	Q9v8y6	drosophila	336	5	35.7	184	2	Q82898	Q82898	escherichia
264	5	35.7	146	2	Q8RD77	Q8rd77	human papil	337	5	35.7	185	2	Q16556	Q16556	caenorhabdi
265	5	35.7	146	2	Q899W9	Q899w9	clostridium	338	5	35.7	185	2	Q8V3H5	Q8v3h5	swinepox vi
266	5	35.7	149	2	Q59021	Q59021	pyrococcus	339	5	35.7	187	2	Q64CV4	Q64cv4	uncultured
267	5	35.7	151	2	Q9NV63	Q9nv63	homo sapien	340	5	35.7	187	2	Q84Y12	Q84y12	capsella ru
268	5	35.7	151	2	Q6SED9	Q6sed9	lactobacill	341	5	35.7	188	2	Q9M448	Q9m448	cicer ariet
269	5	35.7	151	2	Q8EJ21	Q8ej21	shewanella	342	5	35.7	188	2	Q9J3A4	Q9j3a4	hepatitis c
270	5	35.7	151	2	Q85PP8	Q85pp8	lactobacill	343	5	35.7	188	2	Q9J3A5	Q9j3a5	hepatitis c
271	5	35.7	152	2	Q8IEN4	Q8ien4	plasmodium	344	5	35.7	188	2	Q9J3A6	Q9j3a6	hepatitis c
272	5	35.7	152	2	Q8HCR4	Q8hcr4	oryza sativ	345	5	35.7	188	2	Q9J3A7	Q9j3a7	hepatitis c
273	5	35.7	152	2	Q6DAB7	Q6da87	erwinia car	346	5	35.7	188	2	Q9J3A8	Q9j3a8	hepatitis c
274	5	35.7	154	2	Q7RAS1	Q7ra51	plasmodium	347	5	35.7	188	2	Q9J3B1	Q9j3b1	hepatitis c
275	5	35.7	154	2	Q7RCG8	Q7rcg8	plasmodium	348	5	35.7	188	2	Q9J3B2	Q9j3b2	hepatitis c
276	5	35.7	154	2	Q8W628	Q8w628	cyanophage	349	5	35.7	188	2	Q9J3B3	Q9j3b3	hepatitis c
277	5	35.7	154	2	Q92CE7	Q92ce7	listeria mo	350	5	35.7	188	2	Q9J3B4	Q9j3b4	hepatitis c
278	5	35.7	154	2	Q720G5	Q720g5	listeria mo	351	5	35.7	188	2	Q9J3B5	Q9j3b5	hepatitis c
279	5	35.7	154	2	Q72T44	Q72t44	leptospiro	352	5	35.7	189	2	Q7QEH6	Q7qeh6	anopheles g
280	5	35.7	154	2	Q7AP06	Q7ap06	listeria in	353	5	35.7	189	2	Q93I96	Q93i96	staphylococ
281	5	35.7	154	2	Q8F2B0	Q8f2b0	leptospiro	354	5	35.7	190	2	Q8JPH1	Q8jph1	hepatitis c
282	5	35.7	154	2	Q7T0K7	Q7t0k7	ambystoma m	355	5	35.7	190	2	Q9Q3W1	Q9q3w1	hepatitis c
283	5	35.7	155	2	Q9HDZ6	Q9hdz6	schizosacch	356	5	35.7	190	2	Q9Q3W2	Q9q3w2	hepatitis c
284	5	35.7	155	2	Q6EVE2	Q6eve2	avena insul	357	5	35.7	190	2	Q9Q3W3	Q9q3w3	hepatitis c
285	5	35.7	155	2	Q6EVE3	Q6eve3	avena longi	358	5	35.7	190	2	Q9Q3W4	Q9q3w4	hepatitis c
286	5	35.7	156	2	Q97U00	Q97u00	sulfolobus	359	5	35.7	190	2	Q7ZZP4	Q7zzp4	agkistrodon
287	5	35.7	156	2	Q884V2	Q884v2	arabidopsis	360	5	35.7	191	2	Q8N1Y3	Q8n1y3	homo sapien
288	5	35.7	156	2	Q888C9	Q888c9	arabidopsis	361	5	35.7	191	2	Q6R9G2	Q6r9g2	zea mays (m
289	5	35.7	160	1	THY1_CHICK	Q07212	gallus gall	362	5	35.7	191	2	Q8JPG8	Q8jpg8	hepatitis c
290	5	35.7	160	1	TPC2_CAEBL	Q09665	caenorhabdi	363	5	35.7	191	2	Q8JPH2	Q8jph2	hepatitis c
291	5	35.7	160	2	Q6ZW30	Q6zw30	homo sapien	364	5	35.7	191	2	Q8JPH4	Q8jph4	hepatitis c
292	5	35.7	160	2	Q7PN38	Q7pn38	anopheles g	365	5	35.7	191	2	Q8JPH5	Q8jph5	hepatitis c
293	5	35.7	160	2	Q97TE5	Q97te5	clostridium	366	5	35.7	191	2	Q8JPH6	Q8jph6	hepatitis c
294	5	35.7	160	2	Q7T252	Q7t252	gallus gall	367	5	35.7	191	2	Q8JPH7	Q8jph7	hepatitis c
295	5	35.7	162	2	Q6MRRO	Q6mrro	bdellovibri	368	5	35.7	191	2	Q8JPH8	Q8jph8	hepatitis c
296	5	35.7	162	2	Q89PC2	Q89pc2	bradyrhizob	369	5	35.7	191	2	Q8JPI0	Q8jpi0	hepatitis c
297	5	35.7	163	1	EMP3_HUMAN	P54852	homo sapien	370	5	35.7	191	2	Q8JPI1	Q8jpi1	hepatitis c
298	5	35.7	163	1	EMP3_MOUSE	Q35912	mus musculu	371	5	35.7	191	2	Q8JPI3	Q8jpi3	hepatitis c
299	5	35.7	163	1	EMP3_RAT	Q9qy5	rattus norv	372	5	35.7	191	2	Q8JPI4	Q8jpi4	hepatitis c
300	5	35.7	163	2	Q61BD3	Q61bd3	homo sapien	373	5	35.7	191	2	Q8JPI5	Q8jpi5	hepatitis c
301	5	35.7	164	2	Q97BF3	Q97bf3	thermoplas	374	5	35.7	191	2	Q8JPI7	Q8jpi7	hepatitis c
302	5	35.7	164	2	Q8N204	Q8n204	homo sapien	375	5	35.7	191	2	Q8JPI8	Q8jpi8	hepatitis c
303	5	35.7	165	2	Q975U1	Q975u1	sulfolobus	376	5	35.7	191	2	Q8JPI0	Q8jpi0	hepatitis c
304	5	35.7	165	2	Q893X4	Q893x4	clostridium	377	5	35.7	191	2	Q8JPI2	Q8jpi2	hepatitis c
305	5	35.7	166	2	Q89CK5	Q89ck5	arabidopsis	378	5	35.7	191	2	Q8JPI4	Q8jpi4	hepatitis c
306	5	35.7	167	2	Q8ENNS	Q8enn5	oceanobacil	379	5	35.7	191	2	Q8BBK9	Q8bbk9	hepatitis c
307	5	35.7	167	2	Q6URK9	Q6urk9	bothrops ja	380	5	35.7	191	2	Q8BBM1	Q8bbm1	hepatitis c
308	5	35.7	168	2	Q6ZL83	Q6zlb3	oryza sativ	381	5	35.7	191	2	Q8BBM3	Q8bbm3	hepatitis c
309	5	35.7	168	2	Q6TCD9	Q6tcd9	lactobacill	382	5	35.7	191	2	Q8BBM5	Q8bbm5	hepatitis c
310	5	35.7	170	2	Q639P8	Q639f8	bacillus ce	383	5	35.7	191	2	Q8BBM7	Q8bbm7	hepatitis c
311	5	35.7	170	2	Q8INL1	Q8inl1	bacillus an	384	5	35.7	191	2	Q8BBM8	Q8bbm8	hepatitis c
312	5	35.7	170	2	Q6HGR7	Q6hgr7	bacillus th	385	5	35.7	191	2	Q8BBM9	Q8bbm9	hepatitis c
313	5	35.7	171	2	Q847C9	Q847c9	nodularia s	386	5	35.7	191	2	Q8BBN0	Q8bbn0	hepatitis c
314	5	35.7	171	2	Q9CVY4	Q9cvy4	mus musculu	387	5	35.7	191	2	Q8BBN1	Q8bbn1	hepatitis c
315	5	35.7	172	2	Q8LKCA	Q8lkca	malus pruni	388	5	35.7	191	2	Q8BBN3	Q8bbn3	hepatitis c
316	5	35.7	172	2	Q7VGM0	Q7vgm0	helicobacte	389	5	35.7	191	2	Q8BBN4	Q8bbn4	hepatitis c
317	5	35.7	173	2	Q76P34	Q76p34	dictyosteli	390	5	35.7	191	2	Q8BBN6	Q8bbn6	hepatitis c
318	5	35.7	173	2	Q86E13	Q86e13	schistosoma	391	5	35.7	191	2	Q8BBN7	Q8bbn7	hepatitis c
319	5	35.7	173	2	Q735G3	Q735g3	bacillus ce	392	5	35.7	191	2	Q8BBN8	Q8bbn8	hepatitis c
320	5	35.7	173	2	Q81BL3	Q81bl3	bacillus ce	393	5	35.7	191	2	Q8BBN9	Q8bbn9	hepatitis c
321	5	35.7	174	2	Q9AI91	Q9ai91	helicobacte	394	5	35.7	192	2	Q7S2P5	Q7s2p5	neurospora
322	5	35.7	174	2	Q9AI91	Q9ai91	helicobacte	395	5	35.7	192	2	Q81496	Q81496	hepatitis c
323	5	35.7	175	2	Q9FI91	Q9fi91	arabidopsis	396	5	35.7	192	2	Q81499	Q81499	hepatitis c

397	5	35.7	192	2	Q81502	Q81502 hepatitis c	470	5	35.7	210	2	Q8ARN6	Q8ARN6 human immun
398	5	35.7	192	2	Q81505	Q81505 hepatitis c	471	5	35.7	212	2	Q8H8G3	Q8H8G3 cryza sativ
399	5	35.7	192	2	Q81511	Q81511 hepatitis c	472	5	35.7	213	2	Q93XJ4	Q93XJ4 putunia hyb
400	5	35.7	192	2	Q81514	Q81514 hepatitis c	473	5	35.7	213	2	Q7VF26	Q7VF26 helicobacte
401	5	35.7	192	2	Q81517	Q81517 hepatitis c	474	5	35.7	214	2	Q884V4	Q884V4 arabisdopsis
402	5	35.7	192	2	Q81520	Q81520 hepatitis c	475	5	35.7	214	2	Q84RK0	Q84RK0 arabisdopsis
403	5	35.7	192	2	Q81523	Q81523 hepatitis c	476	5	35.7	214	2	Q8XAE9	Q8XAE9 escherichia
404	5	35.7	192	2	Q81526	Q81526 hepatitis c	477	5	35.7	216	1	VSPB_LACMU	P84036 lachesis mu
405	5	35.7	192	2	Q81529	Q81529 hepatitis c	478	5	35.7	216	1	Q6U9M9	Q6U9M9 bacterioph
406	5	35.7	192	2	Q81535	Q81535 hepatitis c	479	5	35.7	217	1	KAD_BACSU	P16304 bacillus su
407	5	35.7	192	2	Q81538	Q81538 hepatitis c	480	5	35.7	217	2	Q75VL4	Q75VL4 cryptotomia
408	5	35.7	192	2	Q81539	Q81539 hepatitis c	481	5	35.7	217	2	Q8FQR9	Q8FQR9 corynebacte
409	5	35.7	192	2	Q81540	Q81540 hepatitis c	482	5	35.7	218	2	Q73W12	Q73W12 mycobacteri
410	5	35.7	192	2	Q81541	Q81541 hepatitis c	483	5	35.7	218	2	Q7TFH4	Q7TFH4 rhesus cyto
411	5	35.7	192	2	Q81542	Q81542 hepatitis c	484	5	35.7	219	2	Q7MWD7	Q7MWD7 porphyromon
412	5	35.7	192	2	Q81543	Q81543 hepatitis c	485	5	35.7	220	2	Q7DIC1	Q7DIC1 staphylococ
413	5	35.7	192	2	Q81544	Q81544 hepatitis c	486	5	35.7	220	2	Q48363	Q48363 staphylococ
414	5	35.7	192	2	Q81545	Q81545 hepatitis c	487	5	35.7	220	2	Q7A6M5	Q7A6M5 staphylococ
415	5	35.7	192	2	Q81546	Q81546 hepatitis c	488	5	35.7	220	2	Q8EN55	Q8EN55 oceanobacil
416	5	35.7	192	2	Q81547	Q81547 hepatitis c	489	5	35.7	220	2	Q6GKQ1	Q6GKQ1 staphylococ
417	5	35.7	192	2	Q81548	Q81548 hepatitis c	490	5	35.7	221	1	TCPP_VIBCH	P29485 vibrio chol
418	5	35.7	192	2	Q81549	Q81549 hepatitis c	491	5	35.7	221	2	Q9ANX8	Q9ANX8 vibrio chol
419	5	35.7	192	2	Q81550	Q81550 hepatitis c	492	5	35.7	221	2	Q9ANX9	Q9ANX9 vibrio chol
420	5	35.7	192	2	Q81551	Q81551 hepatitis c	493	5	35.7	222	1	TPIS_METFE	Q9JW5 methanother
421	5	35.7	192	2	Q81552	Q81552 hepatitis c	494	5	35.7	222	1	Q9JF74	Q9JF74 rhizobium l
422	5	35.7	192	2	Q81553	Q81553 hepatitis c	495	5	35.7	222	2	Q99XD8	Q99XD8 staphylococ
423	5	35.7	192	2	Q81554	Q81554 hepatitis c	496	5	35.7	222	2	Q7A8C0	Q7A8C0 staphylococ
424	5	35.7	192	2	Q81555	Q81555 hepatitis c	497	5	35.7	222	2	Q7N7R7	Q7N7R7 photorhabdu
425	5	35.7	192	2	Q81556	Q81556 hepatitis c	498	5	35.7	223	2	Q9VRC7	Q9VRC7 drosophila
426	5	35.7	192	2	Q81557	Q81557 hepatitis c	499	5	35.7	223	2	Q8JN68	Q8JN68 snake adeno
427	5	35.7	192	2	Q81558	Q81558 hepatitis c	500	5	35.7	224	2	Q8PW78	Q8PW78 methanosarc
428	5	35.7	192	2	Q81559	Q81559 hepatitis c	501	5	35.7	224	2	Q8T201	Q8T201 methanopyru
429	5	35.7	192	2	Q81560	Q81560 hepatitis c	502	5	35.7	224	2	Q6FSS5	Q6FSS5 candida gla
430	5	35.7	192	2	Q81561	Q81561 hepatitis c	503	5	35.7	224	2	Q9WPM0	Q9WPM0 tomato leaf
431	5	35.7	192	2	Q81562	Q81562 hepatitis c	504	5	35.7	225	2	Q7PG92	Q7PG92 anopheles g
432	5	35.7	192	2	Q81563	Q81563 hepatitis c	505	5	35.7	225	2	Q7QNH7	Q7QNH7 anopheles g
433	5	35.7	192	2	Q81564	Q81564 hepatitis c	506	5	35.7	225	2	Q803X9	Q803X9 brachydanio
434	5	35.7	192	2	Q81565	Q81565 hepatitis c	507	5	35.7	226	2	Q6CFT6	Q6CFT6 yarrowia li
435	5	35.7	192	2	Q81566	Q81566 hepatitis c	508	5	35.7	226	2	Q7RVP3	Q7RVP3 neurospora
436	5	35.7	192	2	Q81567	Q81567 hepatitis c	509	5	35.7	226	2	Q20613	Q20613 caenorhabdi
437	5	35.7	192	2	Q81568	Q81568 hepatitis c	510	5	35.7	226	2	Q79Y26	Q79Y26 streptococc
438	5	35.7	192	2	Q81569	Q81569 hepatitis c	511	5	35.7	227	1	VCLJ_BACSU	Q79Y26 streptococc
439	5	35.7	192	2	Q81570	Q81570 hepatitis c	512	5	35.7	228	2	Q8S4V3	Q8S4V3 bacillus su
440	5	35.7	192	2	Q81571	Q81571 hepatitis c	513	5	35.7	228	2	Q7QTH6	Q7QTH6 giardia lam
441	5	35.7	192	2	Q81572	Q81572 hepatitis c	514	5	35.7	228	2	Q8S4V3	Q8S4V3 arabisdopsis
442	5	35.7	192	2	Q81573	Q81573 hepatitis c	515	5	35.7	228	2	Q54084	Q54084 streptococc
443	5	35.7	192	2	Q81574	Q81574 hepatitis c	516	5	35.7	228	2	Q8Y719	Q8Y719 listeria mo
444	5	35.7	192	2	Q81575	Q81575 hepatitis c	517	5	35.7	228	2	Q92BK6	Q92BK6 listeria in
445	5	35.7	192	2	Q81576	Q81576 hepatitis c	518	5	35.7	228	2	Q71G3	Q71G3 listeria in
446	5	35.7	192	2	Q81577	Q81577 hepatitis c	519	5	35.7	229	2	Q9K0B6	Q9K0B6 neisseria m
447	5	35.7	192	2	Q81578	Q81578 hepatitis c	520	5	35.7	231	1	VSP1_AGKCO	Q9K0B6 neisseria m
448	5	35.7	192	2	Q81579	Q81579 hepatitis c	521	5	35.7	231	2	Q6NE79	Q6NE79 agkistrodon
449	5	35.7	192	2	Q81580	Q81580 hepatitis c	522	5	35.7	231	2	Q73N32	Q73N32 treponema d
450	5	35.7	192	2	Q81581	Q81581 hepatitis c	523	5	35.7	231	2	Q9JVC1	Q9JVC1 neisseria m
451	5	35.7	192	2	Q81582	Q81582 hepatitis c	524	5	35.7	232	1	VSP1_BOTJA	P81824 bothrops ja
452	5	35.7	192	2	Q81583	Q81583 hepatitis c	525	5	35.7	232	1	VSPA_BOTJA	P81661 bothrops ja
453	5	35.7	192	2	Q81584	Q81584 hepatitis c	526	5	35.7	232	2	Q8INZ8	Q8INZ8 drosophila
454	5	35.7	192	2	Q81585	Q81585 hepatitis c	527	5	35.7	233	2	Q6YR86	Q6YR86 onion yello
455	5	35.7	192	2	Q81586	Q81586 hepatitis c	528	5	35.7	233	2	Q8C7Y3	Q8C7Y3 mus musculu
456	5	35.7	192	2	Q81587	Q81587 hepatitis c	529	5	35.7	233	2	Q6IWF1	Q6IWF1 bothrops al
457	5	35.7	192	2	Q81588	Q81588 hepatitis c	530	5	35.7	233	2	Q9PT51	Q9PT51 agkistrodon
458	5	35.7	192	2	Q81589	Q81589 hepatitis c	531	5	35.7	234	1	VSP2_AGKCO	P82981 agkistrodon
459	5	35.7	192	2	Q81590	Q81590 hepatitis c	532	5	35.7	234	2	Q61132	Q61132 plasmodium
460	5	35.7	192	2	Q81591	Q81591 hepatitis c	533	5	35.7	234	2	Q97NR6	Q97NR6 streptococc
461	5	35.7	192	2	Q81592	Q81592 hepatitis c	534	5	35.7	234	2	Q8UNF5	Q8UNF5 streptococc
462	5	35.7	192	2	Q81593	Q81593 hepatitis c	535	5	35.7	234	2	Q8UJ1	Q8UJ1 agkistrodon
463	5	35.7	192	2	Q81594	Q81594 hepatitis c	536	5	35.7	234	2	Q7S2E2	Q7S2E2 agkistrodon
464	5	35.7	192	2	Q81595	Q81595 hepatitis c	537	5	35.7	234	2	Q9YGS1	Q9YGS1 agkistrodon
465	5	35.7	192	2	Q81596	Q81596 hepatitis c	538	5	35.7	235	1	VSP2_AGKBI	Q8CC20 mus musculu
466	5	35.7	192	2	Q81597	Q81597 hepatitis c	539	5	35.7	235	2	Q8CC20	Q8CC20 mus musculu
467	5	35.7	192	2	Q81598	Q81598 hepatitis c	540	5	35.7	236	1	CYSA_CHLVU	P56344 chlorella v
468	5	35.7	192	2	Q81599	Q81599 hepatitis c	541	5	35.7	236	1	P27K_GALME	P83632 galliera me
469	5	35.7	192	2	Q81600	Q81600 hepatitis c	542	5	35.7	236	2	Q7V6W5	Q7V6W5 prochloroco

543	5	35.7	237	2	Q6L2U4	Q6L2u4 picrophilus	616	5	35.7	257	2	Q6DSZ5	Q6dsz5 helicobacte
544	5	35.7	237	2	Q6NQK8	Q6ngk8 arabidopsis	617	5	35.7	257	2	Q8QH62	Q8jh62 vipera lebe
545	5	35.7	237	2	Q83421	Q83421 agkistrodon	618	5	35.7	257	2	Q8QH86	Q8gq86 bothrops in
546	5	35.7	237	2	Q8VUU2	P8uu1j2 agkistrodon	619	5	35.7	257	2	Q71QH8	Q71qh8 trimeresuru
547	5	35.7	238	1	VSP1_AKGHA	P8u1176 agkistrodon	620	5	35.7	257	2	Q71Q13	Q71q13 trimeresuru
548	5	35.7	239	1	GRPE_PROMP	Q7v3q4 prochloroco	621	5	35.7	257	2	Q9PTL3	Q9pl13 agkistrodon
549	5	35.7	239	2	Q7AR84	Q7ar84 campylobact	622	5	35.7	257	2	Q9YGU9	Q9ygj9 agkistrodon
550	5	35.7	239	2	Q6T5L0	Q6t5l0 gloydilus sh	623	5	35.7	258	1	KC2C_YEAST	P38930 saccharomyc
551	5	35.7	240	2	O51151	O51151 borrellia bu	624	5	35.7	258	1	VSP1_TRIGA	O13059 trimeresuru
552	5	35.7	240	2	Q894J9	Q894j9 clostridium	625	5	35.7	258	1	VSP1_TRIST	O15156 trimeresuru
553	5	35.7	241	2	Q75JT5	Q75jt5 dictyosteli	626	5	35.7	258	1	VSP2_AGKAC	Q918x1 agkistrodon
554	5	35.7	241	2	Q9K198	Q9k198 neisseria m	627	5	35.7	258	1	VSP2_AGKRH	Q47797 agkistrodon
555	5	35.7	241	2	Q6APJ4	Q6apj4 desulfotale	628	5	35.7	258	1	VSP2_TRIJE	Q9df67 trimeresuru
556	5	35.7	242	2	Q8E0E7	Q8e0e7 streptococc	629	5	35.7	258	1	VSP3_BOTJA	Q9pcu8 bothrops ja
557	5	35.7	242	2	Q8B621	Q8b621 streptococc	630	5	35.7	258	1	Q71LQ5	Q71lq5 mycobacteri
558	5	35.7	242	2	Q68UW9	Q68uw9 ageratum ye	631	5	35.7	258	2	Q8P4E8	Q8p4e8 xanthomonas
559	5	35.7	243	2	Q6L2N4	Q6l2n4 picrophilus	632	5	35.7	258	2	Q8PG10	Q8pg10 xanthomonas
560	5	35.7	243	2	Q6ZPW6	Q6zpw6 mus musculu	633	5	35.7	258	2	Q8QHK2	Q8qhk2 crocalus at
561	5	35.7	244	1	FABG_VIBCH	Q9kqh7 vibrio chol	634	5	35.7	258	2	Q9HTT5	Q9ht5 agkistrodon
562	5	35.7	244	1	FABG_VIBHA	P55336 vibrio harv	635	5	35.7	258	2	Q71QH6	Q71qh6 trimeresuru
563	5	35.7	244	1	MABC_RAT	P08661 rattus norv	636	5	35.7	258	2	Q71QH7	Q71qh7 trimeresuru
564	5	35.7	244	1	Q94190	Q94190 caenorhabdi	637	5	35.7	258	2	Q71Q11	Q71q11 trimeresuru
565	5	35.7	244	2	Q87N22	Q87n22 vibrio para	638	5	35.7	258	2	Q71Q12	Q71q12 trimeresuru
566	5	35.7	245	2	Q6AV58	Q6av58 oryza sativ	639	5	35.7	258	2	Q7SZE1	Q7sze1 gloydius sa
567	5	35.7	246	1	PCNA_THEAC	Q9hjq0 thermoplasma	640	5	35.7	258	2	Q8AY78	Q8ay78 trimeresuru
568	5	35.7	246	1	PCNA_THEVO	Q97982 thermoplasma	641	5	35.7	258	2	Q8AY80	Q8ay80 trimeresuru
569	5	35.7	246	2	Q970G3	Q970g3 sulfolobus	642	5	35.7	258	2	Q91961	Q91961 agkistrodon
570	5	35.7	246	2	Q8RV42	Q8rv42 arabidopsis	643	5	35.7	258	2	Q9W7S1	Q9w7s1 agkistrodon
571	5	35.7	246	2	Q8BPH3	Q8bph3 oceanobacil	644	5	35.7	259	2	Q8PVX0	Q8pvx0 methanoearc
572	5	35.7	247	2	P95849	P95849 sulfolobus	645	5	35.7	259	2	Q04819	Q04819 salmonella
573	5	35.7	248	1	VGLZ_EBV	P03218 epstein-bar	646	5	35.7	259	2	Q89WX4	Q89wx4 bradyrhizob
574	5	35.7	248	1	Q9BS20	Q9bs20 homo sapien	647	5	35.7	259	2	Q8UUK2	Q8uuk2 crocalus ad
575	5	35.7	248	2	Q67RY1	Q67ry1 symbiobacte	648	5	35.7	260	1	VSP1_AGKAC	Q918x2 agkistrodon
576	5	35.7	248	2	Q9BUG8	Q9bug8 salmonella	649	5	35.7	260	1	VSP1_TRIFL	P05620 trimeresuru
577	5	35.7	248	2	Q7M7J8	Q7m7j8 vibrio vuln	650	5	35.7	260	1	VSP2_AGKHP	Q9yp16 agkistrodon
578	5	35.7	248	2	Q8D8G8	Q8d8g8 vibrio vuln	651	5	35.7	260	1	VSP2_VIPLE	Q9pc40 vipera lebe
579	5	35.7	248	2	Q777B4	Q777b4 human herpe	652	5	35.7	260	1	VSP6_TRIMU	Q9d983 trimeresuru
580	5	35.7	249	2	Q6VED7	Q6ved7 emilliania h	653	5	35.7	260	2	Q662N6	Q662n6 borrellia ga
581	5	35.7	249	2	Q8RJB2	Q8rjb2 bacillus ce	654	5	35.7	260	2	Q8YTA1	Q8yta1 anabaena sp
582	5	35.7	249	2	Q8RS28	Q8rs28 bacillus ce	655	5	35.7	260	2	Q73800	Q73800 agkistrodon
583	5	35.7	250	2	Q9GKE2	Q9gke2 sus scrofa	656	5	35.7	260	2	Q93502	Q93502 agkistrodon
584	5	35.7	251	2	Q7PP50	Q7pp50 anopheles g	657	5	35.7	260	2	Q8UVX1	Q8uvx1 agkistrodon
585	5	35.7	252	1	TP1S_MYCGA	Q7naq4 mycoplasma	658	5	35.7	260	2	Q6T6S7	Q6t6s7 bitis gabon
586	5	35.7	252	1	Q68726	Q68726 yersinia pe	659	5	35.7	260	2	Q71QH9	Q71qh9 trimeresuru
587	5	35.7	252	2	O05582	O05582 mycobacteri	660	5	35.7	260	2	Q71Q14	Q71q14 trimeresuru
588	5	35.7	252	2	Q93GS4	Q93gs4 salmonella	661	5	35.7	260	2	Q71Q12	Q71q12 trimeresuru
589	5	35.7	252	2	Q72VQ2	Q72vq2 leptospira	662	5	35.7	260	2	Q71QJ4	Q71qj4 trimeresuru
590	5	35.7	252	2	Q7U0V7	Q7u0v7 mycobacteri	663	5	35.7	260	2	Q7T229	Q7t229 bothrops ja
591	5	35.7	252	2	Q7UK23	Q7uk23 rhodopirell	664	5	35.7	260	2	Q8AY81	Q8ay81 trimeresuru
592	5	35.7	252	2	Q7UK24	Q7uk24 rhodopirell	665	5	35.7	262	1	VSP1_AGKCA	Q91053 agkistrodon
593	5	35.7	252	2	Q8FP9A	Q8fp9a leptospira	666	5	35.7	262	2	O61131	Q61131 plasmodium
594	5	35.7	252	2	Q9A5Z1	Q9a5z1 caulobacter	667	5	35.7	262	2	Q7RNH6	Q7rnhe plasmodium
595	5	35.7	253	2	Q9SN32	Q9sn32 arabidopsis	668	5	35.7	262	2	Q8L9Y2	Q8l9y2 arabidopsis
596	5	35.7	253	2	Q88FZ3	Q88fz3 pseudomonas	669	5	35.7	262	2	Q93WT2	Q93wt2 sorghum bic
597	5	35.7	253	2	Q8UZE2	Q8uze2 cercopithec	670	5	35.7	262	2	Q941I5	Q941i5 sorghum bic
598	5	35.7	254	2	Q8XL23	Q8xl23 clostridium	671	5	35.7	262	2	Q94EL4	Q94el4 sorghum aru
599	5	35.7	254	2	Q6MU28	Q6mu28 mycoplasma	672	5	35.7	262	2	Q8QHK3	Q8qhk3 crocalus at
600	5	35.7	254	2	Q88DG3	Q88dg3 pseudomonas	673	5	35.7	263	2	Q98BD9	Q98bd9 rhizobium l
601	5	35.7	255	1	VSPA_BOTAT	P04971 bothrops at	674	5	35.7	263	2	Q6LLH2	Q6llh2 photobacter
602	5	35.7	255	2	Q8T5W3	Q8t5w3 methanosarc	675	5	35.7	264	2	Q7Q5I3	Q7q5i3 anopheles g
603	5	35.7	255	2	Q9BZ16	Q9bz16 homo sapien	676	5	35.7	264	2	Q6Z386	Q6z386 oryza sativ
604	5	35.7	255	2	Q6YQ34	Q6yq34 onion yello	677	5	35.7	264	2	Q88IL0	Q88il0 pseudomonas
605	5	35.7	256	2	Q81B17	Q81b17 plasmodium	678	5	35.7	265	2	Q9RIE1	Q9rie1 yersinia pe
606	5	35.7	257	1	VSP1_TRIMU	Q91507 trimeresuru	679	5	35.7	265	2	Q98SR5	Q98sr5 neospora ca
607	5	35.7	257	1	VSP2_BOTJA	O13069 bothrops ja	680	5	35.7	266	1	1433_NEOCA	Q25538 tabacco ca
608	5	35.7	257	1	VSP2_TRIMU	Q91508 trimeresuru	681	5	35.7	266	1	MOV_P_TMGW	P18338 tabacco mil
609	5	35.7	257	1	VSP3_AGKAC	Q918x0 agkistrodon	682	5	35.7	266	2	Q60955	Q60955 toxoplasma
610	5	35.7	257	1	VSP3_TRIFL	O13058 trimeresuru	683	5	35.7	266	2	Q8G053	Q8g053 bruceella su
611	5	35.7	257	1	VSP3_TRIMU	Q91509 trimeresuru	684	5	35.7	267	1	HDHA_CLOSO	P50200 clostridium
612	5	35.7	257	1	VSP4_TRIMU	Q91510 trimeresuru	685	5	35.7	267	2	Q7Q4H6	Q7q4h6 anopheles g
613	5	35.7	257	1	VSP5_TRIMU	Q91511 trimeresuru	686	5	35.7	268	2	Q89TW7	Q89tw7 bradyrhizob
614	5	35.7	257	1	VSP7_TRIMU	Q9DG84 trimeresuru	687	5	35.7	269	2	Q8PWN6	Q8pwn6 methanoearc
615	5	35.7	257	2	Q9SNV4	Q9snv4 antirrhinum	688	5	35.7	269	2	O15781	O15781 babesia bov

689	5	35.7	269	2	Q8KK72	Q8kk72 proteus vul	762	5	35.7	294	2	Q9R8S4	Q9r8s4 rhizobium s
690	5	35.7	269	2	Q7UBG4	Q7ubg4 shigella fl	763	5	35.7	294	2	Q9R8T0	Q9r8t0 rhizobium s
691	5	35.7	269	2	Q87M90	Q87m90 vibrio para	764	5	35.7	294	2	Q8FDB0	Q8fdb0 escherichia
692	5	35.7	269	2	Q87R24	Q87r24 vibrio para	765	5	35.7	295	2	Q6LXA8	Q6lxa8 methanococc
693	5	35.7	269	2	Q8VZ73	Q8vz73 canarypox v	766	5	35.7	295	2	Q9P4T9	Q9p4t9 agaricus bi
694	5	35.7	270	1	DAPF_RICCN	Q92141 rickettsia	767	5	35.7	295	2	Q9R8S9	Q9r8s9 rhizobium s
695	5	35.7	270	2	Q6UA71	Q6ua71 flavobacter	768	5	35.7	295	2	Q6NFK5	Q6nfk5 corynebacte
696	5	35.7	270	2	Q7PBT8	Q7pbt8 rickettsia	769	5	35.7	296	2	Q6FRK5	Q6frk5 candida gla
697	5	35.7	270	2	Q8YXL4	Q8yxl4 anabaena sp	770	5	35.7	296	2	Q77092	Q77092 plasmodium
698	5	35.7	270	2	Q8F9S8	Q8f9s8 acinetobact	771	5	35.7	296	2	Q7RI03	Q7ri03 plasmodium
699	5	35.7	271	2	Q83JH8	Q83jh8 shigella fl	772	5	35.7	296	2	Q9VGJ9	Q9vgj9 drosophila
700	5	35.7	272	1	T2AL_RUEGB	Q9khv6 rugeria ge	773	5	35.7	296	2	Q9R8S9	Q9r8s9 rhizobium s
701	5	35.7	272	2	Q93WT1	Q93wt1 sorghum bic	774	5	35.7	296	2	Q9Z3I8	Q9z3i8 rhizobium s
702	5	35.7	272	2	Q8CEY2	Q8cey2 mus musculu	775	5	35.7	296	2	Q9Z3J0	Q9z3j0 rhizobium s
703	5	35.7	273	2	Q8KC15	Q8kc15 chlorobium	776	5	35.7	296	2	Q9Z3J3	Q9z3j3 rhizobium s
704	5	35.7	273	2	Q72U20	Q72u20 leptospira	777	5	35.7	296	2	Q8YHR2	Q8yhr2 brucella me
705	5	35.7	273	2	Q81W84	Q81w84 bacillus an	778	5	35.7	297	2	Q94M25	Q94m25 haemophilus
706	5	35.7	274	2	Q6CS09	Q6cs09 kluyveromyc	779	5	35.7	297	2	Q8S4V5	Q8s4v5 arabidopsis
707	5	35.7	274	2	Q6SAR1	Q6sar1 yerisinia pe	780	5	35.7	297	2	Q9R8S6	Q9r8s6 rhizobium s
708	5	35.7	275	2	Q44584	Q44584 caenorhabdi	781	5	35.7	297	2	Q9Z3J2	Q9z3j2 rhizobium s
709	5	35.7	275	2	Q8MNJ5	Q8mnj5 dictyosteli	782	5	35.7	297	2	Q6F9E6	Q6f9e6 acinetobact
710	5	35.7	276	2	Q97WJ4	Q97wj4 sulfobus	783	5	35.7	297	2	Q83BY6	Q83by6 coxiella bu
711	5	35.7	276	2	Q6CHD9	Q6chd9 yarrowia li	784	5	35.7	297	2	Q8R2D3	Q8r2d3 mus musculu
712	5	35.7	276	2	Q9RFT6	Q9rft6 mesorhizobi	785	5	35.7	298	1	VPO_BPHP1	P51719 bacterioph
713	5	35.7	276	2	Q9RFT7	Q9rft7 mesorhizobi	786	5	35.7	298	2	Q8UR76	Q8ur76 agrobacteri
714	5	35.7	276	2	Q9RFT8	Q9rft8 mesorhizobi	787	5	35.7	299	2	Q82EP3	Q82ep3 streptomyce
715	5	35.7	276	2	Q8PA04	Q8paq4 xanthomonas	788	5	35.7	300	2	Q8R7E5	Q8r7e5 thermocnaer
716	5	35.7	276	2	Q8PMG1	Q8pmg1 xanthomonas	789	5	35.7	300	2	Q6K1B4	Q6k1b4 mycoplasma
717	5	35.7	276	2	Q87DC9	Q87dc9 xyella fas	790	5	35.7	300	2	Q883B5	Q883b5 pseudomonas
718	5	35.7	276	2	Q993Y9	Q993y9 clostridium	791	5	35.7	300	2	Q89ME0	Q89me0 bradyrhizob
719	5	35.7	276	2	Q8EUB1	Q8eub1 mycoplasma	792	5	35.7	301	1	PAL_POLAN	Q9u6w0 polistes an
720	5	35.7	276	2	Q9HXC9	Q9hxc9 pseudomonas	793	5	35.7	302	2	Q6FW12	Q6fw12 candida gla
721	5	35.7	276	2	Q9PD34	Q9pd34 xyella fas	794	5	35.7	302	2	Q7UFJ5	Q7ufj5 rhodopirell
722	5	35.7	278	2	Q7RV73	Q7rv73 neorospira	795	5	35.7	303	2	Q8LPM8	Q8lpm8 arabidopsis
723	5	35.7	278	2	Q6F8B1	Q6f8b1 acinetobact	796	5	35.7	303	2	Q30377	Q30377 aeromonas s
724	5	35.7	280	2	Q6PA84	Q6pa84 xenopus lae	797	5	35.7	304	2	Q6BXX8	Q6bxx8 debaryomyce
725	5	35.7	281	2	Q8BTB0	Q8btb0 mus musculu	798	5	35.7	304	2	Q7P4N4	Q7p4n4 fusobacteri
726	5	35.7	282	2	Q8CAG7	Q8cag7 mus musculu	799	5	35.7	305	2	Q812K2	Q812k2 plasmodium
727	5	35.7	283	2	Q8QFQ2	Q8qfq2 xenopus lae	800	5	35.7	305	2	Q84QG4	Q84qg4 arabidopsis
728	5	35.7	283	2	Q8S4V6	Q8s4v6 arabidopsis	801	5	35.7	305	2	Q9C719	Q9c719 arabidopsis
729	5	35.7	283	2	Q8DM81	Q8dm81 rat cytomeg	802	5	35.7	305	2	Q764A2	Q764a2 helicobacte
730	5	35.7	284	1	PUR7_CHRVO	Q7p1p8 chromobacte	803	5	35.7	306	2	Q86H28	Q86h28 dictyosteli
731	5	35.7	284	2	Q9R8S7	Q9r8s7 rhizobium s	804	5	35.7	307	1	TF2B_METKA	Q8tx21 methanopyru
732	5	35.7	284	2	Q9EWP8	Q9ewp8 streptomyce	805	5	35.7	307	2	Q6LIG4	Q6lig4 photobacter
733	5	35.7	285	2	Q8QFQ2	Q8qfq2 xenopus lae	806	5	35.7	308	2	Q8R2C7	Q8r2c7 mus musculu
734	5	35.7	286	2	Q8S4V6	Q8s4v6 arabidopsis	807	5	35.7	308	2	Q91TS5	Q91ts5 tupaiid her
735	5	35.7	287	1	PUR7_NEIMA	Q91v73 neisseria m	808	5	35.7	309	2	Q8S484	Q8s484 sea mayas (m
736	5	35.7	287	1	PUR7_NEIMB	Q9k063 neisseria m	809	5	35.7	309	2	Q68S26	Q68s26 hepatitis c
737	5	35.7	287	2	Q72E00	Q7zeu0 desulfovibr	810	5	35.7	310	2	Q9SHR6	Q9shr6 arabidopsis
738	5	35.7	288	2	Q881W5	Q881w5 pseudomonas	811	5	35.7	310	2	Q7UNSG	Q7uns6 rhodopirell
739	5	35.7	288	2	Q97S28	Q97s28 streptococc	812	5	35.7	312	1	MCAL_HUMAN	Q12904 homo sapien
740	5	35.7	288	2	Q9ZM23	Q9zm23 helicobacte	813	5	35.7	312	2	Q6G1P0	Q6g1p0 bartonella
741	5	35.7	289	1	EX53_AQUAE	Q87550 aquifex aeo	814	5	35.7	313	2	Q65ZK4	Q65z2k4 caenorhabdi
742	5	35.7	289	1	THTR_CHICK	P25324 gallus gall	815	5	35.7	313	2	Q9ZH27	Q9zh27 thioacallu
743	5	35.7	289	2	Q97WF2	Q97wf2 sulfolobus	816	5	35.7	313	2	Q97ND7	Q97nd7 streptococc
744	5	35.7	289	2	Q6GN00	Q6gn00 xenopus lae	817	5	35.7	313	2	Q8DN48	Q8dn48 streptococc
745	5	35.7	290	2	Q8PSW4	Q8psw4 methanosaar	818	5	35.7	314	2	Q6WAU1	Q6wau1 mentha pipe
746	5	35.7	290	2	Q8YTU4	Q8ytu4 anabaena sp	819	5	35.7	315	2	Q8TMV8	Q8tmv8 methanosaar
747	5	35.7	290	2	Q8CRP9	Q8crr9 staphylococ	820	5	35.7	315	2	Q7R9Y8	Q7r9y8 plasmodium
748	5	35.7	290	2	Q8UIK2	Q8uik2 agrobacteri	821	5	35.7	315	2	Q75GR3	Q75gr3 oryza sativ
749	5	35.7	291	2	Q9HKW7	Q9hk7 thermoplasm	822	5	35.7	316	1	LORI_HUMAN	P23490 homo sapien
750	5	35.7	291	2	Q72LR5	Q72lr5 leptospira	823	5	35.7	316	2	Q6PHY3	Q6phy3 homo sapien
751	5	35.7	291	2	Q89L69	Q89l69 bradyrhizob	824	5	35.7	316	2	Q6Q249	Q6q249 polistes do
752	5	35.7	291	2	Q8EY71	Q8ey71 leptospira	825	5	35.7	316	2	Q6Q250	Q6q250 polistes do
753	5	35.7	292	2	Q8KIQ2	Q8kiq2 escherichia	826	5	35.7	316	2	Q6Q251	Q6q251 polistes do
754	5	35.7	292	2	Q85FX0	Q85fx0 bacillus li	827	5	35.7	316	2	Q86FA4	Q86fa4 drosophila
755	5	35.7	292	2	Q8XAC6	Q8xac6 escherichia	828	5	35.7	316	2	Q89ER1	Q89er1 bradyrhizob
756	5	35.7	293	1	PUR7_BORBR	Q7wml1 bordetella	829	5	35.7	317	2	Q6KZQ1	Q6kzq1 picropophilus
757	5	35.7	293	1	PUR7_BORPA	Q7wb15 bordetella	830	5	35.7	317	2	Q41681	Q41681 vigna radia
758	5	35.7	293	1	PUR7_BORPE	Q7vy42 bordetella	831	5	35.7	317	2	Q7FY62	Q7fy62 phaseolus a
759	5	35.7	293	2	Q9R8T1	Q9r8t1 rhizobium s	832	5	35.7	317	2	Q89V25	Q89v25 bradyrhizob
760	5	35.7	294	1	ATHB_MOUSE	P50992 mus musculu	833	5	35.7	317	2	Q9KM71	Q9km71 vibrio chol
761	5	35.7	294	1	GGFP_BOVIN	P56966 b geranylige	834	5	35.7	317	2	Q8UBZ1	Q8ubz1 agrobacteri

835	5	35.7	318	2	Q8THP8	Q8thp8 methanosarc	908	5	35.7	337	2	Q6GIL9	Q6gil9 staphylococ
836	5	35.7	318	2	Q9HRU5	Q9hrus halobacteri	909	5	35.7	337	2	Q6HLI8	Q6hli8 bacillus th
837	5	35.7	318	2	Q7R5B5	Q7r5b5 giardia lam	910	5	35.7	338	2	Q8TU08	Q8tu08 methanosarc
838	5	35.7	318	2	Q7R5B5	Q7r5b5 giardia lam	911	5	35.7	338	2	Q6O354	Q6o354 homo sapien
839	5	35.7	319	2	Q82QC8	Q82nd5 streptomyce	912	5	35.7	339	2	Q92V85	Q92ve5 rhizobium m
840	5	35.7	319	2	Q6N0V4	Q6n0v4 rhodopseudo	913	5	35.7	339	2	Q6GLG8	Q6glg8 xenopus tro
841	5	35.7	319	2	Q88GL5	Q88gl5 pseudomonas	914	5	35.7	340	2	Q7QPD1	Q7qpd1 anopheles g
842	5	35.7	319	2	Q8BNC2	Q8bk2 oceanobacil	915	5	35.7	340	2	Q33352	Q33352 chorthippus
843	5	35.7	320	2	Q7QWQ8	Q7qwq8 giardia lam	916	5	35.7	340	2	Q33355	Q33355 chorthippus
844	5	35.7	320	2	Q9CAA2	Q9caa2 arabidopsis	917	5	35.7	340	2	Q8ZK50	Q8zk50 salmonella
845	5	35.7	320	2	Q66JE7	Q66je7 xenopus tro	918	5	35.7	340	2	Q6FFV7	Q6ffv7 acinetobact
846	5	35.7	321	2	Q7D3J2	Q7d3j2 agrobacteri	919	5	35.7	341	1	Q6FFV7	Q6ffv7 acinetobact
847	5	35.7	322	2	Q97V31	Q97v31 sulfolobus	920	5	35.7	341	1	Q6FFV7	Q6ffv7 acinetobact
848	5	35.7	322	2	Q6H890	Q6h890 oryza sativ	921	5	35.7	341	1	Q6FFV7	Q6ffv7 acinetobact
849	5	35.7	322	2	Q8HIM6	Q8him6 arabidopsis	922	5	35.7	342	1	Q6GIL9	Q6gil9 staphylococ
850	5	35.7	322	2	Q9LEZ7	Q9lez7 arabidopsis	923	5	35.7	342	2	Q6IGS7	Q6igs7 drosophila
851	5	35.7	322	2	Q92Q36	Q92q36 arabidopsis	924	5	35.7	343	2	Q898X0	Q898x0 clostridium
852	5	35.7	322	2	Q6LPV9	Q6lpv9 photobacter	925	5	35.7	344	1	Q6O354	Q6o354 homo sapien
853	5	35.7	322	2	Q6DIB3	Q6dib3 mus musculu	926	5	35.7	344	2	Q28906	Q28906 archaeoglob
854	5	35.7	322	2	Q6R256	Q6r256 carassius a	927	5	35.7	344	2	Q7Y4E8	Q7y4e8 bacterioph
855	5	35.7	323	2	Q8KDU7	Q8kdj7 chlorobium	928	5	35.7	344	2	Q858W8	Q858w8 bacterioph
856	5	35.7	323	2	Q99H22	Q99h22 helicoverpa	929	5	35.7	344	2	Q9X5D5	Q9x5d5 zymomonas m
857	5	35.7	323	2	Q77K94	Q77k94 helicoverpa	930	5	35.7	345	2	Q8UCR7	Q8ucr7 agrobacteri
858	5	35.7	323	2	Q77LY8	Q77ly8 helicoverpa	931	5	35.7	345	2	Q9VQM9	Q9vqm9 drosophila
859	5	35.7	324	2	Q6IAC9	Q6iac9 homo sapien	932	5	35.7	345	2	Q87J59	Q87j59 vibrio para
860	5	35.7	324	2	Q8EX47	Q8ex47 drosophila	933	5	35.7	346	2	Q6M0N8	Q6m0n8 methanococ
861	5	35.7	324	2	Q9S0M3	Q9s0m3 staphylococ	934	5	35.7	346	2	Q50068	Q50068 arabidopsis
862	5	35.7	324	2	Q90X98	Q9qx98 mus musculu	935	5	35.7	346	2	Q8C4C2	Q8c4c2 mus musculu
863	5	35.7	324	2	Q90YF5	Q9qyf5 mus musculu	936	5	35.7	347	2	Q703W7	Q703w7 thermoprote
864	5	35.7	325	2	Q6Z057	Q6z057 oryza sativ	937	5	35.7	347	2	Q8T651	Q8t651 giardia lam
865	5	35.7	326	2	Q970C6	Q970c6 sulfolobus	938	5	35.7	347	2	Q891X4	Q891x4 clostridium
866	5	35.7	327	2	Q8PSH1	Q8psh1 methanosarc	939	5	35.7	350	1	Q8N543	Q8n543 corynebacte
867	5	35.7	327	2	Q9V4C4	Q9v4c4 drosophila	940	5	35.7	351	2	Q8UYW9	Q8uyw9 aequifex aeo
868	5	35.7	327	2	Q9VAL1	Q9val1 drosophila	941	5	35.7	351	2	Q6PM50	Q6pm50 tomato yell
869	5	35.7	327	2	Q94CX3	Q94cx3 oryza sativ	942	5	35.7	351	2	Q709N7	Q709n7 indian caes
870	5	35.7	328	1	GALE_CORDI	Q94cx3 oryza sativ	943	5	35.7	351	2	Q7T6E9	Q7t6e9 sri lankan
871	5	35.7	328	2	Q86X73	P33119 corynebacte	944	5	35.7	352	2	Q8THN6	Q8thn6 methanosarc
872	5	35.7	328	2	Q8LIN3	Q8lin3 trypanosoma	945	5	35.7	352	2	Q8RG15	Q8rg15 fusobacteri
873	5	35.7	328	2	Q8FPG5	Q8fpg5 corynebacte	946	5	35.7	352	2	Q8XL25	Q8xl25 clostridium
874	5	35.7	329	2	Q27459	Q27459 methanobact	947	5	35.7	353	2	Q7PR97	Q7pr97 anopheles g
875	5	35.7	329	2	Q8S4V7	Q8s4v7 arabidopsis	948	5	35.7	353	2	Q7QED4	Q7qed4 anopheles g
876	5	35.7	329	2	Q9L7P3	Q9l7p3 rhodococcus	949	5	35.7	353	2	Q9FR28	Q9fr28 petroselinu
877	5	35.7	330	2	Q8TMU0	Q8tmu0 methanosarc	950	5	35.7	353	2	Q6L673	Q6l673 alysiya cal
878	5	35.7	330	2	Q9VQNO	Q9vqno drosophila	951	5	35.7	354	2	Q6RCU6	Q6rcu6 pepper yell
879	5	35.7	331	1	TR38_MOUSE	Q7tqa6 mus musculu	952	5	35.7	354	2	Q6RCU6	Q6rcu6 pepper yell
880	5	35.7	331	2	P73723	P73723 synecocyst	953	5	35.7	354	2	Q9IN42	Q9in42 south afric
881	5	35.7	331	2	Q67ES4	Q67es4 rattus norv	954	5	35.7	356	2	Q96B14	Q96b14 homo sapien
882	5	35.7	332	2	Q43977	Q43977 babesia bov	955	5	35.7	356	2	Q655L6	Q655l6 oryza sativ
883	5	35.7	333	2	Q8TKV5	Q6tkv5 escherichia	956	5	35.7	356	2	Q668H0	Q668h0 yersinia ps
884	5	35.7	333	2	Q8M0J6	Q8m0j6 methanococc	957	5	35.7	357	1	CYSA_BACC1	Q8zce3 yersinia pe
885	5	35.7	334	2	Q8HWA3	Q8hwa3 mus musculu	958	5	35.7	357	1	CYSA_BACC1	Q8igul bacillus ce
886	5	35.7	334	2	Q8D205	Q8d205 mus musculu	959	5	35.7	357	2	Q9DJP9	Q9djp9 citrui tris
887	5	35.7	334	2	Q8D205	P63475 staphylococ	960	5	35.7	358	2	Q6GP68	Q6gp68 xenopus lae
888	5	35.7	335	1	ZDH1_STAAM	P93173 staphylococ	961	5	35.7	359	1	VAL1_TYLCU	P27260 tomato yell
889	5	35.7	335	1	ZDH1_STAAM	P93173 staphylococ	962	5	35.7	359	1	VAL1_TYLCU	P38609 tomato yell
890	5	35.7	335	2	Q9F5Q8	Q9f5q8 vibrio chol	963	5	35.7	359	2	Q8JNF1	Q8jnf1 tomato leaf
891	5	35.7	336	2	Q91HQ5	Q91hq5 hepatitis c	964	5	35.7	359	2	Q8JNF7	Q8jnf7 tomato yell
892	5	35.7	336	2	Q7S6P4	Q7s6p4 neurospora	965	5	35.7	359	2	Q8JNG3	Q8jng3 tomato leaf
893	5	35.7	336	2	Q82TS2	Q82ts2 rhizobium m	966	5	35.7	359	2	Q8JVE8	Q8jve8 tomato curl
894	5	35.7	337	2	Q8PX57	Q8px57 methanosarc	967	5	35.7	359	2	Q8UYT3	Q8uyt3 south afric
895	5	35.7	337	2	Q77324	Q77324 plasmodium	968	5	35.7	359	2	Q8V380	Q8v380 east africa
896	5	35.7	337	2	Q6Q252	Q6q252 polistes do	969	5	35.7	359	2	Q91B86	Q91b86 ageratum ye
897	5	35.7	337	2	Q63E13	Q63e13 bacillus ce	970	5	35.7	359	2	Q91M88	Q91m88 tobacco lea
898	5	35.7	337	2	Q61W70	Q61w70 photobacter	971	5	35.7	359	2	Q66UV7	Q66uv7 tomato yell
899	5	35.7	337	2	Q73BB1	Q73bb1 bacillus ce	972	5	35.7	359	2	Q67620	Q67620 tomato yell
900	5	35.7	337	2	Q7A1F6	Q7a1f6 staphylococ	973	5	35.7	359	2	Q6RCV2	Q6rcv2 tomato yell
901	5	35.7	337	2	Q7A2U8	Q7a2u8 staphylococ	974	5	35.7	359	2	Q764D4	Q764d4 tomato yell
902	5	35.7	337	2	Q7A6Q3	Q7a6q3 staphylococ	975	5	35.7	359	2	Q764E0	Q764e0 tomato yell
903	5	35.7	337	2	Q81G49	Q81g49 bacillus ce	976	5	35.7	359	2	Q764E6	Q764e6 tomato yell
904	5	35.7	337	2	Q81TA8	Q81ta8 bacillus an	977	5	35.7	359	2	Q764F2	Q764f2 tomato yell
905	5	35.7	337	2	Q8CPY6	Q8cpy6 staphylococ	978	5	35.7	359	2	Q764F8	Q764f8 tomato yell
906	5	35.7	337	2	Q8Z5C6	Q8z5c6 staphylococ	979	5	35.7	359	2	Q76C58	Q76c58 tomato yell
907	5	35.7	337	2	Q6GB59	Q6gb59 staphylococ	980	5	35.7	359	2	Q77W92	Q77w92 tomato yell

981 5 35.7 359 2 Q7TAT2 Q7tat2 south afric
 982 5 35.7 359 2 Q88942 Q88942 tomato yell
 983 5 35.7 359 2 Q88942 Q88942 tomato yell
 984 5 35.7 359 2 Q8B2Y2 Q8b2y2 tomato yell
 985 5 35.7 359 2 Q8B6S5 Q8b6s5 tomato yell
 986 5 35.7 359 2 Q8B8M8 Q8b8m8 east africa
 987 5 35.7 359 2 Q9YU7 Q9yux7 tomato yell
 988 5 35.7 359 2 Q9YU7 Q9yux7 tomato yell
 989 5 35.7 359 2 Q9YU7 Q9yux7 tomato yell
 990 5 35.7 359 2 Q9YU7 Q9yux7 tomato yell
 991 5 35.7 360 1 Q9YU7 Q9yux7 tomato yell
 992 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 993 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 994 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 995 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 996 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 997 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 998 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 999 5 35.7 360 2 Q9YU7 Q9yux7 tomato yell
 1000 5 35.7 361 2 Q9YU7 Q9yux7 tomato yell

ALIGNMENTS

RESULT 1
 CYCIN HUMAN
 ID CYCIN HUMAN STANDARD; PRT; 377 AA.
 AC Q14094; (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Cyclin I.
 CN Name=CCNI;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Forebrain cortex;
 RX MEDLINE=96086776; PubMed=7493655; DOI=10.1006/excr.1995.1406;
 RA Nakamura T., Sanokawa R., Sasaki Y.F., Ayusawa D., Oishi M., Mori N.;
 RT "Cyclin I: a new cyclin encoded by a gene isolated from human brain.";
 RL Exp. Cell Res. 221:534-542(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Chen J.H., Luo W.Q., Zhou Y., Zhou H.J., Huang X.W., Yuan J.G.,
 RA Qiang B.Q.;
 RT "Isolating a new cDNA coding for human cyclin protein.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT ILE-207.
 RA Kieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
 RA Miyamoto K.E., Nguyen D.A., Poel C.L., Robertson P.D.,
 RA Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RT "NIHES-SNP, environmental genome project, NIHES ES15478, Department
 of Genome Sciences, Seattle, WA (URL: <http://legp.gs.washington.edu>).";
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Muscle;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 FAhey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP SEQUENCE OF 1-178 FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=98381026; PubMed=9705831; DOI=10.1006/bbrc.1998.9052;
 RA Zhu X., Naz R.K.;
 RT "Expression of a novel isoform of cyclin I in human testis.";
 RL Biochem. Biophys. Res. Commun. 249:56-60(1998).
 CC -I- TISSUE SPECIFICITY: Highest levels in adult heart, brain and
 skeletal muscle. Lower levels in adult placenta, lung, kidney and
 pancreas. Also high levels in fetal brain and lower levels in
 fetal lung, liver and kidney. Also abundant in testis and thyroid.
 CC -I- DEVELOPMENTAL STAGE: Expression is independent of the cell cycle
 in lung fibroblasts.
 CC -I- SIMILARITY: Belongs to the cyclin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (see <http://www.isb-sib.ch/announcement/>
 or send an email to license@isb-sib.ch).
 CC EMBL; D50310; BAA08849.1; -
 CC EMBL; AY207372; AA013492.1; -
 CC EMBL; BC000420; AA00420.1; -
 CC EMBL; BC004975; AA04975.1; -
 CC EMBL; AF135162; AAF43786.1; -
 CC PIR; JE0264; JE0264.
 CC Genew; HGNC:1595; CCNI.
 CC H-InvDB; HIX0004313; -
 CC GO; GO:0007283; P: spermatogenesis; NAS.
 CC InterPro; IPR006670; Cyclin.
 CC InterPro; IPR011028; Cyclin like.
 CC InterPro; IPR006671; Cyclin_N.
 CC Pfam; PF00134; Cyclin_N; 1.
 CC SMART; SM00385; CYCLIN; 1.
 CC PROSITE; PS00292; CYCLINS; FALSE_NEG.
 KW Cyclin; Polymorphism.
 FT VARIANT 207 207 V -> I (in dbSNP:4252903).
 FT CONFLICT 9 9 N -> D (in Ref. 5).
 FT CONFLICT 58 58 Q -> R (in Ref. 5).
 FT CONFLICT 75 75 R -> G (in Ref. 5).
 SQ SEQUENCE 377 AA; 42557 MW; 2DE84EFA/4698F6C CRC64;
 Query Match 100.0%; Score 14; DB 1; Length 377;
 Best Local Similarity 100.0%; Pred. No. 5.4e-07;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EDNVSENVGVCVT 14
 Db 343 EDNVSENVGVCVT 356
 RESULT 2
 Q6FHH0 PRELIMINARY; PRT; 377 AA.
 ID Q6FHH0
 AC Q6FHH0 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CCNI protein (Fragment).

GN Name=CCNI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
RA Neubert P., Kstrang K., Schatten R., Shen B., Henze S., Mar W.,
RA Korn B., Zuo D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the cyclin family.
DR EMBL, CR541783; CAG46582.1; -;
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN_N; 1.
DR Cyclin.
KW NON TER 377 377
SQ SEQUENCE 377 AA; 42486 MW; D950A5CCF0D0F514 CRC64;
Query Match 100.0%; Score 14; DB 2; Length 377;
Best Local Similarity 100.0%; Pred.No. 5.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EDNVSENVSVCGT 14
Db 343 EDNVSENVSVCGT 356
|||||
RESULT 3
CYCI_MOUSE
ID CYCI_MOUSE STANDARD; PRT; 377 AA.
AC Q923V9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Cyclin I.
GN Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99172101; PubMed=10072591;
RA Jensen M.R., Audolfsson T., Keck C.L., Zimonjic D.B.,
RA Thorgerirsson S.S.;
RT "Assignment of the cyclin I gene (Ccni) to mouse chromosome 5E3.3-F1.
RT 3 by in situ hybridization.";
RL Cytogenet. Cell Genet. 83:242-243(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20509992; PubMed=11054536; DOI=10.1016/S0378-1119(00)00361-9;
RA Jensen M.R., Audolfsson T., Factor V.M., Thorgerirsson S.S.;
RT "In vivo expression and genomic organization of the mouse cyclin I
RT gene (Ccni).";
RL Gene 256:59-67(2000).
CC -1- SIMILARITY: Belongs to the cyclin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF005886; AAD01253.2; -;
DR EMBL; AF228740; AAF43391.1; -;
DR EMBL; AF228739; AAF43391.1; JOINED.
DR MGD; MGI:1341077; Ccni.

DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin_like.
DR Pfam; PF00134; Cyclin_N.
DR SMART; SM00385; CYCLIN_N; 1.
DR PROSITE; PS00292; CYCLINS; FALSE_NEG.
KW Cyclin.
SQ SEQUENCE 377 AA; 42261 MW; 4151141C6D9AB677 CRC64;
Query Match 64.3%; Score 9; DB 1; Length 377;
Best Local Similarity 100.0%; Pred.No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 ENVSVCVT 14
Db 348 ENVSVCVT 356
|||||
RESULT 4
Q8C7E2
ID Q8C7E2 PRELIMINARY; PRT; 377 AA.
AC Q8C7E2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult pancreas islet cells cDNA, Riken full-length
DE enriched library, clone:C820001G04 product:cyclin I, full insert
DE sequence.
DE Name=Ccni;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanaki M.,


```

RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayaishizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayaishizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; AK050465; BAC34271.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42206 MW; A1B803EBE135B0E8 CRC64;

Query Match 64.3%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ENVGSVCGT 14
DB 348 ENVGSVCGT 356

RESULT 5
Q99LF2 PRELIMINARY; PRT; 377 AA.
AC Q99LF2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Cyclin I.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,

```

```

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the cyclin family.
DR EMBL; BC003290; AAH03290.1; -.
DR MGD; MGI:1341077; Ccni.
DR GO; GO:0000074; P:regulation of cell cycle; TAS.
DR InterPro; IPR006670; Cyclin.
DR InterPro; IPR011028; Cyclin like.
DR InterPro; IPR006671; Cyclin_N.
DR Pfam; PF00134; Cyclin_N; 1.
DR SMART; SM00385; CYCLIN; 1.
KW Cyclin.
SQ SEQUENCE 377 AA; 42227 MW; FDA2D896A5366A9F CRC64;

Query Match 64.3%; Score 9; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 ENVGSVCGT 14
DB 348 ENVGSVCGT 356

RESULT 6
Q6BXL7 PRELIMINARY; PRT; 600 AA.
AC Q6BXL7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Debaryomyces hansenii chromosome B of strain CBS767 of Debaryomyces
DE hansenii.
GN ORFNames=DEHA0801958g;
OS Debaryomyces hansenii CBS767.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Debaryomyces.
OX NCBI_TaxID=284592;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neugeglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swenne D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS767;
RG Genoscope;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; CR382134; CAG85038.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR InterPro; IPR001357; BRCT.

```

```

DR InterPro; IPR010613; Pescadillo.N.
DR Pfam; PF00533; BRCT; 1.
DR Pfam; PF06732; Pescadillo.N; 1.
DR SMART; SMO0292; BRCT; 1.
DR PROSITE; PS01072; BRCT; 1.
SQ SEQUENCE 600 AA; 68399 MW; 028055D2B9277B42 CRC64;

Query Match 57.1%; Score 8; DB 2; Length 600;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EDNVSENV 8
Db 316 EDNVSENV 323
|||||

RESULT 7
ID Q8SVJ3 PRELIMINARY; PRT; 310 AA.
AC Q8SVJ3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE RS66714p.
GN ORFNames=CG14855;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkely;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celisner S.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
DR EMBL; AY071512; AAL49134.1; -.
DR FlyBase; FBgn0038260; CG14855.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR InterPro; IPR005828; Sub transporter.
DR Pfam; PF00083; Sugar_tr_1.
DR PROSITE; PS00850; MFS; 1.
KW Transmembrane.
SQ SEQUENCE 310 AA; 35861 MW; 0A6475F0154AF711 CRC64;

Query Match 50.0%; Score 7; DB 2; Length 310;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 VGSVCVT 14
Db 131 VGSVCVT 137
|||||

RESULT 8
ID Q8GP73 PRELIMINARY; PRT; 423 AA.
AC Q8GP73;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Eps10G.
GN Name=eps10G;
OS Streptococcus thermophilus.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```

```

OC Streptococcus.
OX NCBI_TaxID=1308;
RN [1]
RP SEQUENCE FROM N.A.
RA Rallu F., Ehrlich D.S., Renault P.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF454500; AAN63767.1; -.
SQ SEQUENCE 423 AA; 49055 MW; B9C9BF6895D6DACC CRC64;

Query Match 50.0%; Score 7; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVGS 10
Db 366 VSENVGS 372
|||||

RESULT 9
ID Q9AH92 PRELIMINARY; PRT; 423 AA.
AC Q9AH92;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE WciU.
GN Name=wciU;
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21116929; PubMed=11179285;
RX DOI=10.1128/IAI.69.3.1244-1255.2001;
RA Jiang S.M., Wang L., Reeves P.R.;
RT "Molecular characterization of Streptococcus pneumoniae type 4, 6B, 8,
RT and 18c capsular polysaccharide gene clusters.";
RL Infect. Immun. 69:1244-1255(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA Jiang S.-M., Wang L., Reeves P.R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF316642; AAK20713.1; -.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 423 AA; 532A56D861ED1C4 CRC64;

Query Match 50.0%; Score 7; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VSENVGS 10
Db 366 VSENVGS 372
|||||

RESULT 10
ID YP33 YEAST STANDARD; PRT; 446 AA.
AC P19541;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative transcriptional regulatory protein YPL133C.
GN OrderedLocusNames=YPL133C; ORFNames=LPI12C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;

```

RA Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansong W.,
RA Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA Dietrich F.S., Delius H., Dipaolo T., Dubois E., Duesterhoeft A.,
RA Duncan M., Floeth M., Fortin N., Friese J.D., Fritz C., Goffeau A.,
RA Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.W.,
RA Hunnicke-Smith S., Hyman R., Johnston M., Kalman S., Kleine K.,
RA Komp C., Kurdi O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA Marathe R., Messing F., Mewes H.-W., Mirtipati S., Moestl D.,
RA Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,
RA Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharfe M.,
RA Scherens B., Schramm S., Schroeder M., Sdicu A.M., Tettelin H.,
RA Urrestazu L.A., Ushinsky S., Vierdeels F., Vissers S., Voss H.,
RA Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,
RA Zhong W.W., Zollner A., Vo D.H., Hani J.,
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI,"
RL Nature 387:103-105 (1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c;
RA Marsischky G., Rolfs A., Richardson A., Kane M., Baqui M., Taycher E.,
RA Hu Y., Vamberg E., Weger J., Kramer J., Moreira D., Kelley F.,
RA Zuo D., Raphael J., Hogle C., Jepson D., Williamson J., Camargo A.,
RA Gonzaga L., Vasconcelos A.T., Simpson A., Kolodner R., Harlow E.,
RA LaBaer J.;
RT "Creation of the YFLEX clone resource: cloning of Saccharomyces
RT cerevisiae ORFs in the Gateway recombinational cloning system,"
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-95 FROM N.A.
RX MEDLINE=90360986; PubMed=2167832;
RA Tzagoloff A., Capitano N., Nobrega M.P., Gatti D.;
RT "Cytochrome oxidase assembly in yeast requires the product of COX11, a
RT homolog of the P. denitrificans protein encoded by ORF3,"
RL EMBL J. 9:2759-2764 (1990).
RN [4]
RP PRESENCE OF A ZN(2)-CYS(6) FUNGAL-TYPE BINUCLEAR CLUSTER.
RX MEDLINE=93284106; PubMed=1304897;
RA Borik P., Ouzounis C., Sander C., Scharf M., Schneider R.,
RA Sonhammer E.;
RT "Comprehensive sequence analysis of the 182 predicted open reading
RT frames of yeast chromosome III,"
RL Protein Sci. 1:1677-1690 (1992).
CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43703; AAB68226.1; -;
DR EMBL; AY693168; AAT93187.1; -;
DR EMBL; X55731; CAA39262.1; -;
DR PIR; S69051; S69051.
DR HSP; P12351; 1PVC.
DR InAct; P19541; -;
DR GenOnline; I44115; -;
DR SGD; S00006054; RDS2.
DR GO; GO:0005737; C:nucleus; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0003700; F:transcription factor activity; IMP.
DR GO; GO:0009410; P:response to xenobiotic stimulus; IMP.
DR InterPro; IPR000138; Fungi_Trcsrp_N.
DR InterPro; IPR000172; Zn.clus; 1.
DR Pfam; PF00172; Zn.clus; 1.
DR SMART; SM00066; GAL4; 1.
DR SMART; SM00091; PAS; 1.

DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_Cy6_FUNGAL_2; 1.
KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
KW Transcription regulation; Zinc.
FT DNA BIND 15 45 Zn(2)-Cys(6), fungal-type.
SQ SEQUENCE 446 AA; 50081 MW; C78D3632DDCC3EAO CRC64;
Query Match 50.0%; Score 7; DB 1; Length 446;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 125 VSENVGS 131
RESULT 11
Q6FJY2 PRELIMINARY; PRT; 462 AA.
ID Q6FJY2
AC Q6FJY2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Similar to sp|P19541|Saccharomyces cerevisiae YPL133c.
GN ORFNames=CAGL0M026519;
OS Candida glabrata CBS138.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=284593;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CBS138;
RG Genolevures;
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Catholico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jaumiaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts,"
RL Nature 430:35-44 (2004).
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
CC -!- SIMILARITY: Contains 1 Zn(2)-Cys(6) fungal-type binuclear cluster
CC domain.
DR EMBL; CR380959; CAG62438.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR001138; Fungi_Trcsrp_N.
DR Pfam; PF00172; Zn.clus; 1.
DR SMART; SM00066; GAL4; 1.
DR PROSITE; PS00463; ZN2_Cy6_FUNGAL_1; 1.
DR PROSITE; PS50048; ZN2_Cy6_FUNGAL_2; 1.
KW DNA-binding; Metal-binding; Nuclear protein; Transcription;
KW Transcription regulation; Zinc.
SQ SEQUENCE 462 AA; 52279 MW; 9195A1BCE41626B0 CRC64;
Query Match 50.0%; Score 7; DB 2; Length 462;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 VSENVGS 10
Db 115 VSENVGS 121

```
RESULT 12
Q9VFG2 PRELIMINARY; PRT; 556 AA.
AC
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CG14855-PA.
GN ORFNames=CG14855;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abrell J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Buesam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
RA Glöck A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.B., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam K.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskaas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scher S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence."
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskaas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective."
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review."
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RX FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003706; AAF55098.1; -.
DR IntAct; Q9VFG2; -.
DR FlyBase; FBgn0038260; CG14855.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR007114; MFS.
DR PROSITE; PS00850; MFS; 1.
SQ SEQUENCE 556 AA; 62519 MW; 0CB57217A18D35F5 CRC64;
Query Match 50.0%; Score 7; DB 2; Length 556;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 VGSVCGT 14
DB 131 VGSVCGT 137
|||||
PRELIMINARY; PRT; 1006 AA.
Q9U360
AC Q9U360;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T24A11.1b.
GN Name=ntm-3; Synonyms=T24A11.1b; ORFNames=T24A11.1;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Bristol N2;
RA Percy C.M.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z49072; CAB61017.2; -.
DR HSSP; P40343; 1VRY.
```

DR WormBase; WBGene00003476; mtm-3.
 DR WormPep; T2411.1b; CE28087.
 DR GO; GO:0004721; P:phosphoprotein phosphatase activity; IEA.
 DR GO; GO:0008270; P:zinc ion binding; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR011011; FYVE PHD Znf.
 DR InterPro; IPR010569; Myotub-related.
 DR InterPro; IPR000387; TYR phosphatase.
 DR InterPro; IPR000306; Znf_FYVE.
 DR Pfam; PF01363; FYVE; 1.
 DR Pfam; PF06602; Myotub-related; 1.
 DR SMART; SM00064; FYVE; 1.
 DR PROSITE; PS00383; TYR PHOSPHATASE_1; 1.
 DR PROSITE; PS01178; ZF_FYVE; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 1006 AA; 113613 MW; BEFC03296E74DB1A CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1006;
 Best Local Similarity 100.0%; Pred.No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 DNVSERV 8
 DB 917 DNVSERV 323
 RESULT 14
 Q9J746 PRELIMINARY; PRT; 1069 AA.
 AC Q9J746;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Exodeoxyribonuclease V (EC 3.1.11.5).
 GN Name=recC; OrderedLocNames=NMN1974;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Z2491 / Serogroup A / Serotype 4a;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrell B.G.
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 meningitidis Z2491".
 RL Nature 404:502-506(2000).
 DR EMBL; AL162757; CAB85194.1; --
 DR PIR; D81826; D81826.
 DR GO; GO:0009338; C:exodeoxyribonuclease V complex; IEA.
 DR GO; GO:0008854; F:exodeoxyribonuclease V activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR InterPro; IPR011034; FMT_C_like.
 DR InterPro; IPR006697; RecC.
 DR Pfam; PF04257; Exonuc_V_gamma; 1.
 DR TIGRFAMs; TIGR01450; recC; 1.
 KW Complete proteome; Hydrolase.
 SQ SEQUENCE 1069 AA; 120606 MW; 57C8E76A62FD705C CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1069;
 Best Local Similarity 100.0%; Pred.No. 42;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SENGVSV 11
 DB 317 SENGVSV 323

RESULT 15
 Q9HS95 PRELIMINARY; PRT; 1190 AA.
 AC Q9HS95;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Chromosome segregation.
 GN Name=smcI; OrderedLocNames=VNG0342G;
 OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRC-1 / ATCC 700922 / JCM 11081;
 RX MEDLINE=20504483; PubMed=11016950; DOI=10.1073/pnas.190337797;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Bergquist B., Pan M.,
 RA Shukla H.D., Laskey S.R., Balliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welter R., Goo Y.A.,
 RA Leithauser B., Kellier K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonksi P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ehardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1".
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004993; AAC18913.1; --
 DR PIR; E84193; E84193.
 DR HSP; Q9X0R4; I869.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0042826; F:ATPase activity; IEA.
 DR GO; GO:0005525; F:GTP binding; IEA.
 DR GO; GO:0007059; P:chromosome segregation; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR003439; ABC transporter.
 DR InterPro; IPR005289; GTP-binding.
 DR InterPro; IPR003405; SMC_C.
 DR InterPro; IPR010935; SMC_hinge.
 DR InterPro; IPR003395; SMC_N.
 DR InterPro; IPR000533; Tropomyosin.
 DR Pfam; PF02483; SMC_C; 1.
 DR Pfam; PF06470; SMC_hinge; 1.
 DR Pfam; PF02463; SMC_N; 1.
 DR Pfam; PF02261; Tropomyosin; 1.
 DR ProDom; PD000006; ABC transporter; 1.
 DR TIGRFAMs; TIGR00650; MG442; 1.
 KW Complete proteome.
 SQ SEQUENCE 1190 AA; 131678 MW; 6994631722219EA4 CRC64;
 Query Match 50.0%; Score 7; DB 2; Length 1190;
 Best Local Similarity 100.0%; Pred.No. 46;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SENGVSV 11
 DB 106 SENGVSV 112
 Search completed: February 11, 2005, 03:18:44
 Job time : 28.7238 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:56:46 ; Search time 285.55 Seconds
(without alignments)
2375.673 Million cell updates/sec

Title: US-09-736-250-5
Perfect score: 14
Sequence: 1 EDNVSENVGVCVT 14

Scoring table:
OLIGO Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9400932

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2 1/USPTO.spool/US09736250/runat_07022005_154942_20650/app_query.fasta_1.718
-DB=GenEmbl -QWTF=fastap -SUFFIX=oligo.rge -MINMATCH=0.1 -LOOPCL=0 -LOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=1000
-DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250.cgn 1 1 3890 @runat_07022005_154942_20650 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	14	100.0	136 6	A74835 Sequence 52
2	14	100.0	136 6	A77814 Sequence 52
3	14	100.0	288 6	CQ712652 Sequence
4	14	100.0	350 6	CQ675890 Sequence

AX397198	Sequence	444	6	AX397198	Sequence
AX198885	Sequence	447	6	AX198885	Sequence
AX209412	Sequence	447	6	AX209412	Sequence
BV180201	sgm10841	601	11	BV180201	sgm10841
BD079737	Cancer-as	804	6	BD079737	Cancer-as
CR541783	Homo sapi	1131	6	CR541783	Homo sapi
AR145734	Sequence	1133	6	AR145734	Sequence
AR087353	Sequence	1133	6	AR087353	Sequence
CQ812312	Sequence	1260	6	CQ812312	Sequence
AR281918	Sequence	1260	6	AR281918	Sequence
AR380354	Sequence	1260	6	AR380354	Sequence
D50310	Human mRNA	1260	6	HUMCVI	
AF135162	Homo sapi	1384	9	AF135162	Homo sapi
BD194541	Human nuc	1493	6	BD194541	Human nuc
AX015395	Sequence	1493	6	AX015395	Sequence
BC000420	Homo sapi	1817	20	BC000420	Homo sapi
CQ468129	Sequence	1889	6	CQ468129	Sequence
BC004975	Homo sapi	1889	6	BC004975	Homo sapi
CQ414223	Sequence	2146	6	CQ414223	Sequence
CQ414515	Sequence	2755	6	CQ414515	Sequence
AY207372	Homo sapi	29867	9	AY207372	Homo sapi
AC111196	Homo sapi	35191	9	AC111196	Homo sapi
AP002874	Homo sapi	178916	2	AP002874	Homo sapi
AC079051	Homo sapi	179443	2	AC079051	Homo sapi
AX914031	Sequence	304	6	AX914031	Sequence
BD049564	Sequence	304	6	BD049564	Sequence
CQ696855	Sequence	308	6	CQ696855	Sequence
AC099472	Rattus no	241543	2	AC099472	Rattus no
AC111318	Rattus no	260517	2	AC111318	Rattus no
AC113213	Rattus no	270068	2	AC113213	Rattus no
CQ660642	Sequence	200	6	CQ660642	Sequence
AF005886	Mus muscu	1535	10	AF005886	Mus muscu
BC003290	Mus muscu	2348	10	BC003290	Mus muscu
AF228739S2	Mus muscu	11793	10	AF228739S2	Mus muscu
AC003001	Homo sapi	101981	9	AC003001	Homo sapi
HS398N15	Human DNA s	104002	9	HS398N15	Human DNA s
AC117658	Mus muscu	179333	2	AC117658	Mus muscu
AC134827	Mus muscu	193811	10	AC134827	Mus muscu
AC101881	Mus muscu	200850	2	AC101881	Mus muscu
AC124646	Mus muscu	202228	2	AC124646	Mus muscu
AC110019	Homo sapi	67380	2	AC110019	Homo sapi
Continuation (2 of		110000	8	CR382134_01	
CR382134_01		110000	8	CR382134_01	
EX323884	Zebrafish	137509	5	EX323884	Zebrafish
AC067871	Homo sapi	181118	9	AC067871	Homo sapi
AC073253	Homo sapi	187045	2	AC073253	Homo sapi
AC122199	Mus muscu	202975	10	AC122199	Mus muscu
AC124931	Rattus no	222594	2	AC124931	Rattus no
AC106995	Rattus no	228823	2	AC106995	Rattus no
CR354610	Danio rer	228860	2	CR354610	Danio rer
AC096022	Rattus no	239423	2	AC096022	Rattus no
AC097676	Rattus no	270387	2	AC097676	Rattus no
A74630	Sequence 31	135	6	A74630	Sequence 31
A77609	Sequence 31	135	6	A77609	Sequence 31
A74629	Sequence 31	183	6	A74629	Sequence 31
A77608	Sequence 31	183	6	A77608	Sequence 31
Z57845	H.sapiens C	245	9	HS1A7F	
AX660625	Sequence	845	6	AX660625	Sequence
AY064628	Arabidops	924	6	AY064628	Arabidops
IAN507598	Isoetes a	980	8	IAN507598	Isoetes a
AB119060	Arabidops	1105	8	AB119060	Arabidops
AJ507593	Isoetes 1	1149	8	IAA507593	
AR448407	Sequence	1226	6	AR448407	Sequence
AY042817	Arabidops	1273	8	AY042817	Arabidops
AY085109	Arabidops	1287	8	AY085109	Arabidops
AX684960	Sequence	1338	6	AX684960	Sequence
AY693168	Saccharom	1341	8	AY693168	Saccharom
AF522193	Drosophil	1434	3	AF522193	Drosophil
AY603424	Rattus no	1550	10	AY603424	Rattus no
CQ608643	Sequence	1671	6	CQ608643	Sequence
AY071512	Drosophill	1987	3	AY071512	Drosophill
AF505865	Drosophill	2004	3	AF505865	Drosophill
BC078340	Danio rer	2030	5	BC078340	Danio rer
AK105285	Oryza sat	2137	8	AK105285	Oryza sat

78	7	50.0	2182	8	AK109896	Oryza sat	c	151	7	50.0	157665	9	AC104695	Homo sapi
79	7	50.0	3235	5	AF111857	Gallus ga	152	7	50.0	157843	2	BX950217	Danio rer	
80	7	50.0	3868	6	QF080642	Sequence	153	7	50.0	158214	2	CNS05TC0	Human chr	
81	7	50.0	3912	3	AF031519	Caenorhab	154	7	50.0	158447	9	AC087435	Homo sapi	
82	7	50.0	4685	5	BC076538	Danio rer	155	7	50.0	159284	2	AC084369	Homo sapi	
83	7	50.0	10286	1	AB004993	Halobacte	c	156	7	50.0	161087	9	AC146261	Pan trogl
84	7	50.0	13525	8	AF523678	Hordeum v	c	157	7	50.0	161297	9	BS000531	Pan trogl
85	7	50.0	21648	1	AF316642	Streptoco	c	158	7	50.0	161433	2	AC022047	Homo sapi
86	7	50.0	28170	1	AC092423	Homo sapi	c	159	7	50.0	162481	2	AC091864	Homo sapi
87	7	50.0	29130	1	AF454500	Streptoco	c	160	7	50.0	162681	2	CR788290	Danio rer
88	7	50.0	28170	6	AX283721	Sequence	c	161	7	50.0	162692	5	BX005067	Zebrafish
89	7	50.0	30655	3	CET24A11	Caenorhabdi	c	162	7	50.0	163179	9	AC022541	Homo sapi
90	7	50.0	32960	3	CEX02E11	Caenorhabdi	c	163	7	50.0	163635	2	CR392027	Danio rer
91	7	50.0	33993	9	AL162581	Human DNA	c	164	7	50.0	165638	3	AC148636	Callithr
92	7	50.0	36484	8	SCU43703	Saccharomyc	c	165	7	50.0	167195	9	AC007808	Drosophil
93	7	50.0	40441	2	AC145714	Homo sapi	c	166	7	50.0	167284	9	AC112719	Homo sapi
94	7	50.0	41153	10	AL808114	Mouse DNA	c	167	7	50.0	167852	9	AC072061	Homo sapi
95	7	50.0	46289	9	AC084793	Homo sapi	c	168	7	50.0	168851	9	AC079336	Homo sapi
96	7	50.0	50988	9	AC104776	Homo sapi	c	169	7	50.0	169152	9	AC115100	Homo sapi
97	7	50.0	63114	5	CR377227	Zebrafish	c	170	7	50.0	169819	9	AC078991	Homo sapi
98	7	50.0	66796	2	AC017435	Drosophil	c	171	7	50.0	170807	9	AC124307	Homo sapi
99	7	50.0	76711	2	AC091341	Continuation (8 of	c	172	7	50.0	170966	5	BX000991	Zebrafish
100	7	50.0	78596	2	AC023030	Homo sapi	c	173	7	50.0	171224	2	AC091600	Homo sapi
101	7	50.0	80074	9	AC008389	Homo sapi	c	174	7	50.0	171409	9	CNS07ED4	Human chr
102	7	50.0	85599	8	AB023045	Arabidops	c	175	7	50.0	172148	9	AC146214	Pan trogl
103	7	50.0	92563	6	AX695695	Sequence	c	176	7	50.0	172761	9	AC092764	Pan trogl
104	7	50.0	97982	8	AC140722	Medicago	c	177	7	50.0	174652	2	AC024630	Homo sapi
105	7	50.0	100190	9	AC061992	Homo sapi	c	178	7	50.0	174920	3	AC010701	Drosophil
106	7	50.0	103287	9	AC084034	Homo sapi	c	179	7	50.0	175036	9	AC068069	Homo sapi
107	7	50.0	107977	9	AC002119	Homo sapi	c	180	7	50.0	175468	2	AC147862	Papio anu
108	7	50.0	110797	2	AC120430	Continuation (3 of	c	181	7	50.0	175965	10	AC121921	Mus muscu
109	7	50.0	110000	2	AC151905	Continuation (2 of	c	182	7	50.0	176043	2	AC113393	Homo sapi
110	7	50.0	110000	8	CR380959	Continuation (3 of	c	183	7	50.0	177242	2	AC147237	Mus muscu
111	7	50.0	110000	8	CR380959	Continuation (4 of	c	184	7	50.0	177423	2	CR356242	Danio rer
112	7	50.0	110000	8	CR382134	Continuation (7 of	c	185	7	50.0	178095	2	CR753874	Danio rer
113	7	50.0	110000	8	CR382135	Continuation (11 o	c	186	7	50.0	178344	2	AC149182	Papio anu
114	7	50.0	111004	9	AC128712	Homo sapi	c	187	7	50.0	179876	10	AC102757	Mus muscu
115	7	50.0	115884	2	AC017581	AC017581 Drosophil	c	188	7	50.0	180187	2	AC117965	Rattus no
116	7	50.0	116803	2	AC097718	Homo sapi	c	189	7	50.0	180488	10	AC141632	Mus muscu
117	7	50.0	121946	9	AC114771	Homo sapi	c	190	7	50.0	180573	10	AL831753	Mouse DNA
118	7	50.0	123037	9	AC109443	Homo sapi	c	191	7	50.0	181027	2	CR354600	Danio rer
119	7	50.0	126730	2	CR548621	CR548621 Danio rer	c	192	7	50.0	181319	2	AC110497	Mus muscu
120	7	50.0	126889	10	AC141867	AC141867 Mus muscu	c	193	7	50.0	181328	9	AC104945	Homo sapi
121	7	50.0	127017	10	AC140445	AC140445 Mus muscu	c	194	7	50.0	181842	10	AC137127	Mus muscu
122	7	50.0	130870	10	AL731775	AL731775 Mouse DNA	c	195	7	50.0	182187	2	AC109374	Rattus no
123	7	50.0	133052	9	AL136325	AL136325 Human DNA	c	196	7	50.0	182203	2	AC128779	Rattus no
124	7	50.0	137925	2	BX927391	BX927391 Danio rer	c	197	7	50.0	183936	2	AC149620	Papio anu
125	7	50.0	138851	10	AL645938	AL645938 Mouse DNA	c	198	7	50.0	185138	10	AL845172	Mouse DNA
126	7	50.0	138864	10	AC115832	AC115832 Mus muscu	c	199	7	50.0	187278	2	BX571888	Danio rer
127	7	50.0	139594	2	AC025085	AC025085 Homo sapi	c	200	7	50.0	187341	10	AC117184	Homo sapi
128	7	50.0	142576	9	AC010609	AC010609 Homo sapi	c	201	7	50.0	187415	2	AC110802	Homo sapi
129	7	50.0	142807	9	HS33B19	AC010609 Human DNA	c	202	7	50.0	187490	2	AC048378	Homo sapi
130	7	50.0	143220	9	AL389887	AL389887 Human DNA	c	203	7	50.0	187792	2	CR407545	Danio rer
131	7	50.0	143334	9	AC005293	AC005293 Homo sapi	c	204	7	50.0	188476	10	AC122238	Mus muscu
132	7	50.0	144260	9	AC006998	AC006998 Homo sapi	c	205	7	50.0	189263	10	AC134595	Mus muscu
133	7	50.0	145226	9	AP004284	AP004284 Homo sapi	c	206	7	50.0	189771	2	AC112921	Homo sapi
134	7	50.0	145603	2	AC148823	AC148823 Pan trogl	c	207	7	50.0	190558	2	AC119478	Rattus no
135	7	50.0	145621	2	OSJN001145	AL662933 Oryza sat	c	208	7	50.0	190860	10	AC144776	Mus muscu
136	7	50.0	147521	2	AC013680	AC013680 Homo sapi	c	209	7	50.0	192944	2	AC146902	Callicebu
137	7	50.0	147755	5	EX649434	EX649434 Zebrafish	c	210	7	50.0	193015	2	AC150074	Gallus ga
138	7	50.0	148485	5	AL590147	AL590147 Zebrafish	c	211	7	50.0	194304	9	AC016708	Homo sapi
139	7	50.0	148592	2	AC125190	AC125190 Mus muscu	c	212	7	50.0	194464	2	AC146119	Pan trogl
140	7	50.0	149277	2	AL627207	AL627207 Homc sapi	c	213	7	50.0	194827	2	BX294106	Danio rer
141	7	50.0	149617	2	AC068052	AC068052 Homo sapi	c	214	7	50.0	195563	10	AC123708	Mus muscu
142	7	50.0	150634	2	AC113371	AC113371 Homo sapi	c	215	7	50.0	195673	2	AC102310	Pongo pyg
143	7	50.0	150794	9	AC025211	AC025211 Homo sapi	c	216	7	50.0	197873	2	AC147722	Mouse DNA
144	7	50.0	151406	10	AC122196	AC122196 Mus muscu	c	217	7	50.0	197912	10	AL672070	Mouse DNA
145	7	50.0	152787	2	EX323075	EX323075 Danio rer	c	218	7	50.0	198404	10	AC114621	Mus muscu
146	7	50.0	153087	2	AC020546	AC020546 Homo sapi	c	219	7	50.0	198576	10	AC068908	Mus muscu
147	7	50.0	155299	9	AL161723	AL161723 Human sapi	c	220	7	50.0	198604	10	AC122828	Mus muscu
148	7	50.0	155725	9	AL161723	Human DNA	c	221	7	50.0	198759	2	AC020772	Homo sapi
149	7	50.0	155775	9	AL011943	AL011943 Homo sapi	c	222	7	50.0	198838	2	AC093647	Rattus no
150	7	50.0	155819	9	AL358372	Human DNA	c	223	7	50.0	198893	2	AC133116	Rattus no

C 224	7	50.0	199946	2	AC135863	AC135863 Mus muscu	297	7	50.0	257396	2	AC130569	AC130569 Rattus no
C 225	7	50.0	200187	5	BX510327	Zebrafish	298	7	50.0	257398	2	AC131885	AC131885 Rattus no
C 226	7	50.0	200679	10	AC112662	Mus muscu	C 299	7	50.0	258873	2	AC096935	AC096935 Rattus no
C 227	7	50.0	200688	2	AC112757	AC112757 Rattus no	300	7	50.0	260168	2	AC094547	AC094547 Rattus no
C 228	7	50.0	200688	10	AL671963	AL671963 Mouse DNA	C 301	7	50.0	260625	2	AC096018	AC096018 Rattus no
C 229	7	50.0	200841	10	AC108830	AC108830 Mus muscu	C 302	7	50.0	260925	2	AC110478	AC110478 Rattus no
C 230	7	50.0	201239	2	AC135866	AC135866 Rattus no	C 303	7	50.0	261089	2	AC094807	AC094807 Rattus no
C 231	7	50.0	202236	10	AC14513	AC14513 Mus muscu	C 304	7	50.0	264473	2	AC132979	AC132979 Rattus no
C 232	7	50.0	203221	10	AC102689	AC102689 Mus muscu	C 305	7	50.0	264754	2	AC128542	AC128542 Rattus no
C 233	7	50.0	203480	2	AC146136	AC146136 Pan trogl	C 306	7	50.0	269670	2	AC121698	AC121698 Rattus no
C 234	7	50.0	203802	2	AC133417	AC133417 Rattus no	C 307	7	50.0	272055	2	AC118859	AC118859 Rattus no
C 235	7	50.0	204191	10	AC099615	AC099615 Mus muscu	C 308	7	50.0	272606	2	AC095738	AC095738 Rattus no
C 236	7	50.0	204478	10	AC127306	AC127306 Mus muscu	C 309	7	50.0	277621	2	AC095191	AC095191 Rattus no
C 237	7	50.0	205702	2	AC145116	AC145116 Mus muscu	C 310	7	50.0	284471	2	AC095933	AC095933 Rattus no
C 238	7	50.0	206331	2	CR388075	CR388075 Danio rer	C 311	7	50.0	299180	1	AP005080	AP005080 Vibrio pa
C 239	7	50.0	207126	2	AC140461	AC140461 Mus muscu	C 312	7	50.0	310137	2	AC111625	AC111625 Rattus no
C 240	7	50.0	207206	9	AC090260	AC090260 Homo sapi	C 313	7	50.0	314906	3	AE003594	AE003594 Drosophil
C 241	7	50.0	207295	2	AC101998	AC101998 Mus muscu	C 314	7	50.0	324430	2	AC118529	AC118529 Rattus no
C 242	7	50.0	207563	2	AC116577	AC116577 Mus muscu	C 315	7	50.0	326301	1	NMA622491	AL162257 Neisseria
C 243	7	50.0	210018	2	AC015557	AC015557 Homo sapi	C 316	7	50.0	347286	2	AC102740	AC102740 Mus muscu
C 244	7	50.0	210018	2	AC015557	AC015557 Homo sapi	C 317	7	50.0	348174	3	CR382399	CR382399 Plasmodiu
C 245	7	50.0	210854	2	AC123995	AC123995 Mus muscu	C 318	6	42.9	19	6	AR294906	AR294906 Sequence
C 246	7	50.0	212284	2	AC131732	AC131732 Mus muscu	C 319	6	42.9	60	6	CQ546488	CQ546488 Sequence
C 247	7	50.0	212421	2	AC109591	AC109591 Homo sapi	C 320	6	42.9	100	6	AX989903	AX989903 Sequence
C 248	7	50.0	213178	10	AC148021	AC148021 Mus muscu	C 321	6	42.9	108	6	CQ081052	CQ081052 Sequence
C 249	7	50.0	214049	2	AC130983	AC130983 Rattus no	C 322	6	42.9	108	6	CQ115545	CQ115545 Sequence
C 250	7	50.0	216449	2	AC115772	AC115772 Mus muscu	C 323	6	42.9	108	6	CQ154345	CQ154345 Sequence
C 251	7	50.0	216851	2	AC146740	AC146740 Callithri	C 324	6	42.9	108	6	CQ186913	CQ186913 Sequence
C 252	7	50.0	217769	2	AC102447	AC102447 Mus muscu	C 325	6	42.9	108	6	CQ237598	CQ237598 Sequence
C 253	7	50.0	217777	2	AC113891	AC113891 Rattus no	C 326	6	42.9	108	6	CQ275218	CQ275218 Sequence
C 254	7	50.0	218157	2	AC134263	AC134263 Rattus no	C 327	6	42.9	108	6	CQ312196	CQ312196 Sequence
C 255	7	50.0	219683	2	AC103126	AC103126 Rattus no	C 328	6	42.9	108	6	CQ349602	CQ349602 Sequence
C 256	7	50.0	220788	2	AC130904	AC130904 Rattus no	C 329	6	42.9	159	6	AX719130	AX719130 Sequence
C 257	7	50.0	222251	2	AC110936	AC110936 Rattus no	C 330	6	42.9	159	6	AX766254	AX766254 Sequence
C 258	7	50.0	222292	2	AC118839	AC118839 Rattus no	C 331	6	42.9	169	10	RAJ10024	RAJ10024 Rattus no
C 259	7	50.0	222330	2	AC096255	AC096255 Rattus no	C 332	6	42.9	171	6	CQ448299	CQ448299 Sequence
C 260	7	50.0	222965	2	AC115879	AC115879 Mus muscu	C 333	6	42.9	174	6	CQ695388	CQ695388 Sequence
C 261	7	50.0	223061	2	AC098658	AC098658 Rattus no	C 334	6	42.9	175	11	AU050020	AU050020 Rattus no
C 262	7	50.0	224400	2	AC111100	AC111100 Mus muscu	C 335	6	42.9	194	1	AB080996	AB080996 Salmonell
C 263	7	50.0	224561	2	AC103154	AC103154 Rattus no	C 336	6	42.9	201	6	AR387165	AR387165 Sequence
C 264	7	50.0	225066	2	AC112674	AC112674 Mus muscu	C 337	6	42.9	201	11	BV169998	BV169998 sqnm28245
C 265	7	50.0	226351	2	AC106508	AC106508 Rattus no	C 338	6	42.9	201	11	BV183159	BV183159 sqnm13661
C 266	7	50.0	226650	2	AC120485	AC120485 Rattus no	C 339	6	42.9	255	8	AY298897	AY298897 Trichoder
C 267	7	50.0	228051	2	AC097434	AC097434 Rattus no	C 340	6	42.9	256	6	AX911508	AX911508 Sequence
C 268	7	50.0	230236	10	AC093366	AC093366 Mus muscu	C 341	6	42.9	256	6	BD047041	BD047041 Sequence
C 269	7	50.0	230448	2	AC128463	AC128463 Rattus no	C 342	6	42.9	256	9	HSRPN133	AY000377 Homo sapi
C 270	7	50.0	230993	2	AC150072	AC150072 Gallus ga	C 343	6	42.9	257	9	AY530102	AY530102 Gorilla g
C 271	7	50.0	231234	2	AC134014	AC134014 Rattus no	C 344	6	42.9	258	9	AY530103	AY530103 Gorilla g
C 272	7	50.0	233097	10	AL772239	AL772239 Mouse DNA	C 345	6	42.9	260	11	BV183203	BV183203 sqnm13702
C 273	7	50.0	233141	2	AC128327	AC128327 Rattus no	C 346	6	42.9	263	6	CQ671671	CQ671671 Sequence
C 274	7	50.0	233345	2	AC150066	AC150066 Gallus ga	C 347	6	42.9	273	9	GORMTDLOOP	L76749 Gorilla gor
C 275	7	50.0	234526	2	AC120414	AC120414 Mus muscu	C 348	6	42.9	277	9	GORMTDLOOR	L76751 Gorilla gor
C 276	7	50.0	234526	2	AC111227	AC111227 Rattus no	C 349	6	42.9	279	6	CQ667273	CQ667273 Sequence
C 277	7	50.0	237260	2	AC095010	AC095010 Rattus no	C 350	6	42.9	283	9	GORMTDLOOQ	L76750 Gorilla gor
C 278	7	50.0	238896	2	AC137226	AC137226 Rattus no	C 351	6	42.9	287	9	GORMTDLOOS	L76752 Gorilla gor
C 279	7	50.0	240350	2	AC124154	AC124154 Rattus no	C 352	6	42.9	289	6	CQ670575	CQ670575 Sequence
C 280	7	50.0	240992	2	AC131467	AC131467 Rattus no	C 353	6	42.9	293	6	AR272809	AR272809 Sequence
C 281	7	50.0	242413	2	AC106264	AC106264 Rattus no	C 354	6	42.9	293	6	AR276390	AR276390 Sequence
C 282	7	50.0	242510	2	AC128507	AC128507 Rattus no	C 355	6	42.9	293	6	AR406665	AR406665 Sequence
C 283	7	50.0	242974	2	AC103570	AC103570 Rattus no	C 356	6	42.9	293	6	AR440515	AR440515 Sequence
C 284	7	50.0	243252	2	AC120850	AC120850 Mus muscu	C 357	6	42.9	293	6	AR472673	AR472673 Sequence
C 285	7	50.0	243545	2	AC135739	AC135739 Rattus no	C 358	6	42.9	293	6	AR543326	AR543326 Sequence
C 286	7	50.0	246083	2	AC106313	AC106313 Rattus no	C 359	6	42.9	293	6	AX062911	AX062911 Sequence
C 287	7	50.0	246369	2	AC125707	AC125707 Rattus no	C 360	6	42.9	293	6	AX367828	AX367828 Sequence
C 288	7	50.0	246805	2	AC098750	AC098750 Rattus no	C 361	6	42.9	305	11	G49065	G49065 SHGC-82968
C 289	7	50.0	247469	2	AC096287	AC096287 Rattus no	C 362	6	42.9	308	6	CQ437347	CQ437347 Sequence
C 290	7	50.0	249791	5	BX537133	BX537133 Zebrafish	C 363	6	42.9	308	10	MMU81277	MMU81277 Mus musculu
C 291	7	50.0	250277	2	AC122757	AC122757 Mus muscu	C 364	6	42.9	309	6	CQ697708	CQ697708 Sequence
C 292	7	50.0	251914	2	AC111366	AC111366 Rattus no	C 365	6	42.9	313	11	G22286	G22286 human STS W
C 293	7	50.0	252843	2	AC096261	AC096261 Rattus no	C 366	6	42.9	316	11	G36015	G36015 STS h14a147
C 294	7	50.0	254400	2	AC096497	AC096497 Rattus no	C 367	6	42.9	346	6	CQ656116	CQ656116 Sequence
C 295	7	50.0	254961	3	AE003706	AE003706 Drosophil	C 368	6	42.9	346	6	CQ690011	CQ690011 Sequence
C 296	7	50.0	257258	2	AC105322	AC105322 Mus muscu	C 369	6	42.9	347	4	ECA272106	ECA272106 Equus cab

C 370	6	42.9	347	6	CQ691350 Sequence	CQ691350 Sequence	443	550	7	STSP02	X01583 Bacterioph
C 371	6	42.9	349	11	Z51386 H. sapiens	Z51386 H. sapiens	444	552	1	UBA309652	AJ309652 Unculture
C 372	6	42.9	357	6	AX414007 Sequence	AX414007 Sequence	C 445	556	6	BD151108	BD151108 Primer fo
C 373	6	42.9	357	6	AX415799 Sequence	AX415799 Sequence	C 446	556	6	AX871046	AX871046 Sequence
C 374	6	42.9	358	5	AF373872 Sequence	AF373872 Sequence	C 447	557	3	AME509690	AJ509690 Apis mell
C 375	6	42.9	358	6	BD059685 Sequence	BD059685 Sequence	C 448	557	6	AX341833	AX341833 Sequence
C 376	6	42.9	360	1	AY015541 Unculture	AY015541 Unculture	C 449	559	11	G78268	G78268 S209P6075FF
C 377	6	42.9	361	11	AV088295 Sequence	AV088295 Sequence	C 450	560	6	CQ782375	CQ782375 Sequence
C 378	6	42.9	361	11	AV097338 Sequence	AV097338 Sequence	C 451	560	6	BD127084	BD127084 Primer fo
C 379	6	42.9	362	10	MUSURF44	MUSURF44	C 452	563	6	AX237376	AX237376 Sequence
C 380	6	42.9	368	6	AX451492 Sequence	AX451492 Sequence	C 453	563	6	AX237504	AX237504 Sequence
C 381	6	42.9	374	9	AF089820	AF089820	C 454	563	6	AX237673	AX237673 Sequence
C 382	6	42.9	380	11	G36260	G36260	C 455	565	5	AY216588	AY216588 Danio rer
C 383	6	42.9	398	6	CQ675091	CQ675091	C 456	575	14	AF529736	AF529736 Hepatitis
C 384	6	42.9	400	11	G16689	G16689	C 457	578	11	AV098575	AV098575 RPAMSEQO
C 385	6	42.9	401	6	CQ218447	CQ218447	C 458	581	9	HS4430600	HS4430600 Homo sapi
C 386	6	42.9	401	6	CQ257059	CQ257059	C 459	585	6	CQ594120	CQ594120 Sequence
C 387	6	42.9	401	11	AV193531	AV193531	C 460	593	11	G96850	G96850 S208P6100FF
C 388	6	42.9	402	8	AY558316	AY558316	C 461	594	6	AX437779	AX437779 Sequence
C 389	6	42.9	408	11	AV179335	AV179335	C 462	594	6	AX437779	AX437779 Sequence
C 390	6	42.9	414	8	BT004730	BT004730	C 463	597	9	HS8PT087	HS8PT087
C 391	6	42.9	425	4	AF140590	AF140590	C 464	598	9	HS4326609	HS4326609 Homo sapi
C 392	6	42.9	429	6	CQ468289	CQ468289	C 465	598	11	G75913	G75913 S208P693RB
C 393	6	42.9	432	1	USA428143	USA428143	C 466	601	11	AV021655	AV021655 S212P6237
C 394	6	42.9	436	6	CQ671069	CQ671069	C 467	601	11	AV179336	AV179336 sqm10491
C 395	6	42.9	445	6	CQ711533	CQ711533	C 468	603	8	AK118607	AK118607 Arabidops
C 396	6	42.9	446	6	AX332954	AX332954	C 469	603	11	AV070510	AV070510 S212P6238
C 397	6	42.9	446	6	AX334706	AX334706	C 470	606	11	G97070	G97070 S208P6379FC
C 398	6	42.9	446	6	AX335909	AX335909	C 471	607	11	AV020847	AV020847 S212P6864
C 400	6	42.9	448	11	G37471	G37471	C 472	610	5	AF402828	AF402828 Ictallurus
C 401	6	42.9	450	6	CQ477457	CQ477457	C 473	615	9	AF032900	AF032900 Homo sapi
C 402	6	42.9	465	6	CQ736493	CQ736493	C 474	619	11	G88550	G88550 S208P6113FC
C 403	6	42.9	471	6	CQ671835	CQ671835	C 475	622	9	AF374413	AF374413 Homo sapi
C 404	6	42.9	471	6	CQ672032	CQ672032	C 476	627	1	AY029581	AY029581 Ascomonas
C 405	6	42.9	475	6	AX072032	AX072032	C 477	628	5	BC042226	BC042226 Xenopus l
C 406	6	42.9	477	6	CQ070005	CQ070005	C 478	629	8	AB108388	AB108388 Phleum pr
C 407	6	42.9	477	6	CQ097608	CQ097608	C 479	630	6	AX370934	AX370934 Sequence
C 408	6	42.9	477	6	CQ136449	CQ136449	C 480	635	10	AF053770	AF053770 Mus muscu
C 409	6	42.9	477	6	CQ174429	CQ174429	C 481	639	6	AR387211	AR387211 Sequence
C 410	6	42.9	477	6	CQ219755	CQ219755	C 482	644	11	AV074312	AV074312 S212P6014
C 411	6	42.9	477	6	CQ258218	CQ258218	C 483	646	11	AV071612	AV071612 S212P6008
C 412	6	42.9	477	6	CQ295562	CQ295562	C 484	649	11	PM3A3B	PM3A3B
C 413	6	42.9	477	6	CQ332151	CQ332151	C 485	650	11	AV056242	AV056242 S212P6039
C 414	6	42.9	478	6	CQ498660	CQ498660	C 486	651	5	CR389463	CR389463 Gallus ga
C 415	6	42.9	478	6	CQ507634	CQ507634	C 487	651	11	AV018666	AV018666 S212P6046
C 416	6	42.9	480	6	BD209567	BD209567	C 488	654	10	AF080580	AF080580 Mus muscu
C 417	6	42.9	480	6	BD209658	BD209658	C 489	655	11	AV018096	AV018096 S208P6653
C 418	6	42.9	480	6	AR341373	AR341373	C 490	656	11	AV033488	AV033488 S212P6039
C 419	6	42.9	480	6	AR341464	AR341464	C 491	660	10	AF551099	AF551099 Mus muscu
C 420	6	42.9	482	11	G63503	G63503	C 492	661	10	AF551146	AF551146 Mus muscu
C 421	6	42.9	491	9	HS430598	HS430598	C 493	662	10	AF551025	AF551025 Mus muscu
C 422	6	42.9	496	11	G56059	G56059	C 494	664	10	AF551186	AF551186 Mus muscu
C 423	6	42.9	498	6	BD210362	BD210362	C 495	664	11	AF551125	AF551125 Mus muscu
C 424	6	42.9	499	11	G87047	G87047	C 496	664	11	G94347	G94347 S208P6022RF
C 425	6	42.9	504	6	CQ720891	CQ720891	C 497	667	11	AV042472	AV042472 S212P6052
C 426	6	42.9	506	8	ATH532204	ATH532204	C 498	675	5	SHXCRP	SHXCRP
C 427	6	42.9	519	5	MTHS2ADH6	MTHS2ADH6	C 499	677	1	UBA309604	UBA309604 Unculture
C 428	6	42.9	520	6	CQ071852	CQ071852	C 500	694	11	AV017936	AV017936 S212P6029
C 429	6	42.9	520	6	CQ102482	CQ102482	C 501	702	1	UBA309603	UBA309603 Unculture
C 430	6	42.9	520	6	CQ141401	CQ141401	C 502	706	9	HUMEBUR03	HUMEBUR03
C 431	6	42.9	520	6	CQ177039	CQ177039	C 503	708	6	AF377545	AF377545 Sequence
C 432	6	42.9	520	6	CQ224688	CQ224688	C 504	710	3	AF385460	AF385460 Paracalan
C 433	6	42.9	520	6	CQ262703	CQ262703	C 505	710	6	BD021649	BD021649 Novel gen
C 434	6	42.9	520	6	CQ299763	CQ299763	C 506	710	6	BD101587	BD101587 Novel gen
C 435	6	42.9	520	6	CQ336930	CQ336930	C 507	714	5	AX930534	AX930534 Gallus ga
C 436	6	42.9	521	6	CQ781334	CQ781334	C 508	717	8	AF028523	AF028523 Bombax bu
C 437	6	42.9	521	6	BD126043	BD126043	C 509	720	8	BT000530	BT000530 Arabidops
C 438	6	42.9	532	10	AF551020	AF551020	C 510				
C 439	6	42.9	532	10	AF551031	AF551031	C 511				
C 440	6	42.9	533	6	AX244776	AX244776	C 512				
C 441	6	42.9	536	6	AX390656	AX390656	C 513				
C 442	6	42.9	541	11	G81105	G81105	C 514				
							C 515				

C 662	6	42.9	1458	3	DME295625	AJ295625 Drosophila	735	1893	14	AF239269	AF239269 Avian inf
C 663	6	42.9	1467	3	AV264367	AV264367 Ixodes sc	736	1893	14	AF239270	AF239270 Avian inf
C 664	6	42.9	1469	9	BC016149	BC016149 Homo sapi	737	1893	14	AF239271	AF239271 Avian inf
C 665	6	42.9	1472	9	HSPAX71	X96744 H. sapiens P	738	1893	14	AF239272	AF239272 Avian inf
C 666	6	42.9	1473	3	TBR308033	AJ308033 Trypanoso	739	1893	14	AF239273	AF239273 Avian inf
C 667	6	42.9	1473	3	TBR308034	AJ308034 Trypanoso	740	1893	14	AF239274	AF239274 Avian inf
C 668	6	42.9	1473	3	TBR308036	AJ308036 Trypanoso	741	1893	14	AF239275	AF239275 Avian inf
C 669	6	42.9	1479	3	AV526243	AV526243 Trypanoso	742	1893	14	AF239276	AF239276 Avian inf
C 670	6	42.9	1480	1	SPU20078	U20078 Streptococ	743	1893	14	AF239277	AF239277 Avian inf
C 671	6	42.9	1483	3	RAC8MENA	X64590 R. americana	744	1893	14	AF239278	AF239278 Avian inf
C 672	6	42.9	1485	4	AF304106	AF304106 Hippopota	745	1893	14	AF239279	AF239279 Avian inf
C 673	6	42.9	1512	5	GGYAP25	X76483 G. gallus (w	746	1893	14	AF239280	AF239280 Avian inf
C 674	6	42.9	1521	5	AF292028	AF292028 Danio rer	747	1893	14	AF239281	AF239281 Avian inf
C 675	6	42.9	1522	5	BX935569	BX935569 Gallus ga	748	1893	14	AF239282	AF239282 Avian inf
C 676	6	42.9	1527	1	NMU19580	UI9580 Neisseria m	749	1893	14	AF239283	AF239283 Avian inf
C 677	6	42.9	1554	6	AV554234	AV554234 Sequence	750	1893	14	AF239284	AF239284 Avian inf
C 678	6	42.9	1601	8	AX087768	AX087768 Arabidops	751	1893	14	AF239285	AF239285 Avian inf
C 679	6	42.9	1610	5	BC048029	BC048029 Danio rer	752	1893	14	AF239286	AF239286 Avian inf
C 680	6	42.9	1635	6	CQ576231	CQ576231 Sequence	753	1893	14	AF239287	AF239287 Avian inf
C 681	6	42.9	1645	11	G07197	G07197 human STS W	754	1899	6	CQ718383	CQ718383 Sequence
C 682	6	42.9	1653	3	AF115255	AF115255 Myxobolus	755	1901	3	AY425470	AY425470 Limnatis
C 683	6	42.9	1654	6	BD269771	BD269771 50 human	756	1902	5	BX950301	BX950301 Gallus ga
C 684	6	42.9	1658	6	BD155889	BD155889 Primer fo	757	1929	9	BC037909	BC037909 Homo sapi
C 685	6	42.9	1658	6	AX876003	AX876003 Sequence	758	1933	6	AR380194	AR380194 Sequence
C 686	6	42.9	1658	9	AX001096	AX001096 Homo sapi	759	1933	6	AR380194	AR380194 Sequence
C 687	6	42.9	1671	5	BC065465	BC065465 Danio rer	760	1933	6	AR380194	AR380194 Sequence
C 688	6	42.9	1696	9	HSM802552	AL162038 Homo sapi	761	1933	6	AR380194	AR380194 Sequence
C 689	6	42.9	1726	6	BD155768	BD155768 Primer fo	762	1933	6	AR380194	AR380194 Sequence
C 690	6	42.9	1726	6	AX875797	AX875797 Sequence	763	1933	6	AR380194	AR380194 Sequence
C 691	6	42.9	1726	9	AX000984	AX000984 Homo sapi	764	1933	6	AR380194	AR380194 Sequence
C 692	6	42.9	1731	6	AX449702	AX449702 Sequence	765	1933	6	AR380194	AR380194 Sequence
C 693	6	42.9	1736	5	AJ719572	AJ719572 Gallus ga	766	1933	6	AR380194	AR380194 Sequence
C 694	6	42.9	1740	5	BC066405	BC066405 Danio rer	767	1933	6	AR380194	AR380194 Sequence
C 695	6	42.9	1740	8	AX099167	AX099167 Oryza sat	768	1933	6	AR380194	AR380194 Sequence
C 696	6	42.9	1748	1	AB126576	AB126576 Bacillus	769	1933	6	AR380194	AR380194 Sequence
C 697	6	42.9	1749	1	AB126568	AB126568 Bacillus	770	1933	6	AR380194	AR380194 Sequence
C 698	6	42.9	1749	1	AB126568	AB126568 Bacillus	771	1933	6	AR380194	AR380194 Sequence
C 699	6	42.9	1749	1	AB126569	AB126569 Bacillus	772	1933	6	AR380194	AR380194 Sequence
C 700	6	42.9	1749	1	AB126572	AB126572 Bacillus	773	1933	6	AR380194	AR380194 Sequence
C 701	6	42.9	1749	1	AB126573	AB126573 Bacillus	774	1933	6	AR380194	AR380194 Sequence
C 702	6	42.9	1749	1	AB126574	AB126574 Bacillus	775	1933	6	AR380194	AR380194 Sequence
C 703	6	42.9	1763	8	AB077765	AB077765 Citrus ja	776	1933	6	AR380194	AR380194 Sequence
C 704	6	42.9	1765	6	AR506063	AR506063 Sequence	777	1933	6	AR380194	AR380194 Sequence
C 705	6	42.9	1781	8	AB051206	AB051206 Chlamydom	778	1933	6	AR380194	AR380194 Sequence
C 706	6	42.9	1787	1	AB126575	AB126575 Bacillus	779	1933	6	AR380194	AR380194 Sequence
C 707	6	42.9	1802	6	AX440493	AX440493 Sequence	780	1933	6	AR380194	AR380194 Sequence
C 708	6	42.9	1802	8	AB072106	AB072106 Oryza sat	781	1933	6	AR380194	AR380194 Sequence
C 709	6	42.9	1813	1	AB126571	AB126571 Bacillus	782	1933	6	AR380194	AR380194 Sequence
C 710	6	42.9	1814	1	AB126535	AB126535 Bacillus	783	1933	6	AR380194	AR380194 Sequence
C 711	6	42.9	1814	1	AB126536	AB126536 Bacillus	784	1933	6	AR380194	AR380194 Sequence
C 712	6	42.9	1814	1	AB126538	AB126538 Bacillus	785	1933	6	AR380194	AR380194 Sequence
C 713	6	42.9	1814	1	AB126539	AB126539 Bacillus	786	1933	6	AR380194	AR380194 Sequence
C 714	6	42.9	1814	1	AB126540	AB126540 Bacillus	787	1933	6	AR380194	AR380194 Sequence
C 715	6	42.9	1814	1	AB126577	AB126577 Bacillus	788	1933	6	AR380194	AR380194 Sequence
C 716	6	42.9	1815	1	AB126534	AB126534 Bacillus	789	1933	6	AR380194	AR380194 Sequence
C 717	6	42.9	1815	1	AB126537	AB126537 Bacillus	790	1933	6	AR380194	AR380194 Sequence
C 718	6	42.9	1815	8	AY242385	AY242385 Citrus si	791	1933	6	AR380194	AR380194 Sequence
C 719	6	42.9	1815	9	HUMFKBP25A	M90820 Human rapam	792	1933	6	AR380194	AR380194 Sequence
C 720	6	42.9	1817	4	BOVKAD	J03759 Bovine bran	793	1933	6	AR380194	AR380194 Sequence
C 721	6	42.9	1818	8	AX128390	AX128390 Arabidops	794	1933	6	AR380194	AR380194 Sequence
C 722	6	42.9	1837	8	SCARDEH	Z17314 Saccharomyc	795	1933	6	AR380194	AR380194 Sequence
C 723	6	42.9	1840	6	CQ783317	CQ783317 Sequence	796	1933	6	AR380194	AR380194 Sequence
C 724	6	42.9	1840	6	BD127585	BD127585 Primer fo	797	1933	6	AR380194	AR380194 Sequence
C 725	6	42.9	1840	9	AK075217	AK075217 Homo sapi	798	1933	6	AR380194	AR380194 Sequence
C 726	6	42.9	1842	6	AR269483	AR269483 Sequence	799	1933	6	AR380194	AR380194 Sequence
C 727	6	42.9	1843	10	AF131949	AF131949 Cavia por	800	1933	6	AR380194	AR380194 Sequence
C 728	6	42.9	1845	9	BC026678	BC026678 Homo sapi	801	1933	6	AR380194	AR380194 Sequence
C 729	6	42.9	1866	9	BC052246	BC052246 Homo sapi	802	1933	6	AR380194	AR380194 Sequence
C 730	6	42.9	1876	9	BC003598	BC003598 Homo sapi	803	1933	6	AR380194	AR380194 Sequence
C 731	6	42.9	1878	8	BT002217	BT002217 Arabidops	804	1933	6	AR380194	AR380194 Sequence
C 732	6	42.9	1890	6	AX714058	AX714058 Sequence	805	1933	6	AR380194	AR380194 Sequence
C 733	6	42.9	1890	9	AK056121	AK056121 Homo sapi	806	1933	6	AR380194	AR380194 Sequence
C 734	6	42.9	1892	14	AF239282	AF239282 Avian inf	807	1933	6	AR380194	AR380194 Sequence

808	6	42.9	2254	6	CQ721114	Sequence	881	6	42.9	2727	9	AF150734	Homo sapi
809	6	42.9	2262	6	CQ715533	Sequence	882	6	42.9	2728	6	BD156421	Primer fo
c 810	6	42.9	2271	6	CQ602048	Sequence	883	6	42.9	2728	6	AX876981	Sequence
811	6	42.9	2272	6	AX406029	Sequence	884	6	42.9	2728	8	AY001555	Homo sapi
812	6	42.9	2272	6	HSPAX7M	Sequence	885	6	42.9	2740	8	AY081293	Arabidops
813	6	42.9	2285	8	AY050954	Arabidops	886	6	42.9	2755	9	BC030686	Homo sapi
814	6	42.9	2288	10	BC025608	Sequence	887	6	42.9	2769	6	AX306106	Sequence
815	6	42.9	2289	3	AF382333	Trypanoso	888	6	42.9	2769	10	MMGRBBP	M.musculus
816	6	42.9	2297	9	BC004149	Homo sapi	889	6	42.9	2772	10	RRU30381	Rattus norv
817	6	42.9	2298	9	HSM801202	Homo sapi	890	6	42.9	2773	14	AY502936	Tomato le
818	6	42.9	2301	10	AF316549	Mus muscu	c 891	6	42.9	2775	5	BC076544	Danio rer
c 819	6	42.9	2305	3	AX113238	Ciona int	892	6	42.9	2778	10	BC047214	Mus muscu
820	6	42.9	2319	6	E021176	DNA sequenc	893	6	42.9	2806	6	CQ719943	Sequence
c 821	6	42.9	2331	3	AX113471	Ciona int	894	6	42.9	2806	8	AX120321	Oryza sat
c 822	6	42.9	2338	3	AF081950	Dictyoste	895	6	42.9	2809	6	AX748342	Sequence
823	6	42.9	2345	6	AK096392	Homo sapi	896	6	42.9	2809	9	AK093861	Homo sapi
824	6	42.9	2358	6	CQ804152	Sequence	897	6	42.9	2809	9	BC015014	Homo sapi
c 825	6	42.9	2381	5	AJ720916	Gallus ga	898	6	42.9	2833	9	BC029350	Homo sapi
c 826	6	42.9	2389	8	AK106702	Oryza sat	899	6	42.9	2838	9	AB006623	Homo sapi
827	6	42.9	2389	8	ATHC10F	Arabidopsis	900	6	42.9	2858	9	AF039019	Homo sapi
828	6	42.9	2392	8	ATHBLA10C	Arabidopsis	901	6	42.9	2892	6	BD156467	Primer fo
829	6	42.9	2395	8	ATHITA01	Arabidopsis	902	6	42.9	2892	6	AX877068	Sequence
830	6	42.9	2412	8	D63463	Arabidopsis	903	6	42.9	2892	9	AK001593	Homo sapi
831	6	42.9	2412	8	ATHCH10E	Arabidopsis	904	6	42.9	2901	8	AY056123	Arabidops
832	6	42.9	2421	8	ATHES0G	Arabidopsis	905	6	42.9	2907	5	AY174870	Pseudople
c 833	6	42.9	2421	6	AX433126	Sequence	c 906	6	42.9	2918	4	AY147192	A.thaliana
c 834	6	42.9	2426	10	MMU80078	Mus musculu	907	6	42.9	2923	8	ATCADH	Sequence
c 835	6	42.9	2429	5	SEOMTCOS3B	Sceloporus	c 908	6	42.9	2930	8	AY122272	Zea mays
c 836	6	42.9	2429	5	SEOMTCOS3D	Sceloporus	909	6	42.9	2952	9	AF432210	Homo sapi
c 837	6	42.9	2429	5	SEOMTCOS3E	Sceloporus	910	6	42.9	2954	6	CQ593861	Sequence
c 838	6	42.9	2429	5	SEOMTCOS3F	Sceloporus	c 911	6	42.9	2955	6	BD160569	Primer fo
c 839	6	42.9	2429	5	SEOMTCOS3G	Sceloporus	c 912	6	42.9	2955	6	AX883855	Sequence
c 840	6	42.9	2429	5	SEOMTCOS3H	Sceloporus	c 913	6	42.9	2955	9	AK024298	Homo sapi
c 841	6	42.9	2429	5	SEOMTCOS3I	Sceloporus	914	6	42.9	2960	6	AX416482	Sequence
c 842	6	42.9	2429	5	SEOMTCOS3J	Sceloporus	915	6	42.9	2962	9	BC050260	Homo sapi
c 843	6	42.9	2429	5	SEOMTCOS3K	Sceloporus	c 916	6	42.9	2970	3	DDU38197	Dictyosteli
c 844	6	42.9	2437	6	I12324	Sequence 5	c 917	6	42.9	2983	10	BC008552	Mus muscu
c 845	6	42.9	2437	6	I70227	Sequence 5	918	6	42.9	2994	6	AX447790	Sequence
c 846	6	42.9	2437	6	AR371464	Sequence	c 919	6	42.9	3005	6	AX714290	Sequence
c 847	6	42.9	2437	9	HUMSRDA	Human stero	920	6	42.9	3005	9	AK056521	Homo sapi
c 848	6	42.9	2443	1	RF1556146	Richettsi	921	6	42.9	3007	5	AF006488	Danio rer
c 849	6	42.9	2462	8	AY048200	Arabidops	922	6	42.9	3007	10	BC026144	Mus muscu
c 850	6	42.9	2464	5	CQ719296	Sequence	923	6	42.9	3010	10	BC006035	Mus muscu
c 851	6	42.9	2465	5	BC076414	Danio rer	c 924	6	42.9	3015	6	CQ598457	Sequence
852	6	42.9	2469	8	D63461	Arabidopsis	925	6	42.9	3016	6	BD175121	Androgen
853	6	42.9	2488	10	BC023291	Mus muscu	926	6	42.9	3016	6	CQ789324	Sequence
854	6	42.9	2490	5	SN0BNHE	Trout sodiu	927	6	42.9	3016	6	AX492926	Sequence
c 855	6	42.9	2491	1	ECRCFGENE	E.chrysanth	c 928	6	42.9	3017	1	AF397144	Listeria
c 856	6	42.9	2491	5	AY485821	Sebastes	929	6	42.9	3023	9	AB056106	Homo sapi
c 857	6	42.9	2538	9	BC040145	Homo sapi	930	6	42.9	3023	9	BC050296	Homo sapi
c 858	6	42.9	2562	6	AX927175	Sequence	931	6	42.9	3032	9	AJ236885	Homo sapi
859	6	42.9	2570	6	BD160561	Primer fo	c 932	6	42.9	3048	1	PSETAM	P.amyiodera
860	6	42.9	2570	6	AX883843	Sequence	c 933	6	42.9	3056	5	BC060902	Danio rer
861	6	42.9	2570	9	AK024291	Homo sapi	c 934	6	42.9	3060	6	CQ595958	Sequence
862	6	42.9	2575	9	H5U23946	Human putat	935	6	42.9	3077	9	HSAL10894	Homo sapi
c 863	6	42.9	2582	6	AX714457	Sequence	936	6	42.9	3089	9	BC002957	Homo sapi
c 864	6	42.9	2582	9	AK056791	Homo sapi	937	6	42.9	3094	9	AF103802	Homo sapi
865	6	42.9	2593	5	AJ719513	Gallus ga	c 938	6	42.9	3116	6	CQ716398	Sequence
866	6	42.9	2625	1	PSEIRMA	Pseudomonas	c 939	6	42.9	3129	8	AY080588	Arabidops
867	6	42.9	2625	6	AI0909	Pseudomonas	940	6	42.9	3135	9	AF091263	Homo sapi
868	6	42.9	2625	6	AK365014	Sequence	941	6	42.9	3141	9	F325326S14	Sequence
869	6	42.9	2625	6	AX089532	Sequence	942	6	42.9	3144	6	CQ574853	Sequence
c 870	6	42.9	2631	10	BC058852	Mus muscu	c 943	6	42.9	3144	6	AB074498	Homo sapi
871	6	42.9	2646	9	AF093250	Homo sapi	c 944	6	42.9	3152	10	RAT5RRHP	Rat 5'-nucl
872	6	42.9	2653	8	AY062555	Arabidops	945	6	42.9	3165	5	TILGH2X	Tilapia nil
873	6	42.9	2667	6	CQ581817	Sequence	946	6	42.9	3180	8	AK099512	Oryza sat
874	6	42.9	2670	10	BC070910	Rattus no	c 947	6	42.9	3188	3	AY014405	Anopheles
875	6	42.9	2683	1	ABCALDH	Acetobacter	948	6	42.9	3189	6	AX076993	Sequence
c 876	6	42.9	2696	5	BC054680	Danio rer	949	6	42.9	3189	6	AX113966	Sequence
877	6	42.9	2704	1	AJ585346	Clostridi	950	6	42.9	3196	5	AJ719417	Gallus ga
878	6	42.9	2706	6	CQ594119	Sequence	951	6	42.9	3208	6	BD249920	human
879	6	42.9	2715	6	AK375386	Sequence	c 952	6	42.9	3210	1	AF175295	Vibrio ch
880	6	42.9	2723	9	HSM804929	Homo sapi	c 953	6	42.9	3221	5	AJ719727	Gallus ga

```

c 954      6 42.9 3239 10 BC025581
955      6 42.9 3250 5 BC068779
956      6 42.9 3266 9 BC022219
957      6 42.9 3268 10 BC024074
958      6 42.9 3280 9 AK122945
959      6 42.9 3284 9 AK095623
960      6 42.9 3306 9 AB094094
961      6 42.9 3320 3 GIU93353
962      6 42.9 3336 6 AR365012
963      6 42.9 3337 8 CRU13168
964      6 42.9 3340 6 C0785752
965      6 42.9 3358 8 AK046016
966      6 42.9 3361 9 AK025223
967      6 42.9 3420 6 AK076995
968      6 42.9 3420 6 AX113968
969      6 42.9 3427 6 C0728177
970      6 42.9 3452 8 TA288RITS
971      6 42.9 3464 6 AK144982
972      6 42.9 3464 6 AX050470
973      6 42.9 3464 9 HUMFOL5
974      6 42.9 3474 5 AF038425
975      6 42.9 3487 6 AX833295
976      6 42.9 3487 9 AK094914
977      6 42.9 3502 6 AR448004
978      6 42.9 3516 1 AB090359
979      6 42.9 3546 5 TRU345039
980      6 42.9 3546 6 AR029518
981      6 42.9 3546 6 AK098471
982      6 42.9 3546 6 I14131
983      6 42.9 3546 6 AR494980
984      6 42.9 3546 6 AX441396
985      6 42.9 3546 6 AX453892
986      6 42.9 3623 6 CQ576768
987      6 42.9 3690 5 AY167041
988      6 42.9 3700 8 AY536888
989      6 42.9 3702 8 PFA544768
990      6 42.9 3709 3 U01842
991      6 42.9 3709 6 AR240582
992      6 42.9 3709 6 AR403854
993      6 42.9 3717 3 DMVAS1HE
994      6 42.9 3723 9 HSM808835
995      6 42.9 3765 10 RNL125
996      6 42.9 3792 6 CQ585768
997      6 42.9 3799 6 AX743766
998      6 42.9 3799 8 YSCTRK2Q
999      6 42.9 3850 5 BC077134
1000     6 42.9 3874 10 AB093260

                                BC025581 Mus muscu
                                BC068779 Xenopus l
                                BC022219 Homo sapi
                                BC024074 Mus muscu
                                AK122945 Homo sapi
                                AK095623 Homo sapi
                                AB094094 Homo sapi
                                GIU93353 Giardia int
                                AR365012 Sequence
                                CRU13168 Chlamydomon
                                C0785752 Sequence
                                AK046016 Arabidops
                                AK025223 Homo sapi
                                AK076995 Sequence
                                AX113968 Sequence
                                C0728177 Sequence
                                Y07979 T.aequale 2
                                AK144982 Sequence
                                AX050470 Sequence
                                J00139 Human dihyd
                                AF038425 Danio rer
                                AX833295 Sequence
                                AK094914 Homo sapi
                                AR448004 Sequence
                                AB090359 Pectobact
                                AJ345039 Takifugu
                                AR029518 Sequence
                                AK098471 Sequence
                                I14131 Sequence 27
                                AR494980 Sequence
                                AX441396 Sequence
                                AX453892 Sequence
                                CQ576768 Sequence
                                AY167041 Pseudople
                                AY536888 Arabidops
                                A5544768 Physcomit
                                U01842 Drosophila
                                AR240582 Sequence
                                AR403854 Sequence
                                X82641 D.melanogas
                                BX648684 Homo sapi
                                X74226 R.norvegicu
                                CQ585768 Sequence
                                AX743766 Sequence
                                M65215 S.cerevisia
                                BC077134 Danio rer
                                AB093260 Mus muscu

ALIGNMENTS

RESULT 1
A74835      A74835      136 bp      DNA      linear      PAT 15-OCT-1999
LOCUS      Sequence 521 from Patent WO9401548.
DEFINITION A74835
ACCESSION  A74835
VERSION    A74835.1 GI:6064849
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 136)
AUTHORS   Sibson,D.R. and Gross,J.
TITLE     HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE,
          PLACENTA OR BONE NARROW
JOURNAL   Patent: WO 9401548-A 521 20-JAN-1994;
          MEDICAL RES COUNCIL (GB); SIBSON DAVID ROSS (GB)
FEATURES   Location/Qualifiers
            source
              1..136
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

ORIGIN

c 954      6 42.9 3239 10 BC025581
955      6 42.9 3250 5 BC068779
956      6 42.9 3266 9 BC022219
957      6 42.9 3268 10 BC024074
958      6 42.9 3280 9 AK122945
959      6 42.9 3284 9 AK095623
960      6 42.9 3306 9 AB094094
961      6 42.9 3320 3 GIU93353
962      6 42.9 3336 6 AR365012
963      6 42.9 3337 8 CRU13168
964      6 42.9 3340 6 C0785752
965      6 42.9 3358 8 AK046016
966      6 42.9 3361 9 AK025223
967      6 42.9 3420 6 AK076995
968      6 42.9 3420 6 AX113968
969      6 42.9 3427 6 C0728177
970      6 42.9 3452 8 TA288RITS
971      6 42.9 3464 6 AK144982
972      6 42.9 3464 6 AX050470
973      6 42.9 3464 9 HUMFOL5
974      6 42.9 3474 5 AF038425
975      6 42.9 3487 6 AX833295
976      6 42.9 3487 9 AK094914
977      6 42.9 3502 6 AR448004
978      6 42.9 3516 1 AB090359
979      6 42.9 3546 5 TRU345039
980      6 42.9 3546 6 AR029518
981      6 42.9 3546 6 AK098471
982      6 42.9 3546 6 I14131
983      6 42.9 3546 6 AR494980
984      6 42.9 3546 6 AX441396
985      6 42.9 3546 6 AX453892
986      6 42.9 3623 6 CQ576768
987      6 42.9 3690 5 AY167041
988      6 42.9 3700 8 AY536888
989      6 42.9 3702 8 PFA544768
990      6 42.9 3709 3 U01842
991      6 42.9 3709 6 AR240582
992      6 42.9 3709 6 AR403854
993      6 42.9 3717 3 DMVAS1HE
994      6 42.9 3723 9 HSM808835
995      6 42.9 3765 10 RNL125
996      6 42.9 3792 6 CQ585768
997      6 42.9 3799 6 AX743766
998      6 42.9 3799 8 YSCTRK2Q
999      6 42.9 3850 5 BC077134
1000     6 42.9 3874 10 AB093260

                                BC025581 Mus muscu
                                BC068779 Xenopus l
                                BC022219 Homo sapi
                                BC024074 Mus muscu
                                AK122945 Homo sapi
                                AK095623 Homo sapi
                                AB094094 Homo sapi
                                GIU93353 Giardia int
                                AR365012 Sequence
                                CRU13168 Chlamydomon
                                C0785752 Sequence
                                AK046016 Arabidops
                                AK025223 Homo sapi
                                AK076995 Sequence
                                AX113968 Sequence
                                C0728177 Sequence
                                Y07979 T.aequale 2
                                AK144982 Sequence
                                AX050470 Sequence
                                J00139 Human dihyd
                                AF038425 Danio rer
                                AX833295 Sequence
                                AK094914 Homo sapi
                                AR448004 Sequence
                                AB090359 Pectobact
                                AJ345039 Takifugu
                                AR029518 Sequence
                                AK098471 Sequence
                                I14131 Sequence 27
                                AR494980 Sequence
                                AX441396 Sequence
                                AX453892 Sequence
                                CQ576768 Sequence
                                AY167041 Pseudople
                                AY536888 Arabidops
                                A5544768 Physcomit
                                U01842 Drosophila
                                AR240582 Sequence
                                AR403854 Sequence
                                X82641 D.melanogas
                                BX648684 Homo sapi
                                X74226 R.norvegicu
                                CQ585768 Sequence
                                AX743766 Sequence
                                M65215 S.cerevisia
                                BC077134 Danio rer
                                AB093260 Mus muscu

us-09-736-250-5 (1-14) x A74835 (1-136)

Alignment Scores:
Pred. No.:      6.03e-08      Length:      136
Score:          14.00         Matches:     14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%      Indels:        0
DB:             6            Gaps:         0

US-09-736-250-5 (1-14) x A74835 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCTCAGAAAATGCGGTCTCTGTGTGGCACT 65

RESULT 2
A77814      A77814      136 bp      DNA      linear      PAT 19-OCT-1999
LOCUS      Sequence 521 from Patent EP0587279.
DEFINITION A77814
ACCESSION  A77814
VERSION    A77814.1 GI:6089479
KEYWORDS   unidentified
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 136)
AUTHORS   Sibson,D.R. and Hadfield,K.M.
TITLE     HUMAN NUCLEIC ACID FRAGMENTS ISOLATED FROM BRAIN, ADRENAL TISSUE,
          PLACENTA OR BONE NARROW AND THEIR USE
JOURNAL   Patent: EP 0587279-A 521 16-MAR-1994;
          MEDICAL RES COUNCIL (GB)
FEATURES   Location/Qualifiers
            source
              1..136
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

ORIGIN

Alignment Scores:
Pred. No.:      6.03e-08      Length:      136
Score:          14.00         Matches:     14
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:    0
Query Match:    100.00%      Indels:        0
DB:             6            Gaps:         0

US-09-736-250-5 (1-14) x A77814 (1-136)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCTCAGAAAATGCGGTCTCTGTGTGGCACT 65

RESULT 3
CQ712652     CQ712652     288 bp      DNA      linear      PAT 03-FEB-2004
LOCUS      Sequence 57578 from Patent WO02070737.
DEFINITION CQ712652
ACCESSION  CQ712652
VERSION    CQ712652.1 GI:42273509
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
REFERENCE  1
AUTHORS     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE      Liew,C.C., Marshall,W.E. and Zhang,H.
JOURNAL    Compositions and methods relating to osteoarthritis
          Patent: WO 02070737-A 57578 12-SEP-2002;
          Chondrogene Inc. (CA)
FEATURES   Location/Qualifiers
            source
              1..288
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

ORIGIN
```

ORIGIN

Alignment Scores:
Pred. No.: 1.26e-07 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ712652 (1-288)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 104

RESULT 4
LOCUS CQ675890 350 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 20816 from Patent WO02070737.
ACCESSION CQ675890
VERSION CQ675890.1 GI:42180044
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 20816 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source
1. 350
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.52e-07 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x CQ675890 (1-350)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 170

RESULT 5
LOCUS AX397198/C 444 bp DNA linear PAT 18-MAY-2002
DEFINITION Sequence 1413 from Patent WO0212328.
ACCESSION AX397198
VERSION AX397198.1 GI:21067945
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212328-A 1413 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
source
1. 444
/organism="Homo sapiens"

ORIGIN

Alignment Scores:
Pred. No.: 1.92e-07 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX397198 (1-444)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 395

RESULT 6
LOCUS AX198885 447 bp DNA linear PAT 29-AUG-2001
DEFINITION Sequence 1340 from Patent WO0151513.
ACCESSION AX198885
VERSION AX198885.1 GI:15389211
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Algate, P.A.
TITLE Ovarian tumor-associated sequences
JOURNAL Patent: WO 0151513-A 1340 19-JUL-2001;
CORIXA CORPORATION (US)
FEATURES
source
1. 447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Alignment Scores:
Pred. No.: 1.94e-07 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX198885 (1-447)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 134

RESULT 7
LOCUS AX209412 447 bp DNA linear PAT 31-AUG-2001
DEFINITION Sequence 1252 from Patent WO0157207.
ACCESSION AX209412
VERSION AX209412.1 GI:15423835
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Algate, P.A. and Mannion, J.
TITLE Compositions and methods for the therapy and diagnosis of ovarian cancer
JOURNAL Patent: WO 0157207-A 1252 09-AUG-2001;
CORIXA CORPORATION (US)
FEATURES
Location/Qualifiers

```
source
1..447
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 1.94e-07 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AX209412 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGTTGGTCTCTGTGTGGCACT 134

RESULT 8
BVI180201/c
LOCUS
DEFINITION sqm108417 Human DNA (Sequenom) Homo sapiens STS genomic, sequence
tagged site.
ACCESSION BVI180201
VERSION BVI180201.1 GI:48017195
KEYWORDS STS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 601)
AUTHORS Nelson,R.M., Marnellos,G., Kammerer,S., Hoyal,C.R., Shi,M.M.,
Cantor,C.R. and Braun,A.
TITLE Large-Scale Validation of Single Nucleotide Polymorphisms in Gene
Regions
JOURNAL Genome Res. (2004) In press
COMMENT Contact: Andreas Braun
Pharmaceuticals division
3595 John Hopkins Court, San Diego, CA 92121, USA
Tel: 18582029018
Fax: 18582029020
Email: abraun@sequenom.com
Primer A: No primer sequence submitted
Primer B: No primer sequence submitted
STS size: 601.
FEATURES
source
Location/Qualifiers
1..601
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone_lib="Human DNA (Sequenom)"
<1..>601

STS
ORIGIN
Alignment Scores:
Pred. No.: 2.59e-07 Length: 601
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x BVI180201 (1-601)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 327 GAAGATAATGCTCAGAAAATGTTGGTCTCTGTGTGGCACT 286

RESULT 9
```

```
BD079737/c
LOCUS
DEFINITION Cancer-associated nucleic acids and polypeptides.
ACCESSION BD079737
VERSION BD079737.1 GI:22625340
KEYWORDS JP 2001516009-A/403.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 804)
AUTHORS Old,L.J., Scanlan,M.J., Stockert,E., Gure,A., Chen,Y.T., Gout,I.,
Oghare,M., Obata,Y., Pfreundschuh,M., Tureci,O. and Sahin,U.
TITLE Cancer-associated nucleic acids and polypeptides
JOURNAL Patent: JP 2001516009-A 403 25-SEP-2001;
LUDWIG INSTITUTE FOR CANCER RESEARCH
COMMENT OS Homo sapiens (human)
PN JP 2001516009-A/403
PD 25-SEP-2001
PF 15-JUL-1998 JP 2000503425
PR 17-JUL-1997 US 08/896164,10-OCT-1997 US 60/061599 PR
10-OCT-1997 US 60/061765,10-OCT-1997 US 08/948705 PR
11-OCT-1997 GB 9721697.2,22-JUN-1998 US 09/102322 PI LLOYD
J OLD,MATTHEW J SCANLAN,ELISABETH STOCKERT,ALI GURE,YAO PI TSENG
CHEN,
PI IVAN GOUT,MICHAEL O'HARE,YUICHI OBATA,MICHAEL PFREUNDSCUH, PI
OZLEM TURECI
PI UGUR SAHIN
PC
GOIN33/574,A61K38/00,A61K39/395,A61K39/395,A61K45/00,A61K48/00, PC
A61P35/00,
PC C07K14/82,C07K16/32,C12N15/09//C07K16/46,C12P21/08,A61K37/02,
PC C12N15/00
CC Cancer-associated nucleic acids and polypeptides. FH Key
Location/Qualifiers
FT source
1..804
/organism="Homo sapiens (human)"
/ol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Alignment Scores:
Pred. No.: 3.45e-07 Length: 804
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x BD079737 (1-804)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 301 GAAGATAATGCTCAGAAAATGTTGGTCTCTGTGTGGCACT 260

RESULT 10
CR541783
LOCUS
DEFINITION Homo sapiens full open reading frame cDNA clone RZPD0834E0730D for
gene CCNI, cyclin I; complete cds, without stopcodon.
ACCESSION CR541783
VERSION CR541783.1 GI:49456522
KEYWORDS Full ORF shuttle clone, Gateway(TM), complete cds.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1131)
AUTHORS Halleck,A., Ebert,L., Mkoundinya,M., Schick,M., Eisenstein,S.,
Neubert,P., Kstrang,K., Schatten,R., Shen,B., Henze,S., Mar,W.,
```

Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Cloning of human full open reading frames in Gateway (TM) system
entry vector (pDONR201)
2 (bases 1 to 1131)
Halleck, A., Ebert, L., Moundinya, M., Schick, M., Eisenstein, S.,
Neubert, P., Kstrang, K., Schatten, R., Shen, B., Henze, S., Mat, W.,
Korn, B., Zuo, D., Hu, Y. and LaBaer, J.
Direct Submission
Submitted (28-JUN-2004) RZPD Deutsches Ressourcenzentrum fuer
Genomforschung GmbH, Im Neuenheimer Feld 580, D-69120 Heidelberg,
Germany
RZPD: RZPD0834E0730D, ORFNo 3592
www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=RZPD0834E0730D RZPDLIB;
Human Full ORF Clones Gateway(TM) - RZPD (kan-resist.) RZPD LIB No.
834
www.rzpd.de/cgi-bin/products/showLib.pl.cgi?response?libNo=834
www.rzpd.de/products/orfclones/
Contact: Inge Arlart
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH,
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 100
Fax: +49 30 32639 111
www.rzpd.de
This clone is available from RZPD;
Contact RZPD (customer.service@rzpd.de) for further information.
Clone name at Harvard Institute of Proteomics
(www.hip.harvard.edu): FLH131015.01L
This CDS clone is part of a collection of human full ORF clones
jointly established and verified by the Harvard Institute of
Proteomics (HIP) and RZPD.
This CDS has been cloned without stopcodon.
The CDS has been inserted into pDONR201 via a BP Clonase (TM)
reaction. Additional sequence has been added in front of the start
codon: att. AAAAAA GCA GGC TCC ACC (ATG).
The last codon is followed by the 3' att site: GACCCAGCTTCTT. .att
The clone is validated by full sequence check.
Compared to the reference sequence NM 006835 (GI:17738314) we found
AA exchange(s) at position (first base of changed triplet):
223(arg->gly) 409(lys->arg)
Clone distribution: http://www.rzpd.de/products/orfclones/
Location/Qualifiers
1. .1131
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="RZPD0834E0730D"
/clone_lib="Human Full ORF Clones Gateway(TM) - RZPD"
/lab_host="DH5Alpha"
/note="vector: pDONR201, Site_1: attP1; Site_2: attP2"
1. .1131
/gene="CCNI"
1. .>1131
/gene="CCNI"
/codon_start=1
/protein_id="CAG46582.1"
/db_xref="GI:4945623"
/translation="MKFPGPLENORLSFLLEKAITREAQMKVNRKMPNSQNVSPSQ
RDEVIOMLAKYQNFYPTFALASLLDGLATVKAHPKLSLCIALSCFFLAQTV
EEDERIPVLKVLARDSFCGSSSEILRMERILDLRLWDLHTATPLFLHFLHAIYS
TRPQLPLSLKLSPSQHLAVTKQLLHMCACNQLQFRGSMALAMVSLNEKCLIPDW
LSLTELQKQAMDSQSLIHCRRELVHHLSTLQSLPLNSVYVYRPLKHLTVTCDKGV
FRLHPSSVPGPDFSKDMSKPEVPVRGTAFAFVHLPLPAASGCKQTSTKRKVEMEVDYF
DGIKRLYNEDNVSNVSGVCTGLSRQEGHASPFPPLQPVSM"

FEATURES
source

gene

CDS

ORIGIN

Alignment Scores:

Pred. No.: 4.82e-07 Length: 1131
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

TITLE Cloning of human full open reading frames in Gateway (TM) system

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

US-09-736-250-5 (1-14) x CR541783 (1-1131)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 1027 GAAGATAATCTCTCAGAAAATGGGTCTGTGTGGCACT 1068

RESULT 11

LOCUS

AR145734 1133 bp DNA linear

DEFINITION

Sequence 2 from patent US 6218115.

ACCESSION

AR145734

VERSION

AR145734.1 GI:15108923

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1133)

AUTHORS

Nakamura, T.

TITLE

Human cyclin I and genes encoding same

JOURNAL

Patent: US 6218115-A 2 17-APR-2001;

FEATURES

Location/Qualifiers

1. .1133

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 4.83e-07 Length: 1133

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AR145734 (1-1133)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 1027 GAAGATAATCTCTCAGAAAATGGGTCTGTGTGGCACT 1068

RESULT 12

LOCUS

AR087353 1260 bp DNA linear

DEFINITION

Sequence 5 from patent US 5986055.

ACCESSION

AR087353

VERSION

AR087353.1 GI:10014116

KEYWORDS

Unknown.

SOURCE

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1260)

AUTHORS

Yang M., Nandabalan, K. and Schultz, V. Peter.

TITLE

CDK2 interactions

JOURNAL

Patent: US 5986055-A 5 16-NOV-1999;

FEATURES

Location/Qualifiers

source

1. .1260

/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Alignment Scores:

Pred. No.: 5.36e-07 Length: 1260

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x AR087353 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14


```
Db      1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068
RESULT 13
LOCUS   CQ812312                1260 bp    DNA        linear    PAT 24-MAY-2004
DEFINITION Sequence 64 from Patent WO2004038020.
ACCESSION CQ812312
VERSION   CQ812312.1 GI:47601932
KEYWORDS
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Wittig R., Poustka A., Mollenhauer J. and Schadendorf, D.
TITLE    Target genes for the diagnosis and treatment of cancer
JOURNAL  Patent: WO 2004038020-A 64 06-MAY-2004;
          Deutsches Krebsforschungszentrum Stiftung des oeffentliche n Rechts
          (DE)
FEATURES             Location/Qualifiers
     source             1..1260
                        /organism="Homo sapiens"
                        /mol_type="unassigned DNA"
     misc_feature       1..1260
                        /note="D50310"
ORIGIN
Alignment Scores:
Pred. No.:             5.36e-07      Length:      1260
Score:                 14.00          Matches:    14
Percent Similarity:    100.00%        Conservative: 0
Best Local Similarity: 100.00%        Mismatches: 0
Query Match:           100.00%        Indels:     0
DB:                    6              Gaps:       0

US-09-736-250-5 (1-14) x CQ812312 (1-1260)

Qy      1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db      1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068

RESULT 14
LOCUS   AR281918                1260 bp    DNA        linear    PAT 10-APR-2003
DEFINITION Sequence 5 from patent US 6521412.
ACCESSION AR281918
VERSION   AR281918.1 GI:29717848
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Yang, M., Nandabalan, K. and Schulz, V. P.
TITLE    HsReq*1 and HsReq*2 proteins and use thereof to detect CDK2
JOURNAL  Patent: US 6521412-A 5 18-FEB-2003;
          Location/Qualifiers
FEATURES             source
                        1..1260
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:             5.36e-07      Length:      1260
Score:                 14.00          Matches:    14
Percent Similarity:    100.00%        Conservative: 0
Best Local Similarity: 100.00%        Mismatches: 0
Query Match:           100.00%        Indels:     0
DB:                    6              Gaps:       0

US-09-736-250-5 (1-14) x AR281918 (1-1260)

Qy      1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db      1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068

RESULT 15
LOCUS   AR380354                1260 bp    DNA        linear    PAT 18-DEC-2003
DEFINITION Sequence 899 from patent US 6607879.
ACCESSION AR380354
VERSION   AR380354.1 GI:40087988
KEYWORDS
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE
AUTHORS Cocks, B.G., Stuart, S.G. and Seilhamer, J.J.
TITLE    Compositions for the detection of blood cell and immunological
          response gene expression
JOURNAL  Patent: US 6607879-A 899 19-AUG-2003;
          Location/Qualifiers
FEATURES             source
                        1..1260
                        /organism="unknown"
                        /mol_type="genomic DNA"
ORIGIN
Alignment Scores:
Pred. No.:             5.36e-07      Length:      1260
Score:                 14.00          Matches:    14
Percent Similarity:    100.00%        Conservative: 0
Best Local Similarity: 100.00%        Mismatches: 0
Query Match:           100.00%        Indels:     0
DB:                    6              Gaps:       0

US-09-736-250-5 (1-14) x AR380354 (1-1260)

Qy      1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db      1027 GAAGATAATGCTCAGAAAATGGGGTTCTGTGTGGCACT 1068

Search completed: February 11, 2005, 14:34:43
Job time : 348.55 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 07:36:40 ; Search time 35.1969 Seconds
(without alignments)
2354.648 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGSVCGT 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8760405

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154941_20640/app_query.fasta_1.718
-DB=N_Geneseq_16Dec04 -QWTF=fastap -SUFFIX=oligo.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09736250 @CGN 1 1 586 @runat_07022005_154941_20640 -ICPU=3
-NO_MMAP -LARGOQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	100.0	136	2	AaQ76921 Human gen
c 2	14	100.0	351	8	AaD51549 Human BCA
3	14	100.0	389	10	ADK61066 Ovarian c
c 4	14	100.0	444	6	ABK45862 CDNA enco
5	14	100.0	447	4	AaE25071 Human ova

6	14	100.0	447	5	AaH83716 Human ova
c 7	14	100.0	597	10	ADK61065 Ovarian c
c 8	14	100.0	804	2	AaX40003 Prostate
9	14	100.0	903	12	ADN01156 Human cel
10	14	100.0	1260	3	AaZ37836 Human cyc
11	14	100.0	1260	6	ABK83672 Human cDN
12	14	100.0	1260	10	ADK61064 Ovarian c
13	14	100.0	1260	11	ADi31573 Human cDN
14	14	100.0	1260	13	ADr25465 Breast ca
15	14	100.0	1328	2	AaT73937 DNA encod
16	14	100.0	1384	8	ACC47339 Human pro
17	14	100.0	1493	2	AaZ41284 Human nor
18	14	100.0	1651	9	ADr57247 Human CGD
19	14	100.0	1889	6	ABL87929 Human ova
20	14	100.0	1890	12	ADP10653 Reference
21	14	100.0	1890	13	ACN38124 Tumour-as
22	14	100.0	2146	5	ADL63082 Human ova
23	14	100.0	2755	5	ADL63374 Human ova
24	13	92.9	304	3	RAC25819 Human sec
25	8	57.1	791	6	ABQ37048 Oligonuc1
c 26	8	57.1	791	6	ABQ37049 Oligonuc1
27	8	57.1	796	6	ABQ34158 Oligonuc1
c 28	8	57.1	796	6	ABQ34159 Oligonuc1
29	7	50.0	135	2	AAQ76716 Human gen
30	7	50.0	183	2	AAQ76715 Human gen
c 31	7	50.0	293	12	ADQ19591 Human sof
32	7	50.0	420	8	ABX44645 Bovine ES
33	7	50.0	578	12	ACH79716 Human gen
c 34	7	50.0	840	8	ACF64409 Human IP1
c 35	7	50.0	845	9	ADA48912 Wheat gen
c 36	7	50.0	1023	12	ADo61772 Transcrip
c 37	7	50.0	1170	3	AAC39327 Arabidops
38	7	50.0	1226	6	ACA03904 cDNA upre
39	7	50.0	1226	12	ADL13381 Human ste
c 40	7	50.0	1287	3	AAC35385 Arabidops
c 41	7	50.0	1338	6	ABN79897 Fungal ZB
c 42	7	50.0	1428	9	ADr57460 Fruit fly
c 43	7	50.0	1671	4	ABL26107 Drosophil
c 44	7	50.0	1682	10	ADr25706 Human cDN
c 45	7	50.0	2321	8	ACA03913 cDNA down
c 46	7	50.0	3204	10	ABZ39157 N. gonorr
47	7	50.0	3573	13	ADr43795 Bacterial
48	7	50.0	3868	4	ABL26106 Drosophil
49	7	50.0	28170	6	ABA01447 Streptoco
c 50	7	50.0	92562	10	ADC85284 Human ITK
c 51	7	50.0	92563	9	ADA02804 Human ITK
c 52	7	50.0	92563	10	ADB72542 Human ITK
c 53	7	50.0	92563	12	ADM74399 Human car
c 54	6	42.9	19	3	AAZ72285 Human bia
55	6	42.9	25	9	ACI50953 Human mic
56	6	42.9	25	12	ADP13757 Renal cel
57	6	42.9	33	2	AAV25500 Primer EV
c 58	6	42.9	41	6	ABK12099 Phytocro
c 59	6	42.9	60	6	ABN43375 Human spl
60	6	42.9	100	8	ACD70096 E. coli K
c 61	6	42.9	108	4	AAI26919 Probe #16
c 62	6	42.9	108	4	ABA75174 Human foe
c 63	6	42.9	108	4	AAI55718 Probe #24
c 64	6	42.9	108	4	ABA39843 Probe #18
c 65	6	42.9	108	4	AAK49810 Human bon
c 66	6	42.9	108	4	AAK23705 Human bra
c 67	6	42.9	108	4	ABs49447 Human liv
c 68	6	42.9	108	6	ABs23310 Human gen
c 69	6	42.9	121	12	ADo60013 Novel hum
70	6	42.9	159	8	ACC69095 Cucumbe
c 71	6	42.9	171	6	ABN22791 Human ORF
72	6	42.9	201	11	ACH98099 Klebsiell
73	6	42.9	201	13	ADQ41814 Myocardia
74	6	42.9	213	10	ACD96463 Human col
75	6	42.9	235	3	AAA31903 Plant mic
c 76	6	42.9	256	3	AAC23296 Human sec
77	6	42.9	279	8	ABX51427 Bovine ES
78	6	42.9	284	12	ADH00536 Kidney di

C 79	6	42.9	293	5	AAF68603	Aaf68603 Human lun	C 152	6	42.9	500	3	AAc93641	Aac93641 Cat flea
C 80	6	42.9	293	6	ABK38514	Abk38514 cDNA enco	153	6	42.9	505	9	ACH32958	Ach32958 Human end
C 81	6	42.9	293	8	ACR10843	Acr10843 Human lun	154	6	42.9	508	6	ABK34612	Abk34612 Human cDN
C 82	6	42.9	293	8	ABX99794	Abx99794 Lung canc	155	6	42.9	510	13	ADT42610	Adt42610 Bacterial
C 83	6	42.9	293	10	ADH46057	Adh46057 Human lun	C 156	6	42.9	520	4	AAI17719	Aai17719 Probe #76
C 84	6	42.9	293	12	ADT1809	Adt1809 Human lun	C 157	6	42.9	520	4	ABA62659	Aba62659 Human foe
C 85	6	42.9	293	13	ADJ19976	Adj19976 Human lun	C 158	6	42.9	520	4	AAI42655	Aai42655 Probe #81
C 86	6	42.9	293	10	ADD89922	Add89922 Murine DN	C 159	6	42.9	520	4	ABA29969	Aba29969 Probe #11
C 87	6	42.9	304	8	ABX43798	Abx43798 Bovine ES	C 160	6	42.9	520	4	AAK36866	Aak36866 Human bon
C 88	6	42.9	308	6	ABN17315	Abn17315 Human ORF	C 161	6	42.9	520	4	AAK11033	Aak11033 Human bra
C 89	6	42.9	328	5	AAAS87978	Aas87978 DNA enco	C 162	6	42.9	520	4	ABS36537	Abs36537 Human liv
C 90	6	42.9	337	4	AAI82014	Aai82014 Human pol	C 163	6	42.9	520	6	ABS10877	Abs10877 Human gen
C 91	6	42.9	343	2	AAAT51191	Aat51191 Human bre	C 164	6	42.9	521	4	AAK93014	Aak93014 Human cDN
C 92	6	42.9	343	4	AAH36304	Aah36304 Human col	C 165	6	42.9	521	12	ADL29441	Adl29441 3' end of
C 93	6	42.9	343	9	ADA57806	Ada57806 Human par	C 166	6	42.9	526	4	AAH99409	Aah99409 Human pro
C 94	6	42.9	348	3	AAA31744	Aaa31744 Plant mic	C 167	6	42.9	526	4	ABA08557	Aba08557 Human gro
C 95	6	42.9	351	3	AAA31500	Aaa31500 Plant mic	C 168	6	42.9	533	3	AAA81834	Aaa81834 N. mening
C 96	6	42.9	353	9	ACH20340	Ach20340 Human adu	C 169	6	42.9	533	4	AAAS30832	Aas30832 Human cDN
C 97	6	42.9	354	13	ADS50742	Ads50742 Bacterial	C 170	6	42.9	536	6	ABN65617	Abn65617 Human can
C 98	6	42.9	357	6	ABQ68185	Abq68185 Listeria	C 171	6	42.9	538	6	ABV98619	Abv98619 Human pan
C 99	6	42.9	357	6	ABQ69977	Abq69977 Listeria	C 172	6	42.9	543	11	ADT96434	Adt96434 Colon can
C 100	6	42.9	358	2	AAV87567	Aav87567 EST clone	C 173	6	42.9	545	4	AAK74167	Aak74167 Human imm
C 101	6	42.9	360	9	ACH20362	Ach20362 Human adu	C 174	6	42.9	549	6	ABQ37879	Abq37879 Oligonuc
C 102	6	42.9	368	6	ABA99099	Aba99099 Human col	C 175	6	42.9	549	6	ABQ37878	Abq37878 Oligonuc
C 103	6	42.9	379	4	AAK74206	Aak74206 Human imm	C 176	6	42.9	556	4	AAH09116	Aah09116 Human cDN
C 104	6	42.9	380	4	AAK74208	Aak74208 Human imm	C 177	6	42.9	557	6	ABL38491	Abi38491 Human col
C 105	6	42.9	382	4	AAK74207	Aak74207 Human imm	C 178	6	42.9	560	4	AAK94055	Aak94055 Human cDN
C 106	6	42.9	386	3	AAA31444	Aaa31444 Plant mic	C 179	6	42.9	560	12	ADL30482	Adl30482 3' end of
C 107	6	42.9	392	4	AAH99207	Aah99207 Human pro	C 180	6	42.9	561	6	ABV88029	Abv88029 Human col
C 108	6	42.9	393	13	ADR61795	Adr61795 Cotton cD	C 181	6	42.9	563	4	AAK54627	Aak54627 Human hae
C 109	6	42.9	399	9	ACH49522	Ach49522 Human leu	C 182	6	42.9	563	4	AAK54755	Aak54755 Human hae
C 110	6	42.9	401	4	ABA57015	Aba57015 Human foe	C 183	6	42.9	563	4	AAK54924	Aak54924 Human hae
C 111	6	42.9	401	4	ABS30296	Abs30296 Human liv	C 184	6	42.9	565	6	ABQ37134	Abq37134 Oligonuc
C 112	6	42.9	406	6	ABQ55831	Abq55831 Human ova	C 185	6	42.9	565	6	ABQ37135	Abq37135 Oligonuc
C 113	6	42.9	414	6	ABK80229	Abk80229 Bacillus	C 186	6	42.9	566	5	AAK74235	Aak74235 DNA enco
C 114	6	42.9	429	5	ABV00164	Abv00164 Human pro	C 187	6	42.9	583	3	AAF10972	Aaf10972 Fusarium
C 115	6	42.9	434	10	ACD96670	Acd96670 Human col	C 188	6	42.9	585	4	ABL16425	Abi16425 Drosophil
C 116	6	42.9	441	9	ACH41591	Ach41591 Human foe	C 189	6	42.9	594	6	ABK78903	Abk78903 Bacillus
C 117	6	42.9	446	6	ABL68081	Abi68081 Ovary can	C 190	6	42.9	608	13	ADQ57592	Adq57592 Novel can
C 118	6	42.9	446	6	ABL65126	Abi65126 Lung canc	C 191	6	42.9	622	8	ACC44873	Acc44873 Human KG-
C 119	6	42.9	446	6	ABL66878	Abi66878 Lung canc	C 192	6	42.9	630	6	ABK53349	Abk53349 Human eos
C 120	6	42.9	446	6	ABT11074	Abt11074 Human bre	C 193	6	42.9	633	10	ACF70015	Acf70015 Photorhab
C 121	6	42.9	450	5	ABV09333	Abv09333 Human pro	C 194	6	42.9	638	6	ABQ22263	Abq22263 Oligonuc
C 122	6	42.9	455	10	ADD33222	Add33222 Human mit	C 195	6	42.9	638	6	ABQ22262	Abq22262 Oligonuc
C 123	6	42.9	458	9	ACH24078	Ach24078 Human adu	C 196	6	42.9	639	11	ACH98145	Ach98145 Klebsiell
C 124	6	42.9	465	9	ACH48012	Ach48012 Human lun	C 197	6	42.9	677	13	ADQ53349	Adq53349 Novel can
C 125	6	42.9	465	9	ACH24024	Ach24024 Human adu	C 198	6	42.9	692	4	AAI18173	Aai18173 Human bre
C 126	6	42.9	469	6	ABL93459	Abi93459 Arabidops	C 199	6	42.9	702	8	ACA36744	Aca36744 Prokaryot
C 127	6	42.9	472	4	AAAC99781	Aac99781 Skin cell	C 200	6	42.9	708	10	ADF02266	Adf02266 Bacterial
C 128	6	42.9	472	6	ABL34933	Abi34933 Murine cD	C 201	6	42.9	710	4	AAI197812	Aai197812 Human neu
C 129	6	42.9	475	5	AAF66748	Aaf66748 Novel hum	C 202	6	42.9	712	6	ABQ35812	Abq35812 Oligonuc
C 130	6	42.9	476	10	ADG90946	Adg90946 Hepatic s	C 203	6	42.9	712	6	ABQ35813	Abq35813 Oligonuc
C 131	6	42.9	477	4	AAI15872	Aai15872 Probe #58	C 204	6	42.9	743	4	AAH06742	Aah06742 Human cDN
C 132	6	42.9	477	4	ABA58174	Aba58174 Human foe	C 205	6	42.9	772	10	ADJ26344	Adj26344 Novel end
C 133	6	42.9	477	4	AAI37781	Aai37781 Probe #64	C 206	6	42.9	772	12	ADM68457	Adm68457 Mosaic vi
C 134	6	42.9	477	4	AAK58740	Aak58740 Human imm	C 207	6	42.9	772	12	ADP26610	Adp26610 Heterodup
C 135	6	42.9	477	4	ABA27359	Aba27359 Probe #58	C 208	6	42.9	772	13	ADQ88432	Adq88432 TMV-U2/To
C 136	6	42.9	477	4	AAK31914	Aak31914 Human bon	C 209	6	42.9	772	13	ADQ88432	Adq88432 TMV-U2/To
C 137	6	42.9	477	4	AAK06254	Aak06254 Human bra	C 210	6	42.9	773	13	ADQ81786	Adq81786 TMV-U2/To
C 138	6	42.9	477	4	AAK31604	Aak31604 Human liv	C 211	6	42.9	810	4	AAAS23014	Aas23014 Cotton cD
C 139	6	42.9	477	6	ABS06676	Abs06676 Human gen	C 212	6	42.9	822	3	AAA81751	Aaa81751 N. mening
C 140	6	42.9	477	10	ADG90945	Adg90945 Hepatic s	C 213	6	42.9	830	12	ADL13129	Adl13129 Human ste
C 141	6	42.9	478	5	ABV39482	Abv39482 Human pro	C 214	6	42.9	846	6	ABN98868	Abn98868 Arabidops
C 142	6	42.9	480	3	AAZ61644	Aaz61644 cDNA enco	C 215	6	42.9	852	4	AAH73329	Aah73329 Human cer
C 143	6	42.9	480	3	AAZ61735	Aaz61735 cDNA enco	C 216	6	42.9	858	10	ADD34369	Add34369 Mouse mit
C 144	6	42.9	480	4	AAAC99668	Aac99668 Skin cell	C 217	6	42.9	862	2	AAV59573	Aav59573 Human sec
C 145	6	42.9	480	4	AAAC99577	Aac99577 Skin cell	C 218	6	42.9	862	8	AAV59573	Aav59573 Human sec
C 146	6	42.9	480	6	ABL34820	Abi34820 Murine cD	C 219	6	42.9	862	8	AAV59573	Aav59573 Human sec
C 147	6	42.9	480	6	ABL34729	Abi34729 Murine cD	C 220	6	42.9	862	8	AAV59573	Aav59573 Human sec
C 148	6	42.9	483	6	ABS69274	Abs69274 Novel mur	C 221	6	42.9	862	9	ACD82703	Acd82703 cDNA sequ
C 149	6	42.9	488	13	ADQ57723	Adq57723 Novel can	C 222	6	42.9	862	10	ADJ22788	Adj22788 cDNA enco
C 150	6	42.9	488	3	AAZ80168	Aaz80168 Human col	C 223	6	42.9	862	12	ADH73790	Adh73790 Human sec
C 151	6	42.9	498	3	AAZ80168	Aaz80168 Human col	C 224	6	42.9	865	4	AAH06834	Aah06834 Human cDN

225	6	42.9	868	6	ABQ68941	Listeria	Abq68941	298	6	42.9	1239	8	ACA26709	Prokaryot
C 226	6	42.9	879	8	ACA53933	Prokaryot	ACA53933	C 299	6	42.9	1309	12	ADO62646	Transcrip
227	6	42.9	880	5	ADL63214	Human ova	ADL63214	C 300	6	42.9	1309	13	ADI43410	Plant tra
228	6	42.9	892	5	ABV22930	Human pro	ABV22930	C 301	6	42.9	1310	12	ADRO3265	Maize cin
229	6	42.9	892	5	ABV28761	Human pro	ABV28761	C 302	6	42.9	1310	12	AXR82082	Human SIG
C 230	6	42.9	894	3	AAF07793	Fusarium	AAF07793	C 303	6	42.9	1341	6	ABQ15051	Oligonucl
231	6	42.9	897	4	ABL19317	Drosophil	ABL19317	C 304	6	42.9	1341	6	ABQ15050	Oligonucl
C 232	6	42.9	905	4	AAK74168	Human imm	AAK74168	C 305	6	42.9	1345	4	AAK56865	Human imm
233	6	42.9	920	2	AXA22225	Human sec	AXA22225	C 306	6	42.9	1351	11	ADL65886	C. glutam
234	6	42.9	920	2	ACD40469	CDNA sequ	ACD40469	C 307	6	42.9	1371	5	AAH77912	DNA encod
C 235	6	42.9	932	2	AAV59733	Human sec	AAV59733	C 308	6	42.9	1371	5	AAH85776	DNA encod
C 236	6	42.9	932	2	ABV57324	Human cDN	ABV57324	C 309	6	42.9	1371	5	AAH74951	DNA encod
C 237	6	42.9	932	2	ACD82867	CDNA sequ	ACD82867	C 310	6	42.9	1378	6	ABZ78076	Human bre
C 238	6	42.9	932	10	ADI22952	CDNA encod	ADI22952	C 311	6	42.9	1383	6	ABN67484	Streptoco
C 239	6	42.9	932	12	ADH73954	Human sec	ADH73954	C 312	6	42.9	1395	3	AAAC48533	Arabiidops
C 240	6	42.9	935	6	ABQ70274	Listeria	ABQ70274	C 313	6	42.9	1413	4	AAH28941	CDNA encod
241	6	42.9	944	3	AAA58789	CDNA encod	AAA58789	C 314	6	42.9	1413	4	AAH30179	DNA encod
242	6	42.9	962	2	AAQ89874	Bryodin-2	AAQ89874	C 315	6	42.9	1413	4	AAH34809	CDNA encod
243	6	42.9	974	3	AAH35170	Arabiidops	AAH35170	C 316	6	42.9	1413	4	AAH19580	Human exp
C 244	6	42.9	974	3	AAH35170	Arabiidops	AAH35170	C 317	6	42.9	1413	4	AAH06435	Human cDN
C 245	6	42.9	976	6	ABN74460	Bovine em	ABN74460	C 318	6	42.9	1413	4	AAI62753	Human cDN
246	6	42.9	990	12	ADO41953	Human DNA	ADO41953	C 319	6	42.9	1413	4	ABK43513	DNA encod
247	6	42.9	991	8	ABZ51858	Aspergill	ABZ51858	C 320	6	42.9	1413	5	AAH29549	Human end
248	6	42.9	1001	3	AAH51126	Human MGS	AAH51126	C 321	6	42.9	1413	5	ADG15105	Human 7 t
249	6	42.9	1001	3	AAH51127	Human MGS	AAH51127	C 322	6	42.9	1413	6	ABT07776	Novel hum
C 250	6	42.9	1002	12	ADO41949	Human DNA	ADO41949	C 323	6	42.9	1413	6	ABV83772	Human pol
C 251	6	42.9	1007	13	ADH13110	Human can	ADH13110	C 324	6	42.9	1413	8	ACD01434	Human pol
252	6	42.9	1054	3	ABK47317	Peroxidred	ABK47317	C 325	6	42.9	1413	10	ADH45967	Human neo
C 253	6	42.9	1077	8	ACA00711	C. glutam	ACA00711	C 326	6	42.9	1413	12	ADH45967	Human neo
254	6	42.9	1083	4	AAH35118	DNA #68 e	AAH35118	C 327	6	42.9	1455	2	AAH35937	Streptoco
255	6	42.9	1083	4	AAH35118	DNA #68 e	AAH35118	C 328	6	42.9	1485	12	ADO41947	Human DNA
256	6	42.9	1083	4	AAI64007	Human pol	AAI64007	C 329	6	42.9	1512	2	AAH30346	Chicken Y
257	6	42.9	1083	4	ABA06842	Human gen	ABA06842	C 330	6	42.9	1530	12	ADO41962	Human DNA
258	6	42.9	1083	6	ABQ66820	Human pol	ABQ66820	C 331	6	42.9	1554	8	ADA70781	Rice gene
259	6	42.9	1083	6	ABV84179	Human pol	ABV84179	C 332	6	42.9	1554	12	ADO41951	Human DNA
260	6	42.9	1083	10	ADC11107	Human DNA	ADC11107	C 333	6	42.9	1599	3	AAH51542	Arabiidops
261	6	42.9	1083	10	ADC46560	Human neo	ADC46560	C 334	6	42.9	1600	10	ADC30763	Human nov
C 262	6	42.9	1083	12	ADM24722	Human PRO	ADM24722	C 335	6	42.9	1601	3	AAH38735	Arabiidops
C 263	6	42.9	1089	4	ABL03581	Drosophil	ABL03581	C 336	6	42.9	1618	3	AAH15836	Human pro
264	6	42.9	1096	6	ABQ16834	Oligonucl	ABQ16834	C 337	6	42.9	1635	4	ABL04499	Drosophil
C 265	6	42.9	1096	6	ABQ16835	Oligonucl	ABQ16835	C 338	6	42.9	1654	3	AAH59710	Human sec
266	6	42.9	1112	8	ABX63464	Human cDN	ABX63464	C 339	6	42.9	1658	4	AAH13897	Human cDN
C 267	6	42.9	1113	13	ADT42478	Bacterial	ADT42478	C 340	6	42.9	1726	4	AAH13776	Human cDN
C 268	6	42.9	1122	5	AAH67243	C. glutami	AAH67243	C 341	6	42.9	1726	13	ADH51537	Bacterial
269	6	42.9	1129	5	AAH89999	Human bon	AAH89999	C 342	6	42.9	1731	12	ADL02680	DNA encod
C 270	6	42.9	1131	10	ACF71571	Phototrab	ACF71571	C 343	6	42.9	1782	3	AAH21846	Human bre
271	6	42.9	1140	4	AAH28997	Genomic s	AAH28997	C 344	6	42.9	1802	6	ABA99136	HPDE-1 en
C 272	6	42.9	1140	4	AAH30240	DNA encod	AAH30240	C 345	6	42.9	1809	8	ACA24185	Prokaryot
273	6	42.9	1140	4	AAH30740	DNA #24 e	AAH30740	C 346	6	42.9	1840	4	AAH94556	Human ful
274	6	42.9	1140	4	ABA06807	Human gen	ABA06807	C 347	6	42.9	1840	12	ADL31424	Full leng
275	6	42.9	1140	4	AAI62821	Human gen	AAI62821	C 348	6	42.9	1842	10	ACA55448	Signallin
276	6	42.9	1140	4	ABK44026	Genomic D	ABK44026	C 349	6	42.9	1842	12	ADH55244	Human pol
277	6	42.9	1140	5	AAH29741	Human end	AAH29741	C 350	6	42.9	1845	13	ACN41006	Tumour-as
C 278	6	42.9	1140	5	ADG15170	Human 7 t	ADG15170	C 351	6	42.9	1888	13	ADH62059	Bacterial
279	6	42.9	1140	6	ABT07832	Novel hum	ABT07832	C 352	6	42.9	1890	10	ADH53174	Human cod
280	6	42.9	1140	6	ABZ14195	Arabiidops	ABZ14195	C 353	6	42.9	1902	8	ACA24848	Prokaryot
281	6	42.9	1140	6	ABV84144	Human pol	ABV84144	C 354	6	42.9	1913	3	AAH54237	Arabiidops
282	6	42.9	1140	8	ACD01495	Human gen	ACD01495	C 355	6	42.9	1932	10	ADH67263	Human can
283	6	42.9	1140	8	ADA67859	Arabiidops	ADA67859	C 356	6	42.9	1932	10	ADH67261	Human can
C 284	6	42.9	1140	10	ADC46516	Human neo	ADC46516	C 357	6	42.9	1932	11	ADH131413	Human cDN
285	6	42.9	1140	12	ADH55011	Novel hum	ADH55011	C 358	6	42.9	1942	6	ABK35809	CDNA sequ
286	6	42.9	1140	12	ADN72612	Thale cre	ADN72612	C 359	6	42.9	1942	12	ADQ25337	Human sof
287	6	42.9	1146	8	ACA36279	Prokaryot	ACA36279	C 360	6	42.9	1947	4	AAH51514	Human pol
C 288	6	42.9	1163	3	ABQ70234	Listeria	ABQ70234	C 361	6	42.9	1947	11	ABD02444	Pseudomon
289	6	42.9	1175	3	AAH13401	Aspergill	AAH13401	C 362	6	42.9	1952	6	ABA93744	Human sig
290	6	42.9	1178	3	AAH33355	Human sec	AAH33355	C 363	6	42.9	1965	4	AAI99552	Human exp
291	6	42.9	1182	5	ABA15955	Human ner	ABA15955	C 364	6	42.9	1965	7	ADH41295	Human CD-
C 292	6	42.9	1198	10	ADI22502	Rat liver	ADI22502	C 365	6	42.9	1965	13	ADH48221	Bacterial
293	6	42.9	1215	6	ABQ41915	Oligonucl	ABQ41915	C 366	6	42.9	1966	4	ABA09105	Human orp
C 294	6	42.9	1215	6	ABQ41914	Oligonucl	ABQ41914	C 367	6	42.9	1966	4	AAH52498	Human pol
C 295	6	42.9	1230	10	ABZ41545	N. gonorr	ABZ41545	C 368	6	42.9	1996	5	AAH29614	Human end
C 296	6	42.9	1230	10	ABZ39752	N. gonorr	ABZ39752	C 369	6	42.9	2000	8	ADA71826	Rice gene
C 297	6	42.9	1236	11	ABD02483	Pseudomon	ABD02483	C 370	6	42.9	2000	12	ADH40860	Plant cDN

c 371	6	42.9	2028	4	AAK69011	Human imm	444	6	42.9	3039	12	ADO41967	Ado41967 Human com
372	6	42.9	2063	4	AAK94190	Human cDN	c 445	6	42.9	3060	4	ABL17650	Abli17650 Drosophil
373	6	42.9	2063	12	ADL30708	Full leng	446	6	42.9	3094	6	AAI64196	AAi64196 Human H37
374	6	42.9	2082	4	AAF64220	Human sec	447	6	42.9	3094	10	AAU58580	Ad58580 Human H37
c 375	6	42.9	2087	6	AAI45897	A thalian	448	6	42.9	3094	10	AAU58579	Ad58579 Human H37
376	6	42.9	2087	12	ADG74901	A thalian	449	6	42.9	3135	6	ABK83510	Abk83510 Human cDN
c 377	6	42.9	2089	2	AAV06591	Arabidops	450	6	42.9	3135	13	ADP23183	Adp23183 PRO polyP
378	6	42.9	2113	11	ACN45171	Human mRN	451	6	42.9	3144	4	ABL01580	Abli01580 Drosophil
c 379	6	42.9	2123	4	ABL22322	Drosophil	c 452	6	42.9	3152	10	AD58397	Ad58397 Toxicity-
380	6	42.9	2136	13	ADR07776	Full leng	453	6	42.9	3189	4	AAF58654	Aaf58654 Human Rep
c 381	6	42.9	2156	13	ACN41468	Human dia	454	6	42.9	3191	12	ADQ87201	Adq87201 Human tum
c 382	6	42.9	2156	13	ACN43123	Human dia	455	6	42.9	3191	13	ADQ4924	Adq4924 Human tum
c 383	6	42.9	2174	12	ADQ64315	Novel hum	c 456	6	42.9	3192	5	AAU75056	Aas75056 DNA encod
384	6	42.9	2175	8	ADA70642	Rice gene	457	6	42.9	3208	3	AAU59068	Aac59068 Human sec
c 385	6	42.9	2217	8	ACA53426	Prokaryot	458	6	42.9	3208	8	ADA97929	Ada97929 Human sec
386	6	42.9	2217	10	ADB31558	Human cDN	459	6	42.9	3208	8	ADA43840	Ada43840 Human sec
387	6	42.9	2220	12	ADQ67221	Novel hum	460	6	42.9	3208	10	ADC20088	Adc20088 Human sec
388	6	42.9	2223	8	ACA52331	Prokaryot	461	6	42.9	3208	10	ADF10558	Adf10558 Human sec
c 389	6	42.9	2235	1	AAU90389	DNA encod	c 462	6	42.9	3255	12	ADM90628	Adm90628 Human DNA
c 390	6	42.9	2271	4	ABL21710	Drosophil	463	6	42.9	3255	12	ADM91046	Adm91046 Human DNA
391	6	42.9	2272	6	ABN60033	Novel hum	464	6	42.9	3260	10	ADP46299	Adp46299 Rat gene
392	6	42.9	2286	5	ABA14652	Human ner	465	6	42.9	3300	12	ADO62058	Ado62058 Transcrip
c 393	6	42.9	2319	1	AAU90816	Membrane-	466	6	42.9	3327	2	AAQ10989	Aaq10989 B lymphoc
394	6	42.9	2347	6	AAU33729	Human sec	467	6	42.9	3330	12	ADI43398	Adi43398 Plant tra
395	6	42.9	2358	12	ADN72668	Thale cre	468	6	42.9	3337	1	AAU91089	Aan91089 Fragment
396	6	42.9	2379	6	ABE64928	Grape rib	469	6	42.9	3339	10	ADB69135	Adb69135 C. neofor
397	6	42.9	2394	6	RAU33706	Human sec	470	6	42.9	3340	12	ADM86615	Adm86615 Mouse and
c 398	6	42.9	2421	6	ABK74250	Bacillus	471	6	42.9	3420	4	AAU58655	Aaf58655 Human IB1
c 399	6	42.9	2437	2	AAU97381	Human typ	472	6	42.9	3464	5	AAU91232	Aac91232 Human DHF
c 400	6	42.9	2437	2	AAU99802	Human gen	473	6	42.9	3487	11	ADM01734	Adm01734 Human cDN
c 401	6	42.9	2437	2	AAU88368	Human typ	474	6	42.9	3502	12	ADL12930	Adl12930 Human ste
c 402	6	42.9	2437	2	AAU88360	Human typ	475	6	42.9	3623	4	ABL04857	Abli04857 Drosophil
c 403	6	42.9	2437	2	AAU88361	Human typ	476	6	42.9	3709	4	AAU78012	Aah78012 Nucleotid
c 404	6	42.9	2437	10	ACF63370	Human SRD	477	6	42.9	3709	10	ADG98861	Adg98861 Fruit fly
405	6	42.9	2448	6	ABQ60808	Human Rep	478	6	42.9	3709	10	ABX14663	Abx14663 Fruitfly
406	6	42.9	2541	10	ABQ60807	Human pro	c 479	6	42.9	3765	10	ADB53672	Adb53672 Primary r
c 407	6	42.9	2562	10	ADF38037	Synchroni	480	6	42.9	3792	4	ABL10857	Abli10857 Drosophil
408	6	42.9	2566	12	ADI40918	Human kin	481	6	42.9	3799	4	AAI66255	Aai66255 S. cerevis
409	6	42.9	2570	4	AAU18569	Human cDN	482	6	42.9	3799	10	ADD02764	Add02764 S. cerevi
410	6	42.9	2575	6	ABK84270	Human cDN	483	6	42.9	3824	2	AAQ11482	Aaq11482 Sequence
411	6	42.9	2575	6	ABK84729	Human ben	484	6	42.9	3851	3	AAU43193	Aac43193 Arabidops
c 412	6	42.9	2582	10	ADA53573	Human cod	485	6	42.9	3887	12	ADL12931	Adl12931 Human ste
413	6	42.9	2606	11	ACN44255	Human mRN	486	6	42.9	3923	4	AAK89586	Aak89586 Human dig
414	6	42.9	2606	12	ADI40919	Human kin	487	6	42.9	3923	4	AAK77765	Aak77765 Human imm
415	6	42.9	2625	4	AAU55430	Nucleotid	488	6	42.9	3923	4	AAU07388	Aal07388 Human rep
416	6	42.9	2625	8	ACA28753	Prokaryot	489	6	42.9	3923	4	ABA08191	Abao8191 Human ova
417	6	42.9	2652	8	ACA28241	Prokaryot	490	6	42.9	3923	10	ADB85072	Adb85072 Farnesyl
418	6	42.9	2667	4	ABL08223	Drosophil	491	6	42.9	3934	11	ADI31740	Adi31740 Human cDN
419	6	42.9	2670	8	ACA29227	Prokaryot	492	6	42.9	3934	13	ADP56041	Adp56041 Human PRO
420	6	42.9	2686	5	AAU73640	DNA encod	493	6	42.9	4011	3	AAU49498	Aac49498 Arabidops
421	6	42.9	2700	8	ACA44711	Prokaryot	494	6	42.9	4053	12	ADO63651	Ado63651 Transcrip
422	6	42.9	2706	4	ABL16424	Drosophil	c 495	6	42.9	4081	2	AAU06585	Aav06585 Arabidops
423	6	42.9	2715	10	ADF00107	Bacterial	496	6	42.9	4094	10	ADD67537	Add67537 Human Lyl
424	6	42.9	2728	4	AAU14429	Human cDN	497	6	42.9	4106	5	AAU80045	Aas80045 DNA encod
425	6	42.9	2769	6	ABU99771	Mouse isc	498	6	42.9	4106	5	AAU89210	Aas89210 DNA encod
426	6	42.9	2778	8	ACC46308	Human dit	499	6	42.9	4156	13	ADO38385	Ado38385 Human SNP
427	6	42.9	2809	10	ADB63713	Human cDN	500	6	42.9	4248	11	ABD11263	Abd11263 Pseudomon
428	6	42.9	2821	12	ADN05153	Antipsori	501	6	42.9	4339	4	ABL20716	Abli20716 Drosophil
429	6	42.9	2892	4	AAU14475	Human cDN	502	6	42.9	4365	12	ADN12096	Adn12096 Murine ca
430	6	42.9	2909	5	ABU15957	Human ner	503	6	42.9	4484	6	ABL68510	Abli68510 Kidney ca
431	6	42.9	2954	4	ABL16252	Drosophil	504	6	42.9	4484	10	ADP81541	Adp81541 Leukemia
c 432	6	42.9	2955	4	AAU18577	Human cDN	505	6	42.9	4530	8	ABX63357	Abx63357 Human cDN
433	6	42.9	2960	6	ABQ70660	Listeria	506	6	42.9	4530	12	ADP77193	Adp77193 Human cDN
c 434	6	42.9	2980	12	ADM44009	Novel hum	c 507	6	42.9	4530	12	ADL161766	Adl161766 Human cDN
435	6	42.9	2994	10	ADL12669	Human ste	c 508	6	42.9	4628	12	ABZ11203	Abz11203 Human pol
436	6	42.9	3005	10	ADA53406	Human cod	c 509	6	42.9	4628	12	ADM43721	Adm43721 Novel hum
c 437	6	42.9	3015	6	ABL19316	Drosophil	510	6	42.9	4709	8	ACC49517	Acc49517 Tumour-as
438	6	42.9	3016	6	ABE53853	Human and	511	6	42.9	4736	6	ABQ70950	Abq70950 Liesteria
439	6	42.9	3016	6	ABE54316	DNA encod	512	6	42.9	4819	8	ABX70845	Abx70845 Novel hum
440	6	42.9	3016	12	ADN00254	Human and	513	6	42.9	5047	12	ADP13275	Adp13275 Renal cel
441	6	42.9	3023	11	ADP65803	Human mRN	514	6	42.9	5047	12	ADQ84256	Adq84256 Human tum
442	6	42.9	3023	11	ADP65723	Human DKF	515	6	42.9	5047	12	ADQ85638	Adq85638 Human tum
c 443	6	42.9	3033	12	ADQ23033	Human sof	516	6	42.9	5047	13	ADQ86737	Adq86737 Human tum

517	6	42.9	5124	4	ABL03554	AbL03554 Drosophil	590	6	42.9	14896	6	ABK24096	Abk24096 Human alp
518	6	42.9	5159	10	ADK41004	Adk41004 Novel hum	591	6	42.9	14896	8	ABZ34885	Abz34885 Coding se
519	6	42.9	5159	13	ADR15718	Adr15718 Kinase 40	592	6	42.9	14896	8	ACA89917	AcA89917 Gene diff
520	6	42.9	5247	4	ABL04498	AbL04498 Drosophil	593	6	42.9	14896	10	ADD14619	AdD14619 Human src
C 521	6	42.9	5298	5	RA889895	RA889895 DNA encod	594	6	42.9	14896	12	ADL15635	AdL15635 Human lip
C 522	6	42.9	5298	5	RA886664	RA886664 DNA encod	595	6	42.9	14899	4	RAK52224	RAK52224 Human pol
C 523	6	42.9	5319	4	ABL05960	AbL05960 Drosophil	596	6	42.9	15449	3	AA81526	AA81526 N. mening
C 524	6	42.9	5406	4	ABL06257	AbL06257 Drosophil	597	6	42.9	15518	6	ABL34172	AbL34172 Human imm
525	6	42.9	5574	4	ABL02492	AbL02492 Drosophil	598	6	42.9	15518	6	ABL34624	AbL34624 Human met
C 526	6	42.9	5595	2	AAQ25810	AAq25810 Insert of	599	6	42.9	15518	6	ABL70607	AbL70607 Chemicall
527	6	42.9	5989	4	RA546535	RAa46535 Tumour su	600	6	42.9	15518	7	AD998885	Ad998885 Bisulphit
C 528	6	42.9	6096	12	ADO78175	Ado78175 Human thr	601	6	42.9	16545	5	ADL19232	AdL19232 Human CGL
C 529	6	42.9	6149	4	ABL04856	AbL04856 Drosophil	602	6	42.9	16545	13	ADS09790	AdS09790 Human the
530	6	42.9	6343	8	ABZ10194	AbZ10194 Haenatopo	603	6	42.9	16559	11	ACN91031	AcN91031 Breast ca
531	6	42.9	6343	13	ADS89670	AdS89670 Oligonuc	604	6	42.9	16842	4	AA846412	AA846412 Tumour su
532	6	42.9	6436	6	ABL33692	AbL33692 Human imm	605	6	42.9	16842	6	ABK31419	AbK31419 Signal tr
533	6	42.9	6436	6	ABK31408	AbK31408 Signal tr	606	6	42.9	16842	6	ABL70384	AbL70384 Chemicall
C 534	6	42.9	6462	4	RAF90037	RAf90037 Nucleotid	607	6	42.9	16842	6	AA861336	AA861336 Human gen
535	6	42.9	6515	12	ADN06015	Adn06015 Antipeori	608	6	42.9	16842	10	ADS54136	AdS54136 Pretreat
C 536	6	42.9	6779	4	ABL10856	AbL10856 Drosophil	609	6	42.9	16842	13	ADS89286	AdS89286 Oligonuc
C 537	6	42.9	6975	4	ABL09610	AbL09610 Drosophil	610	6	42.9	17200	4	AAAL37025	AAa37025 Human mus
538	6	42.9	7069	4	RAA546653	RAa46653 Tumour su	611	6	42.9	17200	8	ABX60013	AbX60013 cDNA enco
539	6	42.9	7069	6	ABL33352	AbL33352 Human imm	612	6	42.9	17200	12	ADJ30763	AdJ30763 Human mus
540	6	42.9	7069	6	ABK31318	AbK31318 Signal tr	613	6	42.9	18404	8	ADJ30763	AdJ30763 Human mus
541	6	42.9	7069	6	ABL70291	AbL70291 Chemicall	614	6	42.9	18888	4	ABL23020	AbL23020 Drosophil
542	6	42.9	7069	6	AA861219	AA861219 Human gen	615	6	42.9	18966	5	ABA20628	ABa20628 Human ner
543	6	42.9	7069	6	ABQ66983	ABq66983 Human ang	616	6	42.9	18966	5	ABA20628	ABa20628 Human ner
544	6	42.9	7183	6	ABN80167	ABn80167 Human che	617	6	42.9	18966	5	ABX59995	AbX59995 cDNA enco
C 545	6	42.9	7421	4	AAK89313	AAk89313 Human dig	618	6	42.9	18966	12	ADJ30745	AdJ30745 Human mus
546	6	42.9	7431	6	ABL32081	AbL32081 Human imm	619	6	42.9	19236	6	ABN80226	ABn80226 Human che
C 547	6	42.9	7431	6	ABL28371	AbL28371 Human che	620	6	42.9	20001	13	ACN37222	AcN37222 Human per
C 548	6	42.9	7522	4	ABL06256	AbL06256 Drosophil	621	6	42.9	20682	2	AAAX20569	AAx20569 Polynucle
549	6	42.9	7551	12	ADN11594	Adn11594 Human CD9	622	6	42.9	21224	5	ABA20544	ABa20544 Human ner
C 550	6	42.9	7783	5	RAA574636	RAa74636 DNA encod	623	6	42.9	21721	2	AAAX83427	AAx83427 Human lip
551	6	42.9	7792	4	ABL08222	AbL08222 Drosophil	624	6	42.9	22976	2	AAAX83426	AAx83426 Genomic r
C 552	6	42.9	7847	8	RAA50965	RAa50965 pMON50201	625	6	42.9	23107	9	ADA02762	AdA02762 Human RUN
C 553	6	42.9	7847	8	RAA50968	RAa50968 pMON50203	626	6	42.9	23107	10	ADB72500	AdB72500 Human Run
C 554	6	42.9	7847	8	RAA50962	RAa50962 pMON50202	627	6	42.9	23107	10	ADC85242	AdC85242 Human Run
C 555	6	42.9	7847	8	RAA50967	RAa50967 pMON50202	628	6	42.9	23107	12	ADM74357	AdM74357 Human car
556	6	42.9	7856	6	ABN80234	ABn80234 Human che	629	6	42.9	23187	3	AAAS0273	AAa50273 Human lip
C 557	6	42.9	8298	6	ABN80190	ABn80190 Human che	630	6	42.9	23187	3	AAF62331	AAf62331 Human lep
558	6	42.9	8325	13	ADS57889	AdS57889 Bacterial	631	6	42.9	26636	4	ABL16650	AbL16650 Drosophil
559	6	42.9	8530	6	ABL32433	AbL32433 Human imm	632	6	42.9	27689	6	AA819494	AA819494 Arabidosp
560	6	42.9	8776	6	ABK40067	AbK40067 Human che	633	6	42.9	30312	10	ACF65384	ACF65384 Continuation (6 of
C 561	6	42.9	9393	6	AB878855	AB878855 E. coli C	634	6	42.9	30625	6	ABK12808	AbK12808 Human tum
C 562	6	42.9	9393	10	ADH80422	ADh80422 Escherich	635	6	42.9	30676	6	ABK12808	AbK12808 Human tum
C 563	6	42.9	9443	4	ABL16121	AbL16121 Drosophil	636	6	42.9	31352	6	AAAL39687	AAa39687 Genomic D
564	6	42.9	9448	4	RAK84656	RAk84656 Human imm	637	6	42.9	31497	8	ABX72626	ABx72626 Human cDN
565	6	42.9	9900	12	ADN11595	Adn11595 Human CD9	638	6	42.9	31946	11	ACN45120	AcN45120 Mouse gen
566	6	42.9	9935	10	AAAS5749	AAa55749 Escherich	639	6	42.9	32328	4	ABL09994	AbL09994 Drosophil
C 567	6	42.9	10308	4	ABL05365	AbL05365 Drosophil	640	6	42.9	33486	6	AB878976	AB878976 E. coli C
C 568	6	42.9	10308	13	ADQ89631	AdQ89631 Antagonis	641	6	42.9	33486	10	ADH80543	ADh80543 Escherich
C 569	6	42.9	10343	4	ABL14246	AbL14246 Drosophil	642	6	42.9	33925	12	ADL70331	AdL70331 Crenarcha
570	6	42.9	11473	6	ABK40030	AbK40030 Human che	643	6	42.9	34071	4	AAF90033	AAf90033 Nucleotid
571	6	42.9	11473	6	ABL33355	AbL33355 Human imm	644	6	42.9	36383	4	ABL05364	AbL05364 Drosophil
C 572	6	42.9	11809	6	RAA597394	RAa97394 Murine SA	645	6	42.9	39003	4	AAF28534	AAf28534 Genomic f
C 573	6	42.9	11809	12	ADMI5732	AdM15732 Murine SA	646	6	42.9	41322	9	AAAL62633	AAa62633 Genomic f
574	6	42.9	12122	4	ABL08612	AbL08612 Drosophil	647	6	42.9	41936	6	ABL67924	AbL67924 Ovary can
575	6	42.9	12192	4	RAA528195	RAa528195 Genomic s	648	6	42.9	42717	4	AAF90032	AAf90032 Nucleotid
576	6	42.9	12192	10	ADG41391	AdG41391 Human res	649	6	42.9	45265	3	RAA246508	RAa246508 Sequence
577	6	42.9	12192	11	ADG197165	AdG197165 Human res	650	6	42.9	45845	6	ABK12809	AbK12809 Human tum
C 578	6	42.9	13260	12	ADN11596	Adn11596 Human CD9	651	6	42.9	45862	8	ABX93110	ABx93110 Genomic D
C 579	6	42.9	13332	5	ABA15106	ABa15106 Human ner	652	6	42.9	49088	11	ACN43856	AcN43856 Mouse gen
580	6	42.9	13635	12	ADJ27129	AdJ27129 Human LRP	653	6	42.9	50460	11	ACN44936	AcN44936 Mouse gen
581	6	42.9	13635	12	ADJ71873	AdJ71873 Human LRP	654	6	42.9	52253	3	AAA81478	AAa81478 N. mening
582	6	42.9	13638	12	ADI27128	AdI27128 Mouse LRP	655	6	42.9	57038	11	ADP65343	ADp65343 Human seq
583	6	42.9	13836	11	ACN44295	AcN44295 Human mRN	656	6	42.9	57082	12	ADP84151	ADp84151 Human CAL
584	6	42.9	14530	4	AAK51849	AAk51849 Human pol	657	6	42.9	57502	12	ADQ97092	AdQ97092 Human can
C 585	6	42.9	14648	4	ABL16120	AbL16120 Drosophil	658	6	42.9	60935	13	ACN37224	AcN37224 Human per
586	6	42.9	14849	6	ABK24094	AbK24094 Mouse alp	659	6	42.9	65042	8	AB855711	AB855711 DNA encod
587	6	42.9	14849	6	ABK12951	AbK12951 DNA encod	660	6	42.9	65042	9	ACA63029	AcA63029 Human gen
588	6	42.9	14887	4	ABA08597	ABa08597 Human LDL	661	6	42.9	65042	13	ADR05761	AdR05761 Human gen
589	6	42.9	14889	6	ABZ35245	ABz35245 Human gen	662	6	42.9	66566	3	AAA53450	AAa53450 Human thi

C 663	6	42.9	66765	12	ADP84154	Adp84154 Human CA1	C 736	6	42.9	304326	13	ADS15253	Adsl5253 Rat senso
C 664	6	42.9	66765	13	ADP72872	Adp72872 Human ova	C 737	6	42.9	304905	11	ADP75180	Adp75180 Human End
C 665	6	42.9	76341	12	ADM97422	Adm97422 Prostate	C 738	6	42.9	321019	13	ADS16450	Ads16450 Human aut
C 666	6	42.9	80251	4	ABL16442	Ab116442 Drosophil	C 739	6	42.9	326014	6	ABK8296	Abk8296 Human gen
C 667	6	42.9	80251	4	ABL16448	Ab116448 Drosophil	C 740	6	42.9	326014	12	ADQ94981	Adq94981 Human kin
C 668	6	42.9	85915	13	ADL15447	Adl15447 Streptomy	C 741	6	42.9	329019	13	ABD32707	Abd32707 Human can
C 669	6	42.9	90220	6	ABK83576	Abk83576 Human cdn	C 742	6	42.9	332234	12	ADQ59437	Adq59437 Human can
C 670	6	42.9	92794	11	ADP65471	Adp65471 Human seq	C 743	6	42.9	339234	12	ADQ59437	Adq59437 Human can
C 671	6	42.9	93631	11	ACN43984_4	Continuation (5 of	C 744	6	42.9	347001	12	ADP43517	Adp43517 Human MAD
C 672	6	42.9	99957	9	ADA03032	Ada03032 Human mCG	C 745	6	42.9	349980	3	AAF21607	Aaf21607 Neisseria
C 673	6	42.9	99957	10	ADB72770	Adb72770 Human CA	C 746	6	42.9	349980	3	AAF21544	Aaf21544 Neisseria
C 674	6	42.9	99957	10	ADC85512	Adc85512 Human gen	C 747	6	42.9	349980	3	AAH68531	Aah68531 C glutami
C 675	6	42.9	99957	12	ADM74627	Adm74627 Human car	C 748	6	42.9	349980	10	ADC86916	Adc86916 Human GPC
C 676	6	42.9	100534	13	ABD32647	Abd32647 Mouse can	C 749	5	35.7	17	2	AAH71526	Aah71526 Human KDR
C 677	6	42.9	104900	13	ABD32848	Abd32848 Human can	C 750	5	35.7	17	6	ABV85695	Abv85695 Human pp-
C 678	6	42.9	106938	13	ABD33432	Abd33432 Human can	C 751	5	35.7	17	6	ABV85693	Abv85693 Human pp-
C 679	6	42.9	106938	13	ABD67034	Abd67034 Human can	C 752	5	35.7	17	6	ABV85694	Abv85694 Human pp-
C 680	6	42.9	107330	12	ADQ97316	Adq97316 Mouse can	C 753	5	35.7	17	8	ABT36868	Abt36868 Tumour su
C 681	6	42.9	110000	2	AAV21209_12	Continuation (13 o	C 754	5	35.7	17	10	ADB40920	Adb40920 Tumour su
C 682	6	42.9	110000	3	AAA81490_01	Continuation (2 of	C 755	5	35.7	17	10	ACC54252	Acc54252 Human tum
C 683	6	42.9	110000	3	AAA81490_03	Continuation (4 of	C 756	5	35.7	19	10	ADG45288	Adg45288 Human oes
C 684	6	42.9	110000	6	ABN71527_02	Continuation (3 of	C 757	5	35.7	19	10	ADF84831	Adf84831 Human ABL
C 685	6	42.9	110000	6	ABQ67196_2	Continuation (3 of	C 758	5	35.7	19	10	ADF84512	Adf84512 Human ABL
C 686	6	42.9	110000	6	ABQ62245_00	Abq62245 Listeria	C 759	5	35.7	19	12	ADQ88337	Adq88337 Human oes
C 687	6	42.9	110000	6	ABA03041_00	AbA03041 Listeria	C 760	5	35.7	20	2	AAV52527	Aav52527 3' primer
C 688	6	42.9	110000	6	ABA03041_08	Continuation (9 of	C 761	5	35.7	20	5	AAH85344	Aah85344 cDNA prim
C 689	6	42.9	110000	6	ABA03041_11	Continuation (12 o	C 762	5	35.7	20	6	ABQ93176	Abq93176 T. tausch
C 690	6	42.9	110000	6	ABA03041_24	Continuation (25 o	C 763	5	35.7	21	4	AAO59942	Aao59942 PCR prime
C 691	6	42.9	110000	10	ADH10017_2	Continuation (3 of	C 764	5	35.7	21	12	ADM96482	Adm96482 PCR prime
C 692	6	42.9	110000	10	ACF65385_1	Continuation (12 o	C 765	5	35.7	22	2	AAQ95801	Aaq95801 Primer B
C 693	6	42.9	110000	10	ACF67367_11	Continuation (12 o	C 766	5	35.7	22	2	AAZ18601	Aaz18601 Primer fo
C 694	6	42.9	110000	10	ACF67367_30	Continuation (31 o	C 767	5	35.7	22	3	AAA80508	Aaa80508 ASTH1 pol
C 695	6	42.9	110000	10	ACF67367_47	Continuation (48 o	C 768	5	35.7	23	10	AAO60653	Aao60653 Pseudomon
C 696	6	42.9	110000	10	ACF65388_00	Acf65388 Photorhab	C 769	5	35.7	23	3	AAA96921	Aaa96921 PCR prime
C 697	6	42.9	110000	11	ADM27081_00	Adm27081 Hypether	C 770	5	35.7	24	3	AAA66376	Aaa66376 Dog genom
C 698	6	42.9	110000	11	ACN43998_00	Acn43998 Human gen	C 771	5	35.7	24	12	ADH68518	Adh68518 Rosa sp r
C 699	6	42.9	110000	12	ADQ97047_2	Continuation (3 of	C 772	5	35.7	24	12	ADO31884	Ado31884 Human CFT
C 700	6	42.9	110000	12	ADQ97047_2	Continuation (3 of	C 773	5	35.7	25	2	AAQ30686	Aaq30686 IL-6 prim
C 701	6	42.9	110000	13	ABD32921_2	Continuation (3 of	C 774	5	35.7	25	2	AAQ47373	Aaq47373 PCR prime
C 702	6	42.9	110000	13	ABD32629_3	Continuation (4 of	C 775	5	35.7	25	2	AAQ40998	Aaq40998 IL-6 prim
C 703	6	42.9	110021	13	ABD32859_5	Abd32859 Mouse can	C 776	5	35.7	25	2	AAQ45681	Aaq45681 Interleuk
C 704	6	42.9	114411	12	ADQ21090	Adq21090 Human sof	C 777	5	35.7	25	3	AAH61178	Aah61178 PCR prime
C 705	6	42.9	115284	11	ACN44296	Acn44296 Mouse gen	C 778	5	35.7	25	6	ABV86462	Abv86462 Human pp-
C 706	6	42.9	117574	6	AAH45288	Aah45288 Human KCN	C 779	5	35.7	25	6	ABV86464	Abv86464 Human pp-
C 707	6	42.9	124884	5	AAH74201	Aah74201 Nucleotid	C 780	5	35.7	25	6	ABV86467	Abv86467 Human pp-
C 708	6	42.9	124884	10	ADA14878	Ada14878 Human her	C 781	5	35.7	25	6	ABV86471	Abv86471 Human pp-
C 709	6	42.9	124884	11	ADL99489	Adl99489 Varicella	C 782	5	35.7	25	6	ABV86465	Abv86465 Human pp-
C 710	6	42.9	125157	5	AAH74202	Aah74202 Nucleotid	C 783	5	35.7	25	6	ABV86470	Abv86470 Human pp-
C 711	6	42.9	127238	11	ACN44372	Acn44372 Mouse gen	C 784	5	35.7	25	6	ABV86468	Abv86468 Human pp-
C 712	6	42.9	127917	13	ADR52731	Adr52731 Drug ther	C 785	5	35.7	25	6	ABV86466	Abv86466 Human pp-
C 713	6	42.9	129021	3	AAF22296	Aaf22296 BAC conta	C 786	5	35.7	25	6	ABV86463	Abv86463 Human pp-
C 714	6	42.9	133955	11	ACN45170	Acn45170 Human gen	C 787	5	35.7	25	6	ABV86469	Abv86469 Human pp-
C 715	6	42.9	160198	10	ADL13962	Adl13962 Osteoarth	C 788	5	35.7	25	6	ABV86472	Abv86472 Human pp-
C 716	6	42.9	170170	10	ADL13643	Adl13643 Osteoarth	C 789	5	35.7	25	9	ACI13277	Act13277 Human mic
C 717	6	42.9	171936	6	ABS55565	Abs55565 Human SUL	C 790	5	35.7	25	9	ACI42181	Act42181 Human mic
C 718	6	42.9	171936	12	ADN16205	Adn16205 Mouse sul	C 791	5	35.7	25	9	ACK26304	Ack26304 Human mic
C 719	6	42.9	172569	11	ACN44758	Acn44758 Human gen	C 792	5	35.7	25	9	ACK22630	Ack22630 Human mic
C 720	6	42.9	176771	12	ADQ97167	Adq97167 Human can	C 793	5	35.7	25	9	ACK22633	Ack22633 Human mic
C 721	6	42.9	191284	12	ADQ97957	Adq97957 Mouse can	C 794	5	35.7	25	9	ACI31478	Act31478 Human mic
C 722	6	42.9	197997	10	AAH54074	Aah54074 Human tra	C 795	5	35.7	25	9	ACI09742	Act09742 Human mic
C 723	6	42.9	203070	11	ACN44012	Acn44012 Mouse gen	C 796	5	35.7	25	9	ACK25729	Ack25729 Human mic
C 724	6	42.9	207433	3	ABX72040	Abx72040 Gene 216	C 797	5	35.7	25	9	ACI53347	Act53347 Human mic
C 725	6	42.9	207433	8	ABX74891	Abx74891 BAC1098L2	C 798	5	35.7	25	9	ACI58441	Act58441 Human mic
C 726	6	42.9	207433	12	ADJ36614	Adj36614 Bacterial	C 799	5	35.7	25	9	ACK24257	Ack24257 Human mic
C 727	6	42.9	207433	12	ADL81193	Adl81193 BAC1098L2	C 800	5	35.7	25	9	ACK27260	Ack27260 Human mic
C 728	6	42.9	210204	13	ADQ18927	Adq18927 Human sof	C 801	5	35.7	25	9	ACI94194	Act94194 Human mic
C 729	6	42.9	219715	12	ABD32692	Abd32692 Mouse can	C 802	5	35.7	25	9	ACI56987	Act56987 Human mic
C 730	6	42.9	236246	12	ADQ97590	Adq97590 Mouse can	C 803	5	35.7	25	9	ACI79973	Act79973 Human mic
C 731	6	42.9	240823	10	ADD69391	Add69391 Human PG-	C 804	5	35.7	25	9	ACI58440	Act58440 Human mic
C 732	6	42.9	240825	4	AAF24497	Aaf24497 Human PG-	C 805	5	35.7	25	9	ACK03647	Ack03647 Human mic
C 733	6	42.9	240825	6	ABQ81802	Abq81802 Human PG-	C 806	5	35.7	25	9	ACK03560	Act03560 Human mic
C 734	6	42.9	254366	8	ABZ23704	Abz23704 Human pho	C 807	5	35.7	25	9	ACT199839	Act199839 Human mic
C 735	6	42.9	256190	13	ABD33276	Abd33276 Human can	C 808	5	35.7	25	9	ACT179492	Act179492 Human mic

C 809	5	35.7	25	9	ACI82705	AcI82705 Human mic	882	5	35.7	51	4	AAL34292	Aal34292 Human SNP
C 810	5	35.7	25	9	ACI44763	AcI44763 Human mic	883	5	35.7	51	4	AAI74156	Aai74156 Human sil
C 811	5	35.7	25	9	ACI94195	AcI94195 Human mic	884	5	35.7	51	4	AAI74268	Aai74268 Human sil
C 812	5	35.7	25	9	ACI02924	AcI02924 Human mic	C 885	5	35.7	51	4	AAI78621	Aai78621 Human sil
C 813	5	35.7	25	9	ACI84193	AcI84193 Human mic	C 886	5	35.7	51	4	AAI78132	Aai78132 Human sil
C 814	5	35.7	25	9	ACI13266	AcI13266 Human mic	C 887	5	35.7	51	4	AAI78620	Aai78620 Human sil
C 815	5	35.7	25	9	ACK30734	AcK30734 Human mic	C 888	5	35.7	51	4	AAI74157	Aai74157 Human sil
C 816	5	35.7	25	9	ACH61126	AcH61126 DNA targe	C 889	5	35.7	54	2	AAQ86781	Aaq86781 SDI-1 mim
C 817	5	35.7	25	9	ACH61252	AcH61252 DNA targe	C 890	5	35.7	54	2	AAQ74004	Aaq74004 SDI-1 mim
C 818	5	35.7	25	9	ACH57727	AcH57727 DNA targe	C 891	5	35.7	59	2	AAV79267	Aav79267 Staphyloc
C 819	5	35.7	25	12	ADP13756	AdP13756 Renal cel	C 892	5	35.7	59	6	ADN33309	Adn33309 pEE14/NIF
C 820	5	35.7	27	2	AAQ10132	AaQ10132 Probe 165	C 893	5	35.7	60	6	ABN41624	Abn41624 Human spl
C 821	5	35.7	27	3	AA53628	Aa53628 Nested pr	C 894	5	35.7	60	6	ABN33030	Abn33030 Human spl
C 822	5	35.7	27	3	AA53648	Aa53648 Round two	C 895	5	35.7	60	6	ABN44783	Abn44783 Human spl
C 823	5	35.7	27	5	AA53648	Aa53648 Round two	C 896	5	35.7	60	6	ABN35375	Abn35375 Human spl
C 824	5	35.7	27	5	AA61784	Aa61784 B. brevis	C 897	5	35.7	60	6	ABN39481	Abn39481 Human spl
C 825	5	35.7	27	5	AA61806	Aa61806 B. brevis	C 898	5	35.7	60	6	ABN41312	Abn41312 Human spl
C 826	5	35.7	27	12	ADQ07396	AdQ07396 Escherich	C 899	5	35.7	60	6	ABN39698	Abn39698 Human spl
C 827	5	35.7	28	2	AAQ63307	AaQ63307 Canine ho	C 900	5	35.7	60	6	ABN58757	Abn58757 Human spl
C 828	5	35.7	28	2	AAQ69066	AaQ69066 Primer fo	C 901	5	35.7	60	6	ABN32666	Abn32666 Human spl
C 829	5	35.7	28	2	AA85503	Aa85503 PCR prime	C 902	5	35.7	60	13	AD53261	Ad53261 Eucalyptu
C 830	5	35.7	30	2	ADJ27342	AdJ27342 Mouse Lac	C 903	5	35.7	60	13	AD53261	Ad53261 Eucalyptu
C 831	5	35.7	30	4	AA90048	Aa90048 PCR prime	C 904	5	35.7	60	13	AD54041	Ad54041 Eucalyptu
C 832	5	35.7	30	4	AA90049	Aa90049 PCR prime	C 905	5	35.7	60	13	AD52779	Ad52779 Eucalyptu
C 833	5	35.7	30	6	ABX67394	Abx67394 Novel Hel	C 906	5	35.7	64	10	ADG42035	Adg42035 Human N33
C 834	5	35.7	30	10	ADD22742	AdD22742 Filamento	C 907	5	35.7	65	2	AAT39538	Aat39538 Nucleotid
C 835	5	35.7	30	10	ADD22726	AdD22726 Filamento	C 908	5	35.7	65	6	ABN28602	Abn28602 Rat splic
C 836	5	35.7	30	12	ADK15571	AdK15571 Hantaan h	C 909	5	35.7	65	6	ABN30892	Abn30892 Rat splic
C 837	5	35.7	30	12	ADO79493	AdO79493 KIAA0783	C 910	5	35.7	65	6	ABN56813	Abn56813 Mouse spl
C 838	5	35.7	31	2	ACA03148	AaC03148 PCR prime	C 911	5	35.7	65	6	ABN54059	Abn54059 Mouse spl
C 839	5	35.7	32	8	ACA61966	AaC61966 Immunolog	C 912	5	35.7	65	6	ABN54265	Abn54265 Mouse spl
C 840	5	35.7	32	12	ADM48508	AdM48508 Human sub	C 913	5	35.7	74	9	ADA73848	Ada73848 Carcinoma
C 841	5	35.7	33	13	ADS80909	AdS80909 Mammalian	C 914	5	35.7	76	10	ADG89178	Adg89178 Cancer de
C 842	5	35.7	33	2	AA25751	Aa25751 VEGF RNA	C 915	5	35.7	77	6	ADA4074	Ada4074 VEGF 126
C 843	5	35.7	33	2	AA25751	Aa25751 VEGF RNA	C 916	5	35.7	77	12	ADP85243	Adp85243 Ligand id
C 844	5	35.7	33	2	AA16217	Aa16217 Serine pr	C 917	5	35.7	79	12	ACH88247	Ach88247 Human gen
C 845	5	35.7	33	3	AA16252	Aa16252 Serine pr	C 918	5	35.7	80	2	AAV33399	Aav33399 Group B c
C 846	5	35.7	33	3	AA16252	Aa16252 Serine pr	C 919	5	35.7	80	10	ADH06230	Adh06230 Coxackie
C 847	5	35.7	33	3	AA16252	Aa16252 Serine pr	C 920	5	35.7	84	2	AA16252	Aa16252 Serine pr
C 848	5	35.7	33	3	AA16252	Aa16252 Serine pr	C 921	5	35.7	85	2	AA16252	Aa16252 Serine pr
C 849	5	35.7	33	4	AA167556	Aa167556 Serine pr	C 922	5	35.7	85	10	ADH06229	Adh06229 Coxackie
C 850	5	35.7	33	4	AA167517	Aa167517 Serine pr	C 923	5	35.7	87	2	AA167517	Aa167517 Serine pr
C 851	5	35.7	33	4	AA167517	Aa167517 Serine pr	C 924	5	35.7	89	4	AA167517	Aa167517 Serine pr
C 852	5	35.7	33	11	ADM44485	AdM44485 human zin	C 925	5	35.7	90	2	AA167517	Aa167517 Serine pr
C 853	5	35.7	34	2	AA167517	Aa167517 Serine pr	C 926	5	35.7	90	6	ABK36905	Abk36905 Human DNA
C 854	5	35.7	34	2	AA167517	Aa167517 Serine pr	C 927	5	35.7	90	9	ADA02322	Ada02322 Mouse car
C 855	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 928	5	35.7	90	10	ADH06229	Adh06229 Coxackie
C 856	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 929	5	35.7	92	6	AA167517	Aa167517 Serine pr
C 857	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 930	5	35.7	92	6	AA167517	Aa167517 Serine pr
C 858	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 931	5	35.7	99	3	AA167517	Aa167517 Serine pr
C 859	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 932	5	35.7	100	2	AA167517	Aa167517 Serine pr
C 860	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 933	5	35.7	100	2	AA167517	Aa167517 Serine pr
C 861	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 934	5	35.7	100	8	ACD79500	AcD79500 E. coli K
C 862	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 935	5	35.7	100	8	ACD79500	AcD79500 E. coli K
C 863	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 936	5	35.7	100	8	ACD79500	AcD79500 E. coli K
C 864	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 937	5	35.7	100	8	ACD79500	AcD79500 E. coli K
C 865	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 938	5	35.7	100	8	ACD79500	AcD79500 E. coli K
C 866	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 939	5	35.7	101	3	AA167517	Aa167517 Serine pr
C 867	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 940	5	35.7	102	6	ABL0662	AbL0662 Human ova
C 868	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 941	5	35.7	103	6	ABL0662	AbL0662 Human ova
C 869	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 942	5	35.7	103	8	ABX54766	AbX54766 Bovine ES
C 870	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 943	5	35.7	104	2	AAV89599	Aav89599 EST clone
C 871	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 944	5	35.7	104	12	ACH88212	Ach88212 Human gen
C 872	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 945	5	35.7	105	4	AAF85481	Aaf85481 Partial n
C 873	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 946	5	35.7	111	10	AB238510	Ab238510 N. gonorr
C 874	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 947	5	35.7	111	10	AB238510	Ab238510 N. gonorr
C 875	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 948	5	35.7	111	10	AB238510	Ab238510 N. gonorr
C 876	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 949	5	35.7	111	10	AB238510	Ab238510 N. gonorr
C 877	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 950	5	35.7	114	2	ADQ13487	AdQ13487 Human car
C 878	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 951	5	35.7	116	12	ADQ13487	AdQ13487 Human car
C 879	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 952	5	35.7	117	10	AB238510	Ab238510 N. gonorr
C 880	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 953	5	35.7	118	4	AAK22587	Aak22587 Human bra
C 881	5	35.7	35	2	AA167517	Aa167517 Serine pr	C 954	5	35.7	119	10	ADQ13487	AdQ13487 Human car
										121	12	ADK93490	AdK93490 Polynucle

955 5 35.7 121 12 ADK91018 Polynucle
 956 5 35.7 121 12 ADK92261 Polynucle
 957 5 35.7 121 12 ADK92288 Polynucle
 958 5 35.7 121 12 ADK93848 Polynucle
 959 5 35.7 124 4 AAI25295 Probe #15
 960 5 35.7 124 4 ABA71214 Human foe
 961 5 35.7 124 4 AAI51447 Probe #20
 962 5 35.7 124 4 ABA37526 Probe #15
 963 5 35.7 124 4 ABA45504 Human bon
 964 5 35.7 124 4 AAK15913 Human bon
 965 5 35.7 124 4 ABA45190 Human liv
 966 5 35.7 124 6 ABA19772 Human gen
 967 5 35.7 124 7 ADS66715 Corn seed
 968 5 35.7 125 8 ABZ09285 Human oli
 969 5 35.7 125 10 ABZ78738 Tumour su
 970 5 35.7 126 4 ABL27169 Drosophil
 971 5 35.7 128 2 AAT19739 Human gen
 972 5 35.7 128 4 AAI23034 Probe #12
 973 5 35.7 128 4 ABA68123 Human foe
 974 5 35.7 128 4 AAI48335 Probe #17
 975 5 35.7 128 4 ABA50188 Human bre
 976 5 35.7 128 4 AAK42262 Human bon
 977 5 35.7 128 4 AAK16509 Human bra
 978 5 35.7 128 4 ABA41869 Human liv
 979 5 35.7 128 5 AAI08693 Probe #86
 980 5 35.7 128 6 ABA16313 Human gen
 981 5 35.7 129 3 ABA45783 Human sec
 982 5 35.7 129 4 ABA99473 Human pro
 983 5 35.7 130 4 AAI26271 Probe #16
 984 5 35.7 130 4 AAI22452 Probe #12
 985 5 35.7 130 4 ABA74589 Human foe
 986 5 35.7 130 4 ABA67528 Human foe
 987 5 35.7 130 4 ABA73970 Human foe
 988 5 35.7 130 4 AAI55071 Probe #23
 989 5 35.7 130 4 AAI54419 Probe #23
 990 5 35.7 130 4 AAI47744 Probe #16
 991 5 35.7 130 4 ABA49625 Human bre
 992 5 35.7 130 4 ABA39383 Probe #17
 993 5 35.7 130 4 ABA39058 Probe #17
 994 5 35.7 130 4 ABA34609 Probe #13
 995 5 35.7 130 4 AAK49235 Human bon
 996 5 35.7 130 4 AAK41699 Human bon
 997 5 35.7 130 4 AAK48590 Human bon
 998 5 35.7 130 4 AAK15954 Human bra
 999 5 35.7 130 4 AAK23058 Human bra
 1000 5 35.7 130 4 AAK22423 Human bra

ALIGNMENTS

RESULT 1
 AAQ76921 standard; DNA; 136 BP.

AC AAQ76921;

DT 25-MAR-2003 (revised)
 DT 23-SEP-1994 (first entry)

DE Human genome fragment.

KW Brain; placenta; bone marrow; genetic analysis; gene mapping; detection;
 KW homology; human; adrenal tissue; ds.

OS Homo sapiens.

PN WO9401548-A2.

PD 20-JAN-1994.

PF 13-JUL-1993; 93WO-GH001467.

PR 13-JUL-1992; 92GB-00014857.

XX (MEDI-) MEDICAL RES COUNCIL.
 PA Sibson DR, Gross J, Hadfield KM, Howells D, Starkey M, Kelly M;
 PI Shaw D;
 DR WPI; 1994-035056/04.
 PT New nucleic acid fragment encoding gene products - can be used for
 PT genetic analysis and mapping.
 XX Claim 1; Page 272; 616pp; English.
 CC Human nucleic acid fragments, isolated from brain adrenal tissue, the
 CC placenta or bone marrow comprise any of: (A) a sequence selected from
 CC (AAQ76401-Q77613), (B) an allelic variation of a sequence as described in
 CC (A), or (C) a sequence complementary to (A) or (B). Updated on 25-MAR-
 CC 2003 to correct PN field.)
 SQ Sequence 136 BP; 36 A; 28 C; 29 G; 43 T; 0 U; 0 Other;
 Alignment Scores:
 Pred. No.: 8.94e-07 Length: 136
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 2 Gaps: 0
 US-09-736-250-5 (1-14) x AAQ76921 (1-136)
 QY 1 GLUAspAsnValSerGluAsnValGlySerValCysGlyThr 14
 DB 24 GAAGATAATCTCTCAGAAATGTCGTTCTGTGTGGCACT 65
 RESULT 2
 AAD51549/c
 ID AAD51549 standard; cDNA; 351 BP.
 AC AAD51549;
 DT 16-APR-2003 (first entry)
 DE Human BCA7 cDNA.
 KW Human; breast cancer-associated gene; BCA-related disorder; lymphoma;
 KW infectious disease; eating disorder; cancer; Ewing's tumour; allergy;
 KW tumour; polycythaemia vera; forensic biology; gene therapy; leukaemia;
 KW bone disease; sarcoma; vaccine; gene; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 CDS 1..351
 FT /*tag= a
 FT /product= "BCA protein"
 FT /transl_except= (pos:22..24, aa:Xaa)
 FT /transl_except= (pos:28..30, aa:Xaa)
 FT /transl_except= (pos:202..204, aa:Xaa)
 FT /transl_except= (pos:313..315, aa:Xaa)
 FT /transl_except= (pos:334..336, aa:Xaa)
 FT /note= "Xaa corresponds to in-frame stop codon; No start
 FT and stop codon"
 FT /partial
 XX WO200287507-A2.
 XX 07-NOV-2002.
 XX 29-APR-2002; 2002WO-US013584.
 XX 27-APR-2001; 2001US-0287170P.

PA (SUNN-) SUNNYBROOK & WOMEN'S COLLEGE HEALTH SCI.
PI Seth A;
XX WPI; 2003-120443/11.
XX P-PSDB; AAE33644.
XX New breast cancer-associated (BCA) genes and polypeptides, useful for
PT preventing, treating, diagnosing or staging breast cancer, or other BCA-
PT related disorders, e.g. prostate cancer, sarcoma, Ewing's tumor, leukemia
PT or lymphomas.
XX Disclosure; Page 188; 195pp; English.
XX The invention relates to human breast cancer-associated (BCA) genes and
XX polypeptides. BCA sequences are useful for preventing or treating breast
CC cancer. Other BCA-related disorders that may be treated include allergy,
CC bone disease, eating disorder, infectious disease, ovarian cancer,
CC prostate cancer, skin cancer or brain cancer, malignant or non-malignant
CC tumours, sarcoma, Ewing's tumour, leukaemia, lymphomas, or polycythaemia
CC vera. BCA sequences are also useful in forensic biology, diagnostic
CC assays, prognostic assays or pharmacogenomics or for monitoring clinical
CC trials. The invention is useful in gene therapy and as vaccines. The
CC present sequence is human BCA cDNA
XX Sequence 351 BP; 98 A; 77 C; 60 G; 116 T; 0 U; 0 Other;
SQ Alignment Scores: 2.05e-06 Length: 351
Pred. No.: 14.00 Matches: 14
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 8 Gaps: 0
DB: 0
US-09-736-250-5 (1-14) x AAD51549 (1-351)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 308 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 267
RESULT 3
ADK61066
ID ADK61066 standard; DNA; 389 BP.
XX AC
XX ADK61066;
XX 06-MAY-2004 (first entry)
XX Ovarian cancer-related DNA #221 with altered ovarian cancer expression.
DE ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
XX gene expression; primer; cancer.
XX Homo sapiens.
XX WO2003068054-A2.
XX 21-AUG-2003.
XX 13-FEB-2003; 2003WO-US004688.
XX 13-FEB-2002; 2002US-0357031P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (SLOK) SLOAN KETTERING INST CANCER RES.
XX Jazaeri AA, Boyd J, Liu ET;
XX WPI; 2003-689589/65.
XX Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT like tumor by determining a pattern of expression in the ovarian tumor of
several markers.
Disclosure; SEQ ID NO 236; 137pp; English.
The invention relates to a method of classifying an ovarian tumor as a
BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
pattern of expression in the ovarian tumor of several markers given in
the specification; and (2) comparing a similarity of the pattern of
expression of the markers in the ovarian tumor to a pattern of expression
of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
like or non-BRCA-like tumor. The method is useful for classifying an
ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
This sequence corresponds to an ovarian cancer-related gene having an
altered pattern of expression in ovarian cancer. (Note: The sequence data
for this patent did not form part of the printed specification but was
obtained in electronic format from WIPO at
ftp.wipo.int/pub/published_pct_sequences).
SQ Sequence 389 BP; 97 A; 99 C; 84 G; 100 T; 0 U; 9 Other;
Alignment Scores: 2.24e-06 Length: 389
Pred. No.: 14.00 Matches: 14
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 10 Gaps: 0
DB: 0
US-09-736-250-5 (1-14) x ADK61066 (1-389)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 286 GAAGATAATGCTCAGAAATGTGGTCTGTGTGGCACT 327
RESULT 4
ABK45862/c
ID ABK45862 standard; cDNA; 444 BP.
XX AC
XX ABK45862;
XX 05-JUN-2002 (first entry)
XX cDNA encoding colon tumour protein, SEQ ID NO 1413.
DE Human; colon tumour; vaccine; colon cancer; immunogenic; immunotherapy;
XX gene; ss.
XX Homo sapiens.
XX WO200212328-A2.
XX 14-FEB-2002.
XX 31-JUL-2001; 2001WO-US024218.
XX 03-AUG-2000; 2000US-0223283P.
XX 28-MAR-2001; 2001US-0279763P.
XX 29-JUN-2001; 2001US-0302051P.
XX (CORI-) CORIYA CORP.
XX King GE, Meagher MJ, Xu J, Secrist H;
XX WPI; 2002-241739/29.
XX New colon cancer polypeptides and polynucleotides, useful as vaccines,
PT for diagnosing, preventing, and treating colon cancer, and as markers for
PT the progression of cancer.
XX Claim 1; SEQ ID NO 1413; 147pp; English.
XX The invention relates to polynucleotides encoding colon tumour proteins.
CC The polynucleotides and encoded polypeptides are useful in pharmaceutical

CC compositions, such as vaccines, for the diagnosis, prevention, and
CC treatment of colon cancer. Polynucleotide sequences may be used as
CC hybridisation probes or primers, and in the design and preparation of
CC ribozyme molecules for inhibiting expression of tumour polypeptides and
CC proteins in tumour cells. The compositions are useful for stimulating an
CC immune response against cancer, particularly for the immunotherapy of
CC colon cancer, and as markers for the progression of cancer. ABK4450-
CC ABK46237 represent coding sequences of human colon tumour proteins of the
CC invention. Note: With the exception of SEQ ID No.1 and 2, the sequence
CC data for this patent did not form part of the printed specification but
CC was supplied by the European Patent Office

XX SQ Sequence 444 BP; 134 A; 81 C; 74 G; 155 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 2.52e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-736-250-5 (1-14) x ABK45862 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 436 GAAGATAATGCTCAGAAATGGGTTCTCTGTGGCACT 395
|||||

RESULT 5

AAS25071

ID AAS25071 standard; cDNA; 447 BP.

XX AC AAS25071;

XX DT 07-NOV-2001 (first entry)

XX DE Human ovarian PCR-subtracted cDNA library clone #1252.
XX KW Immunogenic protein; cancer; ovarian tumour; T-cell stimulation; ss;
XX KW gene therapy; cytostatic; T-cell expansion; nucleic acid hybridisation;
XX KW primer; probe.

XX OS Homo sapiens.

XX PN WO200157207-A2.

XX PD 09-AUG-2001.

XX PF 05-FEB-2001; 2001WO-US003733.

XX PR 04-FEB-2000; 2000US-0180403P.

XX PR 28-MAR-2000; 2000US-0192745P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA, Mannion J;

XX DR WPI; 2001-489879/53.

XX PT New polynucleotides encoding ovarian tumor proteins, useful for treating
XX PT ovarian cancer, and as probes, primers, and markers of cancer
XX PT progression.
XX PS Example 1; Page 304; 378pp; English.

XX CC The invention comprises compositions used for the therapy and diagnosis
XX CC of ovarian cancer. The compositions comprise one or more ovarian tumour
XX CC proteins, their associated polynucleotides, or immunogenic portions of
XX CC the proteins. The ovarian tumour polynucleotides and polypeptides are
XX CC useful for stimulating and/or expanding T cells specific for a tumour
XX CC protein. They are also useful for inhibiting the development of cancer in
XX CC a patient with an ovarian tumour DNA or protein by incubating isolated T-
XX CC cells allowing them to proliferate, and administering to the patient. The

CC sequences can be used as markers for cancer, for example, to monitor
CC ovarian cancer progression. Probes and primers are useful in nucleic acid
CC hybridisation, in detecting the presence of complementary sequences in a
CC given sample, for preparing mutant species and for preparing other
CC genetic constructions. Sequences AAS23820-AAS25231 and AAS25328-AAS25549
XX CC represent human ovarian tumour protein cDNA clones

SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 2.53e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x AAS25071 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
|||||
Db 93 GAAGATAATGCTCAGAAATGGGTTCTCTGTGGCACT 134
|||||

RESULT 6

AAH83716

ID AAH83716 standard; cDNA; 447 BP.

XX AC AAH83716;

XX DT 25-SEP-2001 (first entry)

XX DE Human ovarian tumour associated polynucleotide sequence SEQ ID NO:1340.
XX KW Human; ovarian tumour; ovarian cancer; diagnosis; gene therapy;
XX KW immunogenic; vaccine; ss.

XX OS Homo sapiens.

XX PN WO200151513-A2.

XX PD 19-JUL-2001.

XX PF 16-JAN-2001; 2001WO-US001575.

XX PR 14-JAN-2000; 2000US-0176722P.

XX PA (CORI-) CORIXA CORP.

XX PI Algate PA;

XX DR WPI; 2001-425866/45.

XX FT Novel ovarian tumor proteins, and nucleic acids encoding them, used to
XX FT treat and diagnose cancers, particularly ovarian cancer.
XX PS Claim 5; Page 308; 338pp; English.

XX CC AAH82377 to AAH83878 represent human ovarian tumour-associated
XX CC polynucleotide sequences which encode ovarian tumour proteins. The
XX CC ovarian tumour protein and polynucleotide sequences have cytostatic
XX CC activity, and can be used in gene therapy and vaccine production. The
XX CC ovarian tumour proteins and polynucleotides can be used to inhibit the
XX CC development of cancer, particularly ovarian cancer. They can also be used
XX CC to diagnose the onset and progression of cancer

SQ Sequence 447 BP; 157 A; 79 C; 92 G; 115 T; 0 U; 4 Other;

Alignment Scores:
Pred. No.: 2.53e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

```
DB:          5          Gaps:          0
US-09-736-250-5 (1-14) x AAH83716 (1-447)
Oy  1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db  93 GAAGATAATGTCCTCAGAAATGTGGTCTCTGTGTGGCACT 134

RESULT 7
ADK61065/c
ID  ADK61065 standard; DNA; 597 BP.
XX  AC  ADK61065;
XX  AC  ADK61065;
XX  DT  06-MAY-2004 (first entry)
XX  DE  Ovarian cancer-related DNA #220 with altered ovarian cancer expression.
XX  KW  ds: gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
XX  KW  gene expression; primer; cancer.
XX  OS  Homo sapiens.
XX  PN  WO2003068054-A2.
XX  PD  21-AUG-2003.
XX  PF  13-FEB-2003; 2003WO-US004688.
XX  PR  13-FEB-2002; 2002US-0357031P.
XX  PA  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX  PA  (SLOK ) SLOAN KETTERING INST CANCER RES.
XX  PI  Jazaeri AA, Boyd J, Liu ET;
XX  WPI; 2003-689589/65.
XX  PT  Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
PT  like tumor by determining a pattern of expression in the ovarian tumor of
PT  several markers.
XX  PS  Disclosure; SEQ ID NO 235; 137pp; English.
XX  CC  The invention relates to a method of classifying an ovarian tumor as a
CC  BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC  pattern of expression in the ovarian tumor of several markers given in
CC  the specification; and (2) comparing a similarity of the pattern of
CC  expression of the markers in the ovarian tumor to a pattern of expression
CC  of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC  like or non-BRCA-like tumor. The method is useful for classifying an
CC  ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC  This sequence corresponds to an ovarian cancer -related gene having an
CC  altered pattern of expression in ovarian cancer. (NOTE: The sequence data
CC  for this patent did not form part of the printed specification but was
CC  obtained in electronic format from WIPO at
CC  ftp.wipo.int/pub/published_pct_sequences).
XX  SQ  Sequence 597 BP; 152 A; 126 C; 143 G; 171 T; 0 U; 5 Other;

Alignment Scores:
Pred. No.:      3.26e-06      Length:      597
Score:          14.00        Matches:      14
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              10          Gaps:          0

US-09-736-250-5 (1-14) x ADK61065 (1-597)
Oy  1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db  303 GAAGATAATGTCCTCAGAAATGTGGTCTCTGTGTGGCACT 262
```

```
RESULT 8
AAAX40003/c
ID  AAAX40003 standard; DNA; 804 BP.
XX  AC  AAAX40003;
XX  AC  AAAX40003;
XX  DT  02-JUL-1999 (first entry)
XX  DE  Prostate cancer associated gene.
XX  KW  Cancer associated antigen; diagnosis; research; treatment; human;
XX  KW  breast cancer; colon cancer; gastric cancer; renal cancer; lung cancer;
XX  KW  prostate cancer; ss.
XX  OS  Homo sapiens.
XX  PN  WO9904265-A2.
XX  PD  28-JAN-1999.
XX  PF  15-JUL-1998; 98WO-US014679.
XX  PR  17-JUL-1997; 97US-00896164.
XX  PR  10-OCT-1997; 97US-0061599P.
XX  PR  10-OCT-1997; 97US-0061765P.
XX  PR  10-OCT-1997; 97US-00948705.
XX  PR  11-OCT-1997; 97GB-00021697.
XX  PR  22-JUN-1998; 98US-00102322.
XX  PA  (LUDW-) LUDWIG INST CANCER RES.
XX  PI  Old LJ, Scanlan MJ, Stockert E, Gure A, Chen Y, Gout I;
XX  PI  O'hare M, Obata Y, Pfreundschuh M, Tureci O, Sahin U;
XX  DR  WPI; 1999-132448/11.
XX  PT  New isolated cancer associated nucleic acids and polypeptides - isolated
PT  using sera from cancer patients, used to develop products for the
PT  diagnosis, monitoring or treatment of cancers.
XX  PS  Claim 67; Page 630; 787pp; English.
XX  CC  The invention relates to a method for diagnosing a disorder characterised
CC  by expression of a human cancer associated antigen precursor coded for by
CC  a nucleic acid molecule (NAM). The method comprises: (a) contacting a
CC  biological sample isolated from a subject with an agent that specifically
CC  binds to the NAM, an expression product or a fragment of an expression
CC  product complexed with an HLA molecule; and (b) determining the
CC  interaction between the agent and the NAM or the expression product as a
CC  determination of the disorder. The products and methods can be used in
CC  the diagnosis, monitoring, research, or treatment of conditions
CC  characterised by the expression of various cancer associated antigens.
CC  The invention provides nucleic acid sequences and encoded polypeptides
CC  which are cancer associated antigen precursors expressed in human breast
CC  cancer, renal cancer, colon cancer, gastric cancer, prostate cancer and
CC  lung cancer
XX  SQ  Sequence 804 BP; 208 A; 172 C; 188 G; 222 T; 0 U; 14 Other;

Alignment Scores:
Pred. No.:      4.23e-06      Length:      804
Score:          14.00        Matches:      14
Percent Similarity: 100.00%    Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              2          Gaps:          0

US-09-736-250-5 (1-14) x AAAX40003 (1-804)
Oy  1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
    |||||
Db  301 GAAGATAATGTCCTCAGAAATGTGGTCTCTGTGTGGCACT 260
```

RESULT 9
ADN01156
ID ADN01156 standard; DNA; 903 BP.
XX AC
XX ADN01156;
XX
XX 01-JUL-2004 (first entry)
XX
XX Human cell growth, differentiation, and death-associated coding seq #15.
XX
XX human; cell growth; cell differentiation; cell death; CGDD;
XX cell proliferative disorder; arteriosclerosis; atherosclerosis; bursitis;
XX cirrhosis; hepatitis; polycythemia vera; psoriasis; cancer;
XX developmental disorder; Cushing's syndrome; hypothyroidism;
XX neurological disorder; epilepsy; stroke; Alzheimer's disease;
XX Pick's disease; Huntington's disease; Parkinson's disease;
XX multiple sclerosis; autoimmune disorder; inflammatory disorder; AIDS;
XX allergy; anaemia; asthma; contact dermatitis; diabetes mellitus;
XX reproductive disorder; infertility; endometriosis; uterine fibroid; gene;
XX ds.
XX
XX Homo sapiens.
XX
XX WO2004031364-A2.
XX
XX 15-APR-2004.
XX
XX 03-OCT-2003; 2003WO-US031441.
XX
XX 03-OCT-2002; 2002US-0416205P.
XX 25-OCT-2002; 2002US-0421521P.
XX 21-NOV-2002; 2002US-0428376P.
XX 23-DEC-2002; 2002US-0436288P.
XX 10-JAN-2003; 2003US-0439292P.
XX 13-FEB-2003; 2003US-0447578P.
XX
XX (INCY-) INCYTE CORP.
XX (BURR/) BURRILL J D.
XX
XX Elliott VS, Swarnakar A, Tang YT, Yue H, Lu DAM, Khare R;
XX Chawla NK, Richardson TW, Marquis JP, Lal PG, Nguyen DB, Lee SY;
XX Tran UK, Bhatia UG, Lee S, Blake JJ, Ho A, Zheng W, Gao J, Tran B;
XX Yang YG, Gietzen KJ, Hatfalia AJA;
XX
XX WPI; 2004-330172/30.
XX P-PSDB; ADN01131.
XX
XX New isolated polypeptides associated with cell growth, differentiation
XX and death, useful for diagnosing, treating or preventing e.g.
XX atherosclerosis, psoriasis, cancers, Alzheimer's disease, AIDS, anemia,
XX diabetes mellitus or infertility.
XX
XX Claim 5; SEQ ID NO 40; 213pp; English.
XX
XX The invention comprises the amino acid and coding sequences of human
XX proteins that are associated with cell growth, differentiation, and death
XX (CGDD). The DNA and protein sequences of the invention are useful for
XX diagnosing, treating or preventing disorders associated with aberrant
XX expression of CGDD, such as: cell proliferative disorders (e.g.
XX arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis,
XX polycythemia vera, psoriasis and cancers), developmental disorders (e.g.
XX Cushing's syndrome and hypothyroidism), neurological disorders (e.g.
XX epilepsy, stroke, Alzheimer's disease, Pick's disease, Huntington's
XX disease, Parkinson's disease and multiple sclerosis),
XX autoimmune/inflammatory disorders (e.g. AIDS, allergies, anaemia, asthma,
XX contact dermatitis and diabetes mellitus), and reproductive disorders
XX (e.g. infertility, endometriosis and uterine fibroid). The present DNA
XX sequence encodes a human CGDD-associated protein of the invention.
XX
XX SQ Sequence 903 BP; 247 A; 202 C; 201 G; 253 T; 0 U; 0 Other;
XX
XX Alignment Scores:

Pred. No.: 4.68e-06 Length: 903
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
US-09-736-250-5 (1-14) x ADN01156 (1-903)
QY 1 GLUASpAsnValSerGluAenValGlySerValCysGlyThr 14
DB 797 GAAGATAATCTCTCAGAAAATGTGGGTCTGTGTGTGGCACT 838
RESULT 10
AAZ37836
ID AAZ37836 standard; DNA; 1260 BP.
XX AAZ37836;
XX 09-FEB-2000 (first entry)
XX Human cyclin I nucleotide sequence.
XX Cyclin-dependent kinase 2; CDK2; hsReq; hsReq*-1; hsReq*-2; cyclin I;
XX ERH; cell cycle; proliferation; cancer; hyperproliferative disorder;
XX atherosclerosis; tumour; ss.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1134
XX FT /*tag= a
XX FT /product= "Cyclin_I"
XX
XX W09925829-A2.
XX 27-MAY-1999.
XX 12-NOV-1998; 98WO-US024095.
XX 13-NOV-1997; 97US-00969106.
XX (CURA-) CURAGEN CORP.
XX Yang M, Nandabalan K, Schulz VP;
XX WPI; 2000-061923/05.
XX P-PSDB; AAY52185.
XX New complexes of the cyclin-dependent kinase 2 protein with its
XX interacting proteins, used to treat, e.g. atherosclerosis.
XX Example; Fig 2; 90pp; English.
XX
XX This sequence is the human Cyclin I nucleotide sequence. Cyclin I is
XX expressed at almost constant levels throughout the cell cycle, and is
XX implicated in controlling cell cycle progression and transcriptional
XX control. Cyclins form complexes with cyclin-dependent kinases. CDK2,
XX cyclin-dependent kinase 2, is used in the invention which relates to
XX complexes of the CDK2 protein with other proteins, selected from cyclin
XX I, ERH, hsReq, hsReq*-1 and hsReq*-2 (AAY52185-152188). CDK2 is expressed
XX late in G1 or early in S phase of the cell cycle, and is pivotal for G1/S
XX transition. Compositions containing a CDK2 complex, an antibody targeting
XX the complex, and nucleotide sequences encoding CDK2 or its derivatives
XX can be used therapeutically. The complexes and their nucleotide sequences
XX can be used to treat diseases or disorders associated with increased or
XX decreased levels of the complex. Screening the complex, or a derivative
XX or a modulator of the complex for neoplastic activity by measuring the
XX survival or proliferation of cells from a malignant cell line when in
XX contact with the complex can be used to indicate if the complex has
XX anti-neoplastic activity. Screening for molecules that modulate the
XX formation of the complexes can be used for treating or preventing
XX atherosclerosis or atherosclerosis-associated disease by contacting cells

CC or using a test animal, in which tumour growth or regression is measured
CC to test whether anti-neoplastic activity is displayed. Diseases which can
CC be treated or prevented by molecule/s which modulate the function of the
CC complex include cancer, hyperproliferative disorders and atherosclerosis
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-736-250-5 (1-14) x AA237836 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGCGGTCTGTGTGGCACT 1068

RESULT 11
ID ABK83672 standard; cDNA; 1260 BP.
XX
AC ABK83672;
XX
DT 14-AUG-2002 (first entry)
XX
DE Human cDNA differentially expressed in granulocytic cells #243.
XX
KW Human; ss; granulocytic cell; DNA chip; bacterial infection;
KW viral infection; parasitic infection; protozoal infection;
KW fungal infection; sterile inflammatory disease; psoriasis;
KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;
KW cardiac reperfusion injury; renal reperfusion injury; ARDS;
KW adult respiratory distress syndrome; inflammatory bowel disease;
KW Crohn's disease; ulcerative colitis; periodontal disease;
KW granulocyte activation; chronic inflammation; allergy.
XX
OS Homo sapiens.
XX
PN WO200228999-A2.
XX
PD 11-APR-2002.
XX
PF 03-OCT-2001; 2001WO-US030821.
XX
PR 03-OCT-2000; 2000US-0237189P.
XX
PA (GENE-) GENE LOGIC INC.
XX
PI Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;
XX
DR WPT; 2002-435328/46.
XX

CC Detecting granulocyte activation by detecting differential expression of
CC genes associated with granulocyte activation, which serves as diagnostic
CC markers that is useful for monitoring disease states and drug toxicity.
XX
PS Claim 1; SEQ ID NO 243; 114pp; English.

CC The invention relates to detecting (M1) granulocyte (GC) activation
CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by
CC DNA chip analysis as given in the specification, and comparing the
CC expression level to an expression level in an unactivated GC, where
CC differential expression of Gs is indicative of GCA. Also included are
CC modulating (M2) GA by contacting GC with an agent that alters the
CC expression of at least one gene in Gs; (2) screening (M3) for an agent
CC capable of modulating GCA or an inflammation (especially chronic) in a
CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease using the gene expression
CC profile; (3) detecting (M4) an inflammation (especially chronic) in a

CC tissue, an allergic response in a subject, exposure of a subject to a
CC pathogen or sterile inflammatory disease, by detecting the level of
CC expression in a sample of the tissue of gene(s) from Gs, where the level
CC of expression of the gene is indicative of inflammation; (4) treating
CC (M5) an inflammation (especially chronic) or in a tissue, an allergic
CC response in a subject, exposure of a subject to a pathogen or sterile
CC inflammatory disease, by contacting a tissue having inflammation with an
CC agent that modulates the expression of gene(s) from Gs in the tissue. M1
CC is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
CC for screening an agent capable of modulating GCA preferably in an
CC inflammation in a tissue; M4 is useful for detecting an inflammation
CC (especially chronic) in a tissue, an allergic response in a subject,
CC exposure of a subject to a pathogen or sterile inflammatory disease (e.g.
CC psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis,
CC cardiac reperfusion injury, renal reperfusion injury, ARDS, adult
CC respiratory distress syndrome, inflammatory bowel disease, Crohn's
CC disease, ulcerative colitis, periodontal disease; also bacterial
CC infection, viral infection, parasitic infection, protozoal infection,
CC fungal infection and M5 is useful for treating one of the above
CC conditions. The present sequence represents a gene differentially
CC expressed in granulocytes. Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX

SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservativity: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-736-250-5 (1-14) x ABK83672 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGCGGTCTGTGTGGCACT 1068

RESULT 12
ID ADK61064 standard; DNA; 1260 BP.
XX
AC ADK61064;
XX
DT 06-MAY-2004 (first entry)
XX
DE Ovarian cancer-related DNA #219 with altered ovarian cancer expression.
XX ds; gene; ovarian tumor; BRCA-1-like; BRCA-2-like; non-BRCA-like;
XX gene expression; primer; cancer.
XX
OS Homo sapiens.
XX
PN WO2003068054-A2.
XX
PD 21-AUG-2003.
XX
PF 13-FEB-2003; 2003WO-US004688.
XX
PR 13-FEB-2002; 2002US-0357031P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA (SLOK) SLOAN KETTERING INST CANCER RES.
XX
PI Jazaeri AA, Boyd J, Liu ET;
XX WPT; 2003-689589/65.
XX
PT Classifying an ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-
XX like tumor by determining a pattern of expression in the ovarian tumor of

PT several markers.
XX
PS Disclosure; SEQ ID NO 234; 137pp; English.
XX
CC The invention relates to a method of classifying an ovarian tumor as a
CC BRCA-1-like or BRCA-2-like or non-BRCA-like tumor by: (1) determining a
CC pattern of expression in the ovarian tumor of several markers given in
CC the specification; and (2) comparing a similarity of the pattern of
CC expression of the markers in the ovarian tumor to a pattern of expression
CC of the markers in a comparison tissue of a known BRCA-1-like or BRCA-2-
CC like or non-BRCA-like tumor. The method is useful for classifying an
CC ovarian tumor as a BRCA-1-like or BRCA-2-like or non-BRCA-like tumor.
CC This sequence corresponds to an ovarian cancer -related gene having an
CC altered pattern of expression in ovarian cancer. (Note: The sequence data
CC for this patent did not form part of the printed specification but was
CC obtained in electronic format from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences).
XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-736-250-5 (1-14) x ADK61064 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 1068

RESULT 13
ADI31573
ID ADI31573 standard; cDNA; 1260 BP.
XX AC ADI31573;
XX
XX 17-JUN-2004 (first entry)
XX
XX Human cDNA #899.
XX
XX Human; gene; ss; immunological response; immunopathological condition;
XX Crohn's disease; asthma; ulcerative colitis; hypereosinophilia;
XX irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
XX acute monocytic leukaemia; antiinflammatory; antiasthmatic; antiulcer;
XX osteopathic; antiarthritic; antirheumatic; cytostatic.
XX
XX Homo sapiens.
XX
XX US6607879-B1.
XX
XX 19-AUG-2003.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX 09-FEB-1998; 98US-00023655.
XX
XX (INCY-) INCYTE CORP.
XX
XX Cocks BG, Stuart SG, Seilhamer JJ;
XX
XX WPI; 2003-895307/82.
XX
XX
XX A composition comprising a plurality of cDNAs, useful for detecting
XX altered expression of genes in an immunological response or for
XX diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma
XX or osteoarthritis.
XX
XX Claim 1; SEQ ID NO 899; 50pp; English.
XX
XX

CC The invention relates to a composition comprising a plurality of cDNAs
CC for detecting the altered expression of genes in an immunological
CC response. The invention also relates to a method of diagnosing or
CC monitoring the treatment of an immunopathological condition in a sample,
CC comprising obtaining nucleic acids from a sample, contacting the nucleic
CC acids of the sample with an array comprising the plurality of cDNAs under
CC conditions to form one or more hybridisation complexes, detecting the
CC hybridisation complexes and comparing the levels of the detected
CC hybridisation complexes with the level of hybridisation complexes
CC detected in a non-diseased sample, where an altered level of the detected
CC hybridisation complexes correlates with the presence of an
CC immunopathological condition. Also disclosed are an expression profile
CC comprising a microarray and a plurality of detectable complexes and a
CC method for identifying a plurality of polynucleotide probes. The cDNAs
CC are useful as hybridisable array elements in a microarray for monitoring
CC the expression of target polynucleotides. The microarray can be used in
CC the diagnosis of an immunopathology, such as Crohn's disease, asthma,
CC ulcerative colitis, hypereosinophilia, irritable bowel syndrome,
CC osteoarthritis, rheumatoid arthritis or acute monocytic leukaemia, and in
CC identifying agents for the treatment of the diseases. The microarray may
CC also be used in drug discovery and development, toxicological and
CC carcinogenicity studies, forensics or pharmacogenomics. The composition
CC may also be used in purification of a subpopulation of mRNAs, cDNAs or
CC genomic fragments. This sequence represents a human cDNA of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification but was obtained in electronic format directly
CC from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0

US-09-736-250-5 (1-14) x ADI31573 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTCTCTGTGTGGCACT 1068

RESULT 14
ADR25465
ID ADR25465 standard; DNA; 1260 BP.
XX AC ADR25465;
XX
XX 21-OCT-2004 (first entry)
XX
XX Breast cancer prognosis marker #1326.
XX
XX ds; breast cancer; prognosis; gene expression; diagnosis.
XX
XX Homo sapiens.
XX
XX WO2004065545-A2.
XX
XX 05-AUG-2004.
XX
XX 15-JAN-2004; 2004WO-US001100.
XX
XX 15-JAN-2003; 2003US-00342887.
XX
XX (ROSE-) ROSETTA INPHARMATICS LLC.
XX (NRCA-) NETHERLANDS CANCER INST.
XX Van't Veer LJ, He Y;
XX WPI; 2004-593473/57.
XX

PT Classifying a breast cancer patient according to prognosis comprises
PT determining the similarity between the level of expression of each of
PT five genes in a cell sample taken from patient, to control levels.
XX
XX
PS Disclosure; SEQ ID NO 1326; 226pp; English.

XX The invention relates to a method of classifying a breast cancer patient
CC according to prognosis by determining the similarity between the level of
CC expression of each of five genes for which markers are listed in the
CC specification, in a cell sample taken from the breast cancer patient, to
CC control levels of expression for each respective five genes to obtain a
CC patient similarity value. The methods are useful for classifying a breast
CC cancer patient according to prognosis. Kits and computer program products
CC are useful for data analysis using the diagnostic, prognostic and
CC statistical methods of the invention. This sequence corresponds to a
CC marker used in the method of the invention.

XX
SQ Sequence 1260 BP; 352 A; 283 C; 274 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.26e-06 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x ADR25465 (1-1260)

Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 15

AAT73937
ID AAT73937 standard; DNA; 1328 BP.

XX
AC AAT73937;

XX 02-DEC-1997 (first entry)

XX DNA encoding human cyclin I.

XX human; cyclin I; antisense; probe; neurone; cancer; antibody; ds.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 69..1202
XX /*tag= a

XX WO9712973-A1.

XX 10-APR-1997.

XX 07-OCT-1996; 96WO-JP002905.

XX 05-OCT-1995; 95JP-00284663.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Nakamura T;

XX WPI; 1997-226217/20.
XX P-PSDB; AAW21965.

XX Human cyclin I protein and related (anti:sense) DNA - used for neuron
PT labelling method and cancer cell detection.

XX Example 1; Fig 1; 45pp; Japanese.

XX This sequence encodes human cyclin I. Antisense polynucleotides are
XX useful for as probes and can be labelled and used for detection of

CC neurones by hybridisation with mRNA for cyclin I (contained in the
CC neurones and arising by the expression of the cyclin I gene in these
CC cells). The gene can be used for detection of cancer cells by detecting
CC the expression of the cyclin I gene in these cells. Also antibodies
CC specific for the fragments of the protein (especially AAW21966) can be
CC used for detection

XX
SQ Sequence 1328 BP; 376 A; 292 C; 302 G; 358 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 6.56e-06 Length: 1328
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x AAT73937 (1-1328)

Oy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1095 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 1136

Search completed: February 11, 2005, 10:39:48
Job time : 104.197 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 09:52:50 ; Search time 11.1356 Seconds
(without alignments)
2057.184 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSNVGVCGT 14

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2395371

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09736250/runat_07022005_154942_20670/app.query.fasta_1.718
-DB=Issued_Patents_NA -QWMT=fastap -SUFFIX=oligo.rn1 -MINMATCH=0.1 -LOOPCL=0
-LOPEXT=0 -UNITS=Dits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=1000 -DOCALLIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09736250@cgn 1 1 93 @runat_07022005_154942_20670 -NCPU=6 -ICPU=3
-NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description
	1	14	100.0	1133	3	US-09-054-492B-2		Sequence 2, Appli
	2	14	100.0	1260	2	US-08-969-106-5		Sequence 5, Appli
	3	14	100.0	1260	4	US-09-338-125-5		Sequence 5, Appli
	4	14	100.0	1260	4	US-09-023-655-899		Sequence 899, App
	5	13	92.9	304	4	US-08-513-999C-29994		Sequence 29894, A
	C 6	7	50.0	601	4	US-09-949-016-187337		Sequence 187337,
	C 7	7	50.0	601	4	US-09-949-016-187338		Sequence 187338,
	C 8	7	50.0	601	4	US-09-949-016-187339		Sequence 187339,
	C 9	7	50.0	601	4	US-09-949-016-187340		Sequence 187340,
	10	7	50.0	1226	4	US-08-976-594-1110		Sequence 1110, Ap
	C 11	7	50.0	76563	4	US-09-949-016-17099		Sequence 17099, A
	C 12	7	50.0	78269	4	US-09-949-016-12497		Sequence 12497, A

C 13	6	42.9	19	4	US-09-422-978-6641	Sequence 6641, Ap
C 14	6	42.9	201	4	US-09-489-039A-3894	Sequence 3894, Ap
C 15	6	42.9	256	4	US-09-513-999C-27371	Sequence 27371, A
C 16	6	42.9	293	4	US-09-702-705-538	Sequence 538, App
C 17	6	42.9	293	4	US-09-736-457-538	Sequence 538, App
C 18	6	42.9	293	4	US-09-614-124B-538	Sequence 538, App
C 19	6	42.9	293	4	US-09-671-325-538	Sequence 538, App
C 20	6	42.9	293	4	US-09-589-184-538	Sequence 538, App
C 21	6	42.9	293	4	US-09-658-824-538	Sequence 538, App
C 22	6	42.9	343	5	PCT-US95-08295-13	Sequence 13, Appl
C 23	6	42.9	480	3	US-09-188-930-39	Sequence 39, Appl
C 24	6	42.9	480	3	US-09-188-930-208	Sequence 208, App
C 25	6	42.9	480	4	US-09-312-283C-39	Sequence 39, Appl
C 26	6	42.9	480	4	US-09-312-283C-208	Sequence 208, App
C 27	6	42.9	498	3	US-09-328-111-252	Sequence 252, App
C 28	6	42.9	601	4	US-09-949-016-18756	Sequence 18756, A
C 29	6	42.9	601	4	US-09-949-016-33007	Sequence 33007, A
C 30	6	42.9	601	4	US-09-949-016-33008	Sequence 33008, A
C 31	6	42.9	601	4	US-09-949-016-71298	Sequence 71298, A
C 32	6	42.9	601	4	US-09-949-016-107870	Sequence 107870, A
C 33	6	42.9	601	4	US-09-949-016-133721	Sequence 133721, A
C 34	6	42.9	601	4	US-09-949-016-130929	Sequence 130929, A
C 35	6	42.9	601	4	US-09-949-016-140783	Sequence 140783, A
C 36	6	42.9	601	4	US-09-949-016-164103	Sequence 164103, A
C 37	6	42.9	601	4	US-09-949-016-175780	Sequence 175780, A
C 38	6	42.9	601	4	US-09-949-016-186703	Sequence 186703, A
C 39	6	42.9	639	4	US-09-489-039A-3940	Sequence 3940, Ap
C 40	6	42.9	708	4	US-09-543-681A-2551	Sequence 2551, Ap
C 41	6	42.9	823	4	US-09-949-016-1025	Sequence 1025, Ap
C 42	6	42.9	823	4	US-09-949-016-2692	Sequence 2692, Ap
C 43	6	42.9	830	4	US-09-976-594-858	Sequence 858, App
C 44	6	42.9	862	3	US-09-149-476-73	Sequence 73, Appl
C 45	6	42.9	932	3	US-09-149-476-237	Sequence 237, App
C 46	6	42.9	962	1	US-08-324-301-14	Sequence 14, Appl
C 47	6	42.9	1001	4	US-09-671-317-17	Sequence 17, Appl
C 48	6	42.9	1001	4	US-09-671-317-18	Sequence 18, Appl
C 49	6	42.9	1236	4	US-09-252-991A-1087	Sequence 1087, Ap
C 50	6	42.9	1512	3	US-08-476-509B-1	Sequence 1, Appli
C 51	6	42.9	1626	3	US-08-348-518C-1	Sequence 1, Appli
C 52	6	42.9	1731	4	US-09-540-236-366	Sequence 366, App
C 53	6	42.9	1765	4	US-09-270-767-11023	Sequence 11023, A
C 54	6	42.9	1842	4	US-09-016-434-46	Sequence 46, Appl
C 55	6	42.9	1933	4	US-09-023-655-739	Sequence 739, App
C 56	6	42.9	1947	4	US-09-252-991A-1048	Sequence 1048, Ap
C 57	6	42.9	2253	6	5457037-2	Patent No. 5457037
C 58	6	42.9	2253	6	5457037-2	Patent No. 5457037
C 59	6	42.9	2256	4	US-09-949-016-2427	Sequence 2427, Ap
C 60	6	42.9	2256	4	US-09-949-016-2428	Sequence 2428, Ap
C 61	6	42.9	2437	1	US-07-795-859B-5	Sequence 5, Appli
C 62	6	42.9	2437	1	US-08-457-616-5	Sequence 5, Appli
C 63	6	42.9	2437	3	US-09-235-538-1	Sequence 1, Appli
C 64	6	42.9	2455	4	US-09-949-016-1570	Sequence 1570, Ap
C 65	6	42.9	2625	6	5457037-4	Patent No. 5457037
C 66	6	42.9	2625	6	5457037-4	Patent No. 5457037
C 67	6	42.9	2715	4	US-09-543-681A-392	Sequence 392, App
C 68	6	42.9	2980	4	US-09-799-451-373	Sequence 373, App
C 69	6	42.9	2994	4	US-09-976-594-398	Sequence 398, App
C 70	6	42.9	3189	4	US-09-447-399-1	Sequence 1, Appli
C 71	6	42.9	3336	6	5457037-1	Patent No. 5457037
C 72	6	42.9	3336	6	5457037-1	Patent No. 5457037
C 73	6	42.9	3420	4	US-09-447-399-3	Sequence 3, Appli
C 74	6	42.9	3464	3	US-09-318-448-30	Sequence 30, Appl
C 75	6	42.9	3502	4	US-09-976-594-659	Sequence 659, App
C 76	6	42.9	3546	1	US-07-951-715A-27	Sequence 27, Appl
C 77	6	42.9	3546	2	US-08-459-448A-27	Sequence 27, Appl
C 78	6	42.9	3546	3	US-08-459-595A-27	Sequence 27, Appl
C 79	6	42.9	3546	3	US-08-459-504B-27	Sequence 27, Appl
C 80	6	42.9	3546	3	US-08-459-444-27	Sequence 27, Appl
C 81	6	42.9	3546	3	US-09-547-422-27	Sequence 27, Appl
C 82	6	42.9	3546	3	US-09-968-462-27	Sequence 27, Appl
C 83	6	42.9	3709	3	US-09-541-782-7	Sequence 7, Appli
C 84	6	42.9	3709	3	US-09-723-820-7	Sequence 7, Appli
C 85	6	42.9	3709	4	US-10-270-085-7	Sequence 7, Appli

86	6	42.9	3887	4	US-09-976-594-660	Sequence 660, App	159	6	42.9	1664976	4	US-09-692-570-1	Sequence 1, Appli
87	6	42.9	3934	4	US-09-023-655-1066	Sequence 1066, App	c 160	5	35.7	17	3	US-08-584-040-4276	Sequence 4276, Ap
88	6	42.9	4248	4	US-09-252-991A-9867	Sequence 9867, Ap	c 161	5	35.7	17	4	US-09-371-722B-2043	Sequence 2043, Ap
89	6	42.9	4530	4	US-09-566-921-134	Sequence 134, App	c 162	5	35.7	17	4	US-09-685-664B-2043	Sequence 2043, Ap
90	6	42.9	4530	4	US-09-919-039-358	Sequence 358, App	c 163	5	35.7	20	4	US-09-596-248D-50	Sequence 50, Appl
c 91	6	42.9	4628	4	US-09-799-451-85	Sequence 85, Appl	c 164	5	35.7	21	3	US-09-061-273-10	Sequence 10, Appl
c 92	6	42.9	4819	4	US-09-774-528-72	Sequence 72, Appl	c 165	5	35.7	22	3	US-09-009-913-251	Sequence 251, App
c 93	6	42.9	5595	1	US-07-841-655-1	Sequence 1, Appli	c 166	5	35.7	23	4	US-09-520-538-15	Sequence 15, Appl
c 94	6	42.9	5595	1	US-07-635-965C-1	Sequence 1, Appli	c 167	5	35.7	25	1	US-08-427-862-5	Sequence 5, Appli
c 95	6	42.9	6574	3	US-08-221-017B-1097	Sequence 1097, Ap	c 168	5	35.7	25	4	US-09-396-196G-13143	Sequence 13143, A
c 96	6	42.9	7497	4	US-08-949-016-3114	Sequence 3114, Ap	c 169	5	35.7	25	4	US-09-396-196G-29216	Sequence 29216, A
c 97	6	42.9	16448	4	US-09-902-540-9686	Sequence 9686, Ap	c 170	5	35.7	25	4	US-09-396-196G-29217	Sequence 29217, A
c 98	6	42.9	16450	4	US-09-902-540-1098	Sequence 1098, Ap	c 171	5	35.7	25	4	US-09-396-196G-29218	Sequence 29218, A
c 99	6	42.9	18471	4	US-09-902-540-1167	Sequence 1167, Ap	c 172	5	35.7	25	4	US-09-396-196G-31171	Sequence 31171, A
c 100	6	42.9	21513	4	US-09-949-016-16695	Sequence 16695, A	c 173	5	35.7	25	4	US-09-396-196G-31172	Sequence 31172, A
c 101	6	42.9	21513	4	US-09-949-016-16696	Sequence 16696, A	c 174	5	35.7	25	4	US-09-396-196G-32009	Sequence 32009, A
c 102	6	42.9	21513	4	US-09-949-016-16697	Sequence 16697, A	c 175	5	35.7	25	4	US-09-396-196G-49676	Sequence 49676, A
c 103	6	42.9	21721	4	US-09-269-939A-41	Sequence 41, Appl	c 176	5	35.7	25	4	US-09-396-196G-64202	Sequence 64202, A
c 104	6	42.9	22976	4	US-09-269-939A-19	Sequence 19, Appl	c 177	5	35.7	25	4	US-09-396-196G-64204	Sequence 64204, A
c 105	6	42.9	23187	4	US-09-499-522-1	Sequence 1, Appli	c 178	5	35.7	25	4	US-09-396-196G-64205	Sequence 64205, A
c 106	6	42.9	34312	4	US-09-949-016-12352	Sequence 12352, A	c 179	5	35.7	25	4	US-09-396-196G-68388	Sequence 68388, A
c 107	6	42.9	38575	4	US-09-949-016-12876	Sequence 12876, A	c 180	5	35.7	25	4	US-09-396-196G-70793	Sequence 70793, A
c 108	6	42.9	38575	4	US-09-949-016-13871	Sequence 13871, A	c 181	5	35.7	25	4	US-09-396-196G-76419	Sequence 76419, A
c 109	6	42.9	39003	4	US-09-596-002-21	Sequence 21, Appl	c 182	5	35.7	25	4	US-09-396-196G-76430	Sequence 76430, A
c 110	6	42.9	39293	4	US-09-949-016-12556	Sequence 12556, A	c 183	5	35.7	25	4	US-09-396-196G-102778	Sequence 102778, A
c 111	6	42.9	39295	4	US-09-949-016-16078	Sequence 16078, A	c 184	5	35.7	25	4	US-09-396-196G-102779	Sequence 102779, A
c 112	6	42.9	41639	4	US-09-949-016-15471	Sequence 15471, A	c 185	5	35.7	25	4	US-09-396-196G-106684	Sequence 106684, A
c 113	6	42.9	46902	4	US-09-949-016-13844	Sequence 13844, A	c 186	5	35.7	25	4	US-09-396-196G-106685	Sequence 106685, A
c 114	6	42.9	49526	4	US-09-949-016-12959	Sequence 12959, A	c 187	5	35.7	25	4	US-09-396-196G-114606	Sequence 114606, A
c 115	6	42.9	85269	4	US-09-949-016-17958	Sequence 17958, A	c 188	5	35.7	25	4	US-09-396-196G-124308	Sequence 124308, A
c 116	6	42.9	60417	4	US-09-949-016-13312	Sequence 13312, A	c 189	5	35.7	25	4	US-09-396-196G-124309	Sequence 124309, A
c 117	6	42.9	61399	4	US-09-949-016-14386	Sequence 14386, A	c 190	5	35.7	27	3	US-09-245-248B-25	Sequence 25, Appl
c 118	6	42.9	65042	3	US-09-784-316-3	Sequence 3, Appli	c 191	5	35.7	28	1	US-08-173-510B-12	Sequence 12, Appl
c 119	6	42.9	65042	4	US-10-229-124-3	Sequence 3, Appli	c 192	5	35.7	28	1	US-08-458-218-12	Sequence 12, Appl
c 120	6	42.9	66213	4	US-09-949-016-11803	Sequence 11803, A	c 193	5	35.7	28	2	US-08-450-437-12	Sequence 12, Appl
c 121	6	42.9	66213	4	US-09-949-016-16739	Sequence 16739, A	c 194	5	35.7	28	2	US-08-060-433C-9	Sequence 9, Appli
c 122	6	42.9	67899	4	US-09-949-016-15432	Sequence 15432, A	c 195	5	35.7	28	4	US-08-450-482B-12	Sequence 12, Appl
c 123	6	42.9	67902	4	US-09-949-016-11870	Sequence 11870, A	c 196	5	35.7	28	4	US-08-232-144-2	Sequence 2, Appli
c 124	6	42.9	79578	4	US-09-949-016-16339	Sequence 16339, A	c 197	5	35.7	30	1	US-09-442-349A-101	Sequence 101, App
c 125	6	42.9	85665	4	US-09-949-016-17345	Sequence 17345, A	c 198	5	35.7	30	3	US-09-442-349A-102	Sequence 102, App
c 126	6	42.9	85956	4	US-09-949-016-12994	Sequence 12994, A	c 199	5	35.7	31	3	US-09-044-718-20	Sequence 20, Appl
c 127	6	42.9	85956	4	US-09-949-016-13335	Sequence 13335, A	c 200	5	35.7	31	4	US-10-062-848-20	Sequence 20, Appl
c 128	6	42.9	89220	4	US-09-949-016-12655	Sequence 12655, A	c 201	5	35.7	31	4	US-08-627-706-6	Sequence 6, Appli
c 129	6	42.9	89224	4	US-09-949-016-15572	Sequence 15572, A	c 202	5	35.7	34	1	US-09-103-489-6	Sequence 6, Appli
c 130	6	42.9	90472	4	US-09-949-016-14038	Sequence 14038, A	c 203	5	35.7	34	3	US-09-829-381D-6	Sequence 6, Appli
c 131	6	42.9	96690	4	US-09-949-016-17103	Sequence 17103, A	c 204	5	35.7	34	3	US-08-447-169A-56	Sequence 56, Appl
c 132	6	42.9	101951	4	US-09-949-016-15648	Sequence 15648, A	c 205	5	35.7	35	1	US-08-233-012C-56	Sequence 56, Appl
c 133	6	42.9	107140	4	US-09-949-016-14834	Sequence 14834, A	c 206	5	35.7	35	2	US-09-860-474-56	Sequence 56, Appl
c 134	6	42.9	109159	4	US-09-949-016-14169	Sequence 14169, A	c 207	5	35.7	35	4	US-08-327-874A-33	Sequence 33, Appl
c 135	6	42.9	109159	4	US-09-949-016-14170	Sequence 14170, A	c 208	5	35.7	40	3	US-10-008-960-33	Sequence 33, Appl
c 136	6	42.9	124884	4	US-09-661-596A-76	Sequence 76, Appl	c 209	5	35.7	40	5	PCT-US94-09700-33	Sequence 33, Appl
c 137	6	42.9	124884	4	US-09-913-514-1	Sequence 1, Appli	c 210	5	35.7	41	1	US-08-330-638D-10	Sequence 10, Appl
c 138	6	42.9	125157	4	US-09-913-514-2	Sequence 2, Appli	c 211	5	35.7	41	2	US-08-306-746A-10	Sequence 10, Appl
c 139	6	42.9	125778	4	US-09-949-016-12191	Sequence 12191, A	c 212	5	35.7	41	2	US-09-422-978A-35	Sequence 35, Appl
c 140	6	42.9	132778	4	US-09-949-016-17075	Sequence 17075, A	c 213	5	35.7	47	4	US-08-327-874A-35	Sequence 35, Appl
c 141	6	42.9	132778	4	US-09-949-016-12524	Sequence 12524, A	c 214	5	35.7	54	3	US-10-008-960-35	Sequence 35, Appl
c 142	6	42.9	133358	4	US-09-949-016-16964	Sequence 16964, A	c 215	5	35.7	54	4	PCT-US94-09700-35	Sequence 35, Appl
c 143	6	42.9	133360	4	US-09-949-016-12651	Sequence 12651, A	c 216	5	35.7	54	5	US-08-956-171B-4956	Sequence 4956, Ap
c 144	6	42.9	152524	4	US-09-949-016-12683	Sequence 12683, A	c 217	5	35.7	59	4	US-08-781-986A-4956	Sequence 4956, Ap
c 145	6	42.9	152524	4	US-09-949-016-13194	Sequence 13194, A	c 218	5	35.7	59	4	US-07-967-693-8	Sequence 8, Appli
c 146	6	42.9	154605	4	US-09-949-016-11894	Sequence 11894, A	c 219	5	35.7	63	1	US-08-195-072-6	Sequence 6, Appli
c 147	6	42.9	221545	4	US-09-949-016-13875	Sequence 13875, A	c 220	5	35.7	63	1	US-08-195-735-6	Sequence 6, Appli
c 148	6	42.9	22452	4	US-09-949-016-12968	Sequence 12968, A	c 221	5	35.7	63	1	US-08-195-747-6	Sequence 6, Appli
c 149	6	42.9	254286	4	US-09-949-016-15497	Sequence 15497, A	c 222	5	35.7	63	1	US-08-446-884-6	Sequence 6, Appli
c 150	6	42.9	254366	4	US-09-822-871-3	Sequence 3, Appli	c 223	5	35.7	63	1	US-08-195-073-6	Sequence 6, Appli
c 151	6	42.9	264358	4	US-09-949-016-15725	Sequence 15725, A	c 224	5	35.7	63	1	US-08-198-175-6	Sequence 6, Appli
c 152	6	42.9	276237	4	US-09-949-016-17504	Sequence 17504, A	c 225	5	35.7	63	2	US-08-443-153-6	Sequence 6, Appli
c 153	6	42.9	312957	4	US-09-949-001-31	Sequence 31, Appl	c 226	5	35.7	63	2	US-08-442-807-6	Sequence 6, Appli
c 154	6	42.9	312972	4	US-09-949-001-34	Sequence 34, Appl	c 227	5	35.7	63	3	US-09-191-852-17	Sequence 17, Appl
c 155	6	42.9	346112	4	US-09-949-016-13165	Sequence 13165, A	c 228	5	35.7	65	3	US-08-817-906-17	Sequence 17, Appl
c 156	6	42.9	390890	4	US-09-949-016-14720	Sequence 14720, A	c 229	5	35.7	65	3	PCT-US95-13376-17	Sequence 17, Appl
c 157	6	42.9	421118	4	US-09-949-016-16297	Sequence 16297, A	c 230	5	35.7	65	5	US-08-447-169A-38	Sequence 38, Appl
c 158	6	42.9	1664976	4	US-08-916-421B-1	Sequence 1, Appli	c 231	5	35.7	77	1		

232	5	35.7	77	2	US-08-233-012C-38	Sequence 38, Appl	305	5	35.7	276	4	US-09-489-039A-7135	Sequence 7135, Ap
233	5	35.7	77	4	US-08-860-474-38	Sequence 38, Appl	306	5	35.7	278	4	US-09-270-767-28010	Sequence 28010, A
234	5	35.7	80	3	US-08-812-121-2	Sequence 2, Appl	c 307	5	35.7	279	3	US-09-615-192A-262	Sequence 262, App
235	5	35.7	80	3	US-09-403-672-2	Sequence 2, Appl	308	5	35.7	280	4	US-09-513-999C-10084	Sequence 10084, A
236	5	35.7	85	3	US-08-812-121-1	Sequence 1, Appl	309	5	35.7	285	4	US-09-976-594-932	Sequence 932, App
237	5	35.7	85	3	US-09-403-672-1	Sequence 1, Appl	c 310	5	35.7	287	4	US-09-270-767-25944	Sequence 25944, A
238	5	35.7	100	4	US-08-956-171E-4860	Sequence 4860, Ap	c 311	5	35.7	287	4	US-09-513-999C-3402	Sequence 3402, Ap
239	5	35.7	100	4	US-08-781-986A-4860	Sequence 4860, Ap	c 312	5	35.7	288	4	US-08-956-171E-4433	Sequence 4433, Ap
240	5	35.7	101	4	US-09-513-999C-18462	Sequence 18462, A	c 313	5	35.7	288	4	US-08-781-986A-4433	Sequence 4433, Ap
241	5	35.7	102	4	US-08-956-171E-4831	Sequence 4831, Ap	c 314	5	35.7	290	4	US-09-513-999C-30616	Sequence 30616, A
242	5	35.7	102	4	US-08-781-986A-4831	Sequence 4831, Ap	c 315	5	35.7	293	4	US-09-313-294A-6856	Sequence 6856, Ap
243	5	35.7	114	4	US-08-850-348A-3	Sequence 3, Appl	c 316	5	35.7	294	4	US-09-313-294A-4294	Sequence 4294, Ap
244	5	35.7	153	4	US-09-930-803-24	Sequence 24, Appl	c 317	5	35.7	294	4	US-09-107-532A-3249	Sequence 3249, Ap
245	5	35.7	153	4	US-09-513-999C-17528	Sequence 17528, A	c 318	5	35.7	294	4	US-09-489-039A-3664	Sequence 3664, Ap
246	5	35.7	157	4	US-08-956-171E-3163	Sequence 3163, Ap	c 319	5	35.7	295	4	US-09-313-294A-7316	Sequence 7316, Ap
247	5	35.7	157	4	US-08-781-986A-3163	Sequence 3163, Ap	c 320	5	35.7	296	4	US-09-313-294A-2877	Sequence 2877, Ap
248	5	35.7	159	4	US-09-513-999C-27073	Sequence 27073, A	c 321	5	35.7	296	4	US-09-313-294A-4432	Sequence 4432, Ap
249	5	35.7	165	4	US-09-513-999C-22235	Sequence 22235, A	c 322	5	35.7	297	4	US-09-543-681A-3109	Sequence 3109, Ap
250	5	35.7	171	4	US-09-621-976-10885	Sequence 10885, A	c 323	5	35.7	300	2	US-08-351-316A-9	Sequence 9, Appl
251	5	35.7	175	4	US-09-513-999C-13879	Sequence 13879, A	c 324	5	35.7	300	4	US-09-471-276-699	Sequence 699, App
252	5	35.7	183	4	US-09-248-796A-12054	Sequence 12054, A	c 325	5	35.7	301	3	US-09-439-313-292	Sequence 292, App
253	5	35.7	186	4	US-09-540-236-1147	Sequence 1147, Ap	c 326	5	35.7	301	3	US-09-352-616A-292	Sequence 292, App
254	5	35.7	189	4	US-09-248-796A-7486	Sequence 7486, Ap	c 327	5	35.7	301	3	US-09-232-149A-292	Sequence 292, App
255	5	35.7	192	4	US-09-107-532A-1014	Sequence 1014, Ap	c 328	5	35.7	301	4	US-09-159-812-292	Sequence 292, App
256	5	35.7	192	4	US-09-489-039A-7126	Sequence 7126, Ap	c 329	5	35.7	301	4	US-09-636-215-292	Sequence 292, App
257	5	35.7	195	4	US-09-107-433-2343	Sequence 2343, Ap	c 330	5	35.7	301	4	US-09-685-166A-292	Sequence 292, App
258	5	35.7	198	4	US-09-107-433-2344	Sequence 2344, Ap	c 331	5	35.7	301	4	US-09-688-489-292	Sequence 292, App
259	5	35.7	207	4	US-09-248-796A-11439	Sequence 11439, A	c 332	5	35.7	301	4	US-09-679-426-292	Sequence 292, App
260	5	35.7	209	4	US-09-513-999C-27245	Sequence 27245, A	c 333	5	35.7	301	4	US-09-759-143-292	Sequence 292, App
261	5	35.7	210	4	US-09-248-796A-12381	Sequence 12381, A	c 334	5	35.7	301	4	US-09-651-236-292	Sequence 292, App
262	5	35.7	210	4	US-09-513-999C-9765	Sequence 9765, Ap	c 335	5	35.7	302	4	US-09-513-999C-2676	Sequence 2676, Ap
263	5	35.7	210	4	US-09-471-276-328	Sequence 328, App	c 336	5	35.7	305	4	US-09-513-999C-14109	Sequence 14109, A
264	5	35.7	212	4	US-09-513-999C-2823	Sequence 2823, Ap	c 337	5	35.7	306	3	US-09-134-001C-1107	Sequence 1107, Ap
265	5	35.7	213	4	US-09-313-294A-6651	Sequence 6651, Ap	c 338	5	35.7	307	4	US-09-621-976-8362	Sequence 8362, Ap
266	5	35.7	213	4	US-09-107-532A-938	Sequence 938, App	c 339	5	35.7	307	4	US-09-513-999C-10738	Sequence 10738, A
267	5	35.7	213	4	US-09-107-532A-938	Sequence 938, App	c 340	5	35.7	309	4	US-09-513-999C-13129	Sequence 13129, A
268	5	35.7	214	4	US-09-513-999C-23018	Sequence 23018, A	c 341	5	35.7	312	3	US-09-191-852-20	Sequence 20, Appl
269	5	35.7	214	4	US-09-252-991A-13341	Sequence 13341, A	c 342	5	35.7	312	3	US-08-817-906-20	Sequence 20, Appl
270	5	35.7	222	4	US-09-270-767-30143	Sequence 30143, A	c 343	5	35.7	312	4	US-09-513-999C-10993	Sequence 10993, A
271	5	35.7	228	4	US-08-956-171E-2523	Sequence 2523, Ap	c 344	5	35.7	312	5	PCT-US95-13376-20	Sequence 20, Appl
272	5	35.7	228	4	US-08-781-986A-2523	Sequence 2523, Ap	c 345	5	35.7	314	4	US-09-513-999C-1998	Sequence 1998, Ap
273	5	35.7	230	4	US-09-270-767-10705	Sequence 31075, A	c 346	5	35.7	316	4	US-08-956-171E-4288	Sequence 4288, Ap
274	5	35.7	231	1	US-08-065-845-8	Sequence 8, Appl	c 347	5	35.7	316	4	US-08-781-986A-4288	Sequence 4288, Ap
275	5	35.7	231	1	US-08-429-523-8	Sequence 8, Appl	c 348	5	35.7	321	3	US-09-222-575-54	Sequence 54, Appl
276	5	35.7	231	1	US-08-429-532-8	Sequence 8, Appl	c 349	5	35.7	321	4	US-09-389-681-54	Sequence 54, Appl
277	5	35.7	231	1	US-08-429-522-8	Sequence 8, Appl	c 350	5	35.7	321	4	US-09-620-4058-54	Sequence 54, Appl
278	5	35.7	231	1	US-08-429-520-8	Sequence 8, Appl	c 351	5	35.7	321	4	US-09-339-338-54	Sequence 54, Appl
279	5	35.7	231	3	US-09-065-474-126	Sequence 126, App	c 352	5	35.7	321	4	US-09-433-826B-54	Sequence 54, Appl
280	5	35.7	231	3	US-09-065-474-127	Sequence 127, App	c 353	5	35.7	321	4	US-09-604-287A-54	Sequence 54, Appl
281	5	35.7	231	3	US-09-269-136B-8	Sequence 8, Appl	c 354	5	35.7	321	4	US-09-285-480-54	Sequence 54, Appl
282	5	35.7	231	3	US-09-557-034-126	Sequence 126, App	c 355	5	35.7	321	4	US-09-834-759-54	Sequence 54, Appl
283	5	35.7	231	3	US-09-557-034-127	Sequence 127, App	c 356	5	35.7	321	4	US-09-590-751A-54	Sequence 54, Appl
284	5	35.7	233	4	US-09-513-999C-25651	Sequence 25651, A	c 357	5	35.7	321	4	US-09-551-621-54	Sequence 54, Appl
285	5	35.7	234	4	US-09-489-039A-3465	Sequence 3465, Ap	c 358	5	35.7	324	4	US-08-956-171E-4259	Sequence 4259, Ap
286	5	35.7	234	4	US-09-107-532A-364	Sequence 364, App	c 359	5	35.7	324	4	US-08-956-171E-4337	Sequence 4337, Ap
287	5	35.7	239	4	US-09-016-434-106	Sequence 106, App	c 360	5	35.7	324	4	US-08-781-986A-4259	Sequence 4259, Ap
288	5	35.7	239	4	US-09-513-999C-3102	Sequence 3102, Ap	c 361	5	35.7	324	4	US-08-781-986A-4337	Sequence 4337, Ap
289	5	35.7	243	4	US-08-956-171E-4515	Sequence 4515, Ap	c 362	5	35.7	325	4	US-09-513-999C-31954	Sequence 31954, A
290	5	35.7	243	4	US-08-781-986A-4515	Sequence 4515, Ap	c 363	5	35.7	328	4	US-09-270-767-8036	Sequence 8036, Ap
291	5	35.7	243	4	US-09-513-999C-24203	Sequence 24203, A	c 364	5	35.7	328	4	US-09-270-767-23318	Sequence 23318, A
292	5	35.7	243	4	US-09-513-999C-26106	Sequence 26106, A	c 365	5	35.7	329	4	US-09-513-999C-34427	Sequence 34427, A
293	5	35.7	244	4	US-09-910-099A-282	Sequence 282, App	c 366	5	35.7	330	4	US-09-902-540-8238	Sequence 8238, Ap
294	5	35.7	258	4	US-09-248-796A-13421	Sequence 13421, A	c 367	5	35.7	332	1	US-09-985-799-65	Sequence 65, Appl
295	5	35.7	260	4	US-09-513-999C-32662	Sequence 32662, A	c 368	5	35.7	332	1	US-09-977-371-65	Sequence 65, Appl
296	5	35.7	261	4	US-08-956-171E-4484	Sequence 4484, Ap	c 369	5	35.7	332	1	US-08-594-031-65	Sequence 65, Appl
297	5	35.7	261	4	US-08-781-986A-3859	Sequence 3859, Ap	c 370	5	35.7	339	4	US-09-543-681A-3103	Sequence 3103, Ap
298	5	35.7	261	4	US-09-489-039A-4484	Sequence 4484, Ap	c 371	5	35.7	340	4	US-08-956-171E-4403	Sequence 4403, Ap
299	5	35.7	264	4	US-09-328-352-17	Sequence 17, Appl	c 372	5	35.7	342	3	US-09-306-042-4	Sequence 4, Appl
300	5	35.7	264	4	US-09-270-767-27570	Sequence 27570, A	c 373	5	35.7	342	3	US-09-489-039A-6535	Sequence 6535, Ap
301	5	35.7	269	4	US-09-016-434-141	Sequence 141, App	c 374	5	35.7	342	4	US-08-956-171E-4301	Sequence 4301, Ap
302	5	35.7	272	4	US-09-544-398B-57	Sequence 57, Appl	c 375	5	35.7	348	4	US-08-781-986A-4301	Sequence 4301, Ap
303	5	35.7	272	4	US-09-543-771B-57	Sequence 57, Appl	c 376	5	35.7	348	4	US-09-513-999C-13928	Sequence 13928, A
304	5	35.7	275	4	US-09-513-999C-12140	Sequence 12140, A	c 377	5	35.7	348	4		

C 378	5	35.7	351	4	US-08-956-171E-793	Sequence 793, App	C 451	417	4	US-09-513-999C-11315	Sequence 11315, A
C 379	5	35.7	351	4	US-08-956-171E-4341	Sequence 4341, App	C 452	419	4	US-09-513-999C-31472	Sequence 31472, A
C 380	5	35.7	351	4	US-08-781-986A-793	Sequence 793, App	C 453	420	4	US-09-270-767-28106	Sequence 28106, A
C 381	5	35.7	351	4	US-08-781-986A-4341	Sequence 4341, App	C 454	422	3	US-09-397-787-229	Sequence 229, App
C 382	5	35.7	355	4	US-07-988-945-2	Sequence 2, Appl1	C 455	422	4	US-09-270-767-9619	Sequence 9619, App
C 383	5	35.7	355	4	US-09-621-395A-41	Sequence 18286, A	C 456	422	4	US-09-270-767-24901	Sequence 24901, A
C 384	5	35.7	355	4	US-09-513-999C-1716	Sequence 1716, A	C 457	424	3	US-09-132-316-26	Sequence 26, Appl
C 385	5	35.7	355	4	US-09-513-999C-1716	Sequence 1716, A	C 458	426	4	US-09-270-767-6880	Sequence 6880, App
C 386	5	35.7	356	4	US-09-513-999C-8231	Sequence 8231, App	C 459	426	4	US-09-270-767-22162	Sequence 22162, A
C 387	5	35.7	358	4	US-09-401-064-234	Sequence 234, App	C 460	427	4	US-09-621-976-11351	Sequence 11351, A
C 388	5	35.7	358	4	US-09-401-064-246	Sequence 246, App	C 461	427	4	US-09-919-172-14	Sequence 14, Appl
C 389	5	35.7	360	4	US-09-621-976-8395	Sequence 8395, App	C 462	428	4	US-09-270-767-3723	Sequence 3723, App
C 390	5	35.7	360	4	US-09-107-433-2334	Sequence 2334, App	C 463	428	4	US-09-270-767-19005	Sequence 19005, A
C 391	5	35.7	363	4	US-09-543-681A-3090	Sequence 3090, App	C 464	432	3	US-09-252-991A-9405	Sequence 9405, App
C 392	5	35.7	365	3	US-09-439-313-389	Sequence 389, App	C 465	433	3	US-09-132-316-22	Sequence 22, Appl
C 393	5	35.7	365	3	US-09-352-616A-389	Sequence 389, App	C 466	435	4	US-09-621-976-16911	Sequence 16911, A
C 394	5	35.7	365	4	US-09-636-215-389	Sequence 389, App	C 467	438	4	US-09-134-000C-717	Sequence 717, App
C 395	5	35.7	365	4	US-09-685-166A-389	Sequence 389, App	C 468	438	4	US-09-270-767-3723	Sequence 3723, App
C 396	5	35.7	365	4	US-09-679-426-389	Sequence 389, App	C 469	438	4	US-09-270-767-19005	Sequence 19005, A
C 397	5	35.7	365	4	US-09-759-143-389	Sequence 389, App	C 470	440	4	US-09-252-991A-9405	Sequence 9405, App
C 398	5	35.7	365	4	US-09-651-236-389	Sequence 389, App	C 471	441	4	US-09-132-316-22	Sequence 22, Appl
C 399	5	35.7	369	1	US-09-083-945-3	Sequence 3, Appl1	C 472	442	4	US-09-621-976-13951	Sequence 13951, A
C 400	5	35.7	371	4	US-09-702-705-1141	Sequence 1141, App	C 473	443	4	US-09-134-000C-717	Sequence 717, App
C 401	5	35.7	371	4	US-09-736-457-1141	Sequence 1141, App	C 474	444	4	US-09-513-999C-12012	Sequence 12012, A
C 402	5	35.7	371	4	US-09-614-124B-1141	Sequence 1141, App	C 475	444	4	US-09-179-221D-12	Sequence 12, Appl
C 403	5	35.7	371	4	US-09-671-325-1141	Sequence 1141, App	C 476	444	4	US-09-621-976-12872	Sequence 12872, A
C 404	5	35.7	371	4	US-09-658-824-1141	Sequence 1141, App	C 477	447	4	US-09-252-991A-14798	Sequence 14798, A
C 405	5	35.7	374	4	US-09-270-767-14825	Sequence 14825, A	C 478	447	4	US-09-513-999C-9397	Sequence 9397, App
C 406	5	35.7	375	4	US-09-328-352-1161	Sequence 1161, App	C 479	450	4	US-09-621-976-13951	Sequence 13951, A
C 407	5	35.7	375	4	US-09-302-626B-13	Sequence 13, Appl	C 480	451	4	US-09-912-935-5	Sequence 4006, App
C 408	5	35.7	375	4	US-09-302-626B-15	Sequence 15, Appl	C 481	452	4	US-09-513-999C-32355	Sequence 32355, A
C 409	5	35.7	376	4	US-09-023-655-395	Sequence 395, App	C 482	452	4	US-09-302-540-1485	Sequence 1485, App
C 410	5	35.7	378	4	US-09-248-796A-1918	Sequence 1918, App	C 483	457	4	US-09-270-767-12871	Sequence 12871, A
C 411	5	35.7	378	4	US-09-248-796A-12752	Sequence 12752, A	C 484	460	4	US-09-270-767-7059	Sequence 7059, App
C 412	5	35.7	381	3	US-09-615-192A-174	Sequence 174, App	C 485	460	4	US-09-270-767-22341	Sequence 22341, A
C 413	5	35.7	381	4	US-09-169-789-174	Sequence 174, App	C 486	462	4	US-09-513-999C-13651	Sequence 13651, A
C 414	5	35.7	383	3	US-08-888-998-3	Sequence 3, Appl1	C 487	462	4	US-09-401-064-214	Sequence 214, App
C 415	5	35.7	383	3	US-09-362-633-3	Sequence 3, Appl1	C 488	467	4	US-09-621-976-17211	Sequence 17211, A
C 416	5	35.7	384	4	US-09-270-767-7395	Sequence 7395, App	C 489	468	3	US-09-270-767-11335	Sequence 11335, A
C 417	5	35.7	384	4	US-09-270-767-22677	Sequence 22677, A	C 490	468	3	US-09-132-316-9	Sequence 9, Appl1
C 418	5	35.7	385	4	US-09-270-767-6580	Sequence 6580, App	C 491	469	4	US-09-621-976-18497	Sequence 18497, A
C 419	5	35.7	385	4	US-09-270-767-21862	Sequence 21862, A	C 492	469	4	US-09-513-999C-10642	Sequence 10642, A
C 420	5	35.7	391	4	US-09-902-540-1553	Sequence 1553, App	C 493	471	4	US-09-252-991A-2464	Sequence 2464, App
C 421	5	35.7	392	4	US-09-270-767-6358	Sequence 6358, App	C 494	472	4	US-09-621-976-2240	Sequence 2240, App
C 422	5	35.7	392	4	US-09-270-767-21640	Sequence 21640, A	C 495	472	4	US-09-596-248D-3	Sequence 3, Appl1
C 423	5	35.7	393	4	US-09-621-976-16211	Sequence 16211, A	C 496	474	4	US-09-270-767-11907	Sequence 11907, A
C 424	5	35.7	398	4	US-09-513-999C-3548	Sequence 3548, App	C 497	476	4	US-09-596-248D-4	Sequence 4, Appl1
C 425	5	35.7	399	4	US-09-107-532A-936	Sequence 936, App	C 498	478	4	US-09-270-767-1345	Sequence 1345, App
C 426	5	35.7	399	4	US-09-489-039A-4573	Sequence 4573, App	C 499	478	4	US-09-513-999C-561	Sequence 561, App
C 427	5	35.7	399	4	US-09-513-999C-11884	Sequence 11884, A	C 500	479	3	US-09-621-976-17089	Sequence 17089, App
C 428	5	35.7	399	4	US-09-956-171E-3568	Sequence 3568, App	C 501	480	4	US-08-956-171E-3734	Sequence 3734, App
C 429	5	35.7	400	4	US-08-956-171E-3773	Sequence 3773, App	C 502	480	4	US-08-781-986A-3734	Sequence 3734, App
C 430	5	35.7	400	4	US-08-956-171E-3842	Sequence 3842, App	C 503	482	2	US-08-783-395-1	Sequence 1, Appl1
C 431	5	35.7	400	4	US-08-956-171E-3867	Sequence 3867, App	C 504	484	2	US-08-924-838-7	Sequence 7, Appl1
C 432	5	35.7	400	4	US-08-956-171E-3881	Sequence 3881, App	C 505	484	4	US-09-621-976-15154	Sequence 11034, A
C 433	5	35.7	400	4	US-08-956-171E-3881	Sequence 3881, App	C 506	484	4	Sequence 15154, A	
C 434	5	35.7	400	4	US-08-956-171E-4153	Sequence 4153, App	C 507	486	4	US-09-252-991A-5896	Sequence 5896, App
C 435	5	35.7	400	4	US-08-956-171E-4174	Sequence 4174, App	C 508	486	4	US-09-621-976-879	Sequence 879, App
C 436	5	35.7	400	4	US-08-956-171E-4346	Sequence 4346, App	C 509	487	4	US-09-621-976-17089	Sequence 17089, App
C 437	5	35.7	400	4	US-08-956-171E-4346	Sequence 4346, App	C 510	489	3	US-08-078-271B-5	Sequence 5, Appl1
C 438	5	35.7	400	4	US-08-781-986A-3568	Sequence 3568, App	C 511	489	3	US-08-078-271B-7	Sequence 7, Appl1
C 439	5	35.7	400	4	US-08-781-986A-3773	Sequence 3773, App	C 512	492	3	US-08-600-430-1	Sequence 1, Appl1
C 440	5	35.7	400	4	US-08-781-986A-3842	Sequence 3842, App	C 513	492	3	US-08-600-430-3	Sequence 3, Appl1
C 441	5	35.7	400	4	US-08-781-986A-3867	Sequence 3867, App	C 514	492	3	US-09-621-976-1760	Sequence 1760, App
C 442	5	35.7	400	4	US-08-781-986A-3881	Sequence 3881, App	C 515	492	4	US-09-621-976-17517	Sequence 1517, A
C 443	5	35.7	400	4	US-08-781-986A-4140	Sequence 4140, App	C 516	494	4	US-09-513-999C-1395	Sequence 1395, App
C 444	5	35.7	400	4	US-08-781-986A-4153	Sequence 4153, App	C 517	495	1	US-09-621-976-17517	Sequence 1, Appl1
C 445	5	35.7	400	4	US-08-781-986A-4174	Sequence 4174, App	C 518	495	1	US-08-406-248-1	Sequence 4, Appl1
C 446	5	35.7	400	4	US-08-781-986A-4346	Sequence 4346, App	C 519	495	4	US-09-075-505-4	Sequence 111, App
C 447	5	35.7	400	4	US-09-513-999C-10114	Sequence 10114, A	C 520	495	4	US-09-270-767-15393	Sequence 15393, A
C 448	5	35.7	407	4	US-09-513-999C-30663	Sequence 30663, A	C 521	495	4	US-09-221-268D-4	Sequence 4, Appl1
C 449	5	35.7	408	4	US-09-513-999C-9630	Sequence 9630, App	C 522	495	4	US-09-248-796A-5258	Sequence 5258, App
C 450	5	35.7	414	4	US-09-328-352-3589	Sequence 3589, App	C 523	497	4	US-09-621-976-17681	Sequence 17681, A
			414	4	US-09-134-000C-1924	Sequence 1924, App				US-09-640-211A-1863	Sequence 1863, App

524	5	35.7	501	4	US-09-621-976-18972	Sequence 18972, A	597	4	US-09-949-016-20913	Sequence 20913, A
525	5	35.7	502	4	US-09-544-398B-635	Sequence 635, App	598	4	US-09-949-016-20914	Sequence 20914, A
526	5	35.7	503	4	US-09-543-771B-635	Sequence 635, App	c 599	4	US-09-949-016-21716	Sequence 21716, A
527	5	35.7	504	4	US-09-270-767-2408	Sequence 2408, App	600	4	US-09-949-016-21767	Sequence 21767, A
528	5	35.7	505	4	US-09-270-767-17690	Sequence 17690, App	c 601	4	US-09-949-016-21896	Sequence 21896, A
c 529	5	35.7	506	4	US-09-270-767-4931	Sequence 4931, App	602	4	US-09-949-016-22573	Sequence 22573, A
c 530	5	35.7	507	4	US-09-270-767-20213	Sequence 20213, A	c 603	4	US-09-949-016-23252	Sequence 23252, A
531	5	35.7	508	4	US-09-621-976-16214	Sequence 16214, A	c 604	4	US-09-949-016-23599	Sequence 23599, A
c 532	5	35.7	509	4	US-09-513-999C-1552	Sequence 1552, App	c 605	4	US-09-949-016-23600	Sequence 23600, A
c 533	5	35.7	510	4	US-08-956-171E-3590	Sequence 3590, App	c 606	4	US-09-949-016-23626	Sequence 23626, A
c 534	5	35.7	511	4	US-08-781-986A-3590	Sequence 3590, App	c 607	4	US-09-949-016-23747	Sequence 23747, A
c 535	5	35.7	512	4	US-09-809-665A-53	Sequence 53, Appl	c 608	4	US-09-949-016-24577	Sequence 24577, A
c 536	5	35.7	513	4	US-09-621-976-17682	Sequence 17682, A	c 609	4	US-09-949-016-24729	Sequence 24729, A
537	5	35.7	514	4	US-09-248-736A-13488	Sequence 13488, A	c 610	4	US-09-949-016-24798	Sequence 24798, A
538	5	35.7	515	4	US-09-513-999C-11935	Sequence 11935, A	c 611	4	US-09-949-016-24799	Sequence 24799, A
c 539	5	35.7	516	4	US-09-621-976-18600	Sequence 18600, App	c 612	4	US-09-949-016-24888	Sequence 24888, A
c 540	5	35.7	517	4	US-09-621-976-1040	Sequence 1040, App	613	4	US-09-949-016-25436	Sequence 25436, A
541	5	35.7	518	4	US-09-270-767-1441	Sequence 1441, App	614	4	US-09-949-016-25437	Sequence 25437, A
542	5	35.7	519	4	US-09-270-767-16723	Sequence 16723, A	615	4	US-09-949-016-25438	Sequence 25438, A
c 543	5	35.7	520	4	US-09-023-655-236	Sequence 236, App	616	4	US-09-949-016-25765	Sequence 25765, A
544	5	35.7	521	4	US-09-451-651-20	Sequence 20, Appl	c 617	4	US-09-949-016-26121	Sequence 26121, A
545	5	35.7	522	4	US-09-270-767-7961	Sequence 7961, App	c 618	4	US-09-949-016-26325	Sequence 26325, A
546	5	35.7	523	4	US-09-270-767-23243	Sequence 23243, App	619	4	US-09-949-016-26351	Sequence 26351, A
547	5	35.7	524	4	US-09-902-540-2095	Sequence 2095, App	620	4	US-09-949-016-26899	Sequence 26899, A
c 548	5	35.7	525	4	US-09-270-767-10526	Sequence 10526, A	621	4	US-09-949-016-26900	Sequence 26900, A
549	5	35.7	526	4	US-09-465-558-23	Sequence 23, Appl	c 622	4	US-09-949-016-27257	Sequence 27257, A
c 550	5	35.7	527	4	US-10-101-464A-358	Sequence 358, App	c 623	4	US-09-949-016-27587	Sequence 27587, A
c 551	5	35.7	528	4	US-09-621-976-9313	Sequence 9313, App	624	4	US-09-949-016-27588	Sequence 27588, A
552	5	35.7	529	4	US-09-465-558-19	Sequence 19, Appl	c 625	4	US-09-949-016-27599	Sequence 27599, A
553	5	35.7	530	4	US-09-583-110-2023	Sequence 2023, App	c 626	4	US-09-949-016-28121	Sequence 28121, A
c 554	5	35.7	531	4	US-09-306-042-2	Sequence 2, Appl	c 627	4	US-09-949-016-28122	Sequence 28122, A
c 555	5	35.7	532	4	US-10-101-464A-308	Sequence 308, App	c 628	4	US-09-949-016-28123	Sequence 28123, A
556	5	35.7	533	4	US-09-513-999C-180	Sequence 180, App	629	4	US-09-949-016-28815	Sequence 28815, A
557	5	35.7	534	4	US-09-513-999C-3747	Sequence 3747, App	630	4	US-09-949-016-29352	Sequence 29352, A
558	5	35.7	535	4	US-09-543-681A-2277	Sequence 2277, App	631	4	US-09-949-016-29353	Sequence 29353, A
559	5	35.7	536	4	US-09-134-000C-2786	Sequence 2786, App	c 632	4	US-09-949-016-29399	Sequence 29399, A
560	5	35.7	537	4	US-09-107-433-2030	Sequence 2030, App	c 633	4	US-09-949-016-30102	Sequence 30102, A
561	5	35.7	538	4	US-09-998-416-10905	Sequence 10905, A	634	4	US-09-949-016-30189	Sequence 30189, A
c 562	5	35.7	539	4	US-09-252-991A-10905	Sequence 10905, A	635	4	US-09-949-016-30190	Sequence 30190, A
c 563	5	35.7	540	4	US-09-513-999C-8229	Sequence 8229, App	c 636	4	US-09-949-016-30394	Sequence 30394, A
c 564	5	35.7	541	4	US-09-171-209-30	Sequence 30, Appl	c 637	4	US-09-949-016-30395	Sequence 30395, A
c 565	5	35.7	542	4	US-08-646-273-13	Sequence 13, Appl	c 638	4	US-09-949-016-30396	Sequence 30396, A
c 566	5	35.7	543	4	US-09-543-681A-860	Sequence 860, App	c 639	4	US-09-949-016-31382	Sequence 31382, A
567	5	35.7	544	4	US-09-270-767-2617	Sequence 2617, App	640	4	US-09-949-016-31675	Sequence 31675, A
568	5	35.7	545	4	US-09-270-767-17899	Sequence 17899, A	c 641	4	US-09-949-016-31902	Sequence 31902, A
569	5	35.7	546	4	US-09-270-767-583	Sequence 583, App	c 642	4	US-09-949-016-31903	Sequence 31903, A
570	5	35.7	547	4	US-09-270-767-15865	Sequence 15865, A	c 643	4	US-09-949-016-32237	Sequence 32237, A
c 571	5	35.7	548	4	US-09-248-736A-490	Sequence 490, App	c 644	4	US-09-949-016-32276	Sequence 32276, A
572	5	35.7	549	4	US-09-561-077C-8	Sequence 8, Appl	c 645	4	US-09-949-016-32277	Sequence 32277, A
c 573	5	35.7	550	4	US-09-221-014-8	Sequence 8, Appl	c 646	4	US-09-949-016-33637	Sequence 33637, A
c 574	5	35.7	551	4	US-09-489-039A-5146	Sequence 5146, App	c 647	4	US-09-949-016-33826	Sequence 33826, A
575	5	35.7	552	4	US-09-023-655-922	Sequence 922, App	c 648	4	US-09-949-016-33827	Sequence 33827, A
576	5	35.7	553	4	US-09-461-912A-22	Sequence 22, Appl	c 649	4	US-09-949-016-33828	Sequence 33828, A
577	5	35.7	554	4	US-09-811-825A-27	Sequence 27, Appl	c 650	4	US-09-949-016-34026	Sequence 34026, A
c 578	5	35.7	555	4	US-09-949-016-17836	Sequence 17836, A	651	4	US-09-949-016-34061	Sequence 34061, A
c 579	5	35.7	556	4	US-09-949-016-17837	Sequence 17837, A	c 652	4	US-09-949-016-34201	Sequence 34201, A
c 580	5	35.7	557	4	US-09-949-016-17967	Sequence 17967, A	c 653	4	US-09-949-016-35070	Sequence 35070, A
581	5	35.7	558	4	US-09-949-016-17968	Sequence 17968, A	c 654	4	US-09-949-016-35071	Sequence 35071, A
c 582	5	35.7	559	4	US-09-949-016-18250	Sequence 18250, A	c 655	4	US-09-949-016-35072	Sequence 35072, A
c 583	5	35.7	560	4	US-09-949-016-18251	Sequence 18251, A	c 656	4	US-09-949-016-35073	Sequence 35073, A
c 584	5	35.7	561	4	US-09-949-016-18252	Sequence 18252, A	657	4	US-09-949-016-35074	Sequence 35074, A
c 585	5	35.7	562	4	US-09-949-016-18253	Sequence 18253, A	c 658	4	US-09-949-016-36186	Sequence 36186, A
586	5	35.7	563	4	US-09-949-016-18844	Sequence 18844, A	c 659	4	US-09-949-016-36187	Sequence 36187, A
587	5	35.7	564	4	US-09-949-016-19245	Sequence 19245, A	c 660	4	US-09-949-016-36365	Sequence 36365, A
588	5	35.7	565	4	US-09-949-016-19246	Sequence 19246, A	661	4	US-09-949-016-36367	Sequence 36367, A
589	5	35.7	566	4	US-09-949-016-19247	Sequence 19247, A	c 662	4	US-09-949-016-37613	Sequence 37613, A
c 590	5	35.7	567	4	US-09-949-016-19386	Sequence 19386, A	c 663	4	US-09-949-016-38037	Sequence 38037, A
c 591	5	35.7	568	4	US-09-949-016-19387	Sequence 19387, A	664	4	US-09-949-016-38463	Sequence 38463, A
c 592	5	35.7	569	4	US-09-949-016-19388	Sequence 19388, A	c 665	4	US-09-949-016-38753	Sequence 38753, A
c 593	5	35.7	570	4	US-09-949-016-19389	Sequence 19389, A	c 666	4	US-09-949-016-38754	Sequence 38754, A
594	5	35.7	571	4	US-09-949-016-19573	Sequence 19573, A	c 667	4	US-09-949-016-38755	Sequence 38755, A
c 595	5	35.7	572	4	US-09-949-016-19902	Sequence 19902, A	c 668	4	US-09-949-016-38756	Sequence 38756, A
c 596	5	35.7	573	4	US-09-949-016-20239	Sequence 20239, A	c 669	4	US-09-949-016-38757	Sequence 38757, A

C 670	5	35.7	601	4	US-09-949-016-39740	Sequence 39740, A	C 743	5	35.7	601	4	US-09-949-016-59796	Sequence 59796, A
C 671	5	35.7	601	4	US-09-949-016-39741	Sequence 39741, A	C 744	5	35.7	601	4	US-09-949-016-60124	Sequence 60124, A
C 672	5	35.7	601	4	US-09-949-016-39748	Sequence 39748, A	C 745	5	35.7	601	4	US-09-949-016-60197	Sequence 60197, A
C 673	5	35.7	601	4	US-09-949-016-39749	Sequence 39749, A	C 746	5	35.7	601	4	US-09-949-016-60872	Sequence 60872, A
C 674	5	35.7	601	4	US-09-949-016-39750	Sequence 39750, A	C 747	5	35.7	601	4	US-09-949-016-61190	Sequence 61190, A
C 675	5	35.7	601	4	US-09-949-016-40132	Sequence 40132, A	C 748	5	35.7	601	4	US-09-949-016-61616	Sequence 61616, A
C 676	5	35.7	601	4	US-09-949-016-40607	Sequence 40607, A	C 749	5	35.7	601	4	US-09-949-016-61617	Sequence 61617, A
C 677	5	35.7	601	4	US-09-949-016-40608	Sequence 40608, A	C 750	5	35.7	601	4	US-09-949-016-61618	Sequence 61618, A
C 678	5	35.7	601	4	US-09-949-016-41559	Sequence 41559, A	C 751	5	35.7	601	4	US-09-949-016-61738	Sequence 61738, A
C 679	5	35.7	601	4	US-09-949-016-41706	Sequence 41706, A	C 752	5	35.7	601	4	US-09-949-016-61739	Sequence 61739, A
C 680	5	35.7	601	4	US-09-949-016-41707	Sequence 41707, A	C 753	5	35.7	601	4	US-09-949-016-61740	Sequence 61740, A
C 681	5	35.7	601	4	US-09-949-016-42029	Sequence 42029, A	C 754	5	35.7	601	4	US-09-949-016-62048	Sequence 62048, A
C 682	5	35.7	601	4	US-09-949-016-43099	Sequence 43099, A	C 755	5	35.7	601	4	US-09-949-016-62049	Sequence 62049, A
C 683	5	35.7	601	4	US-09-949-016-44582	Sequence 44582, A	C 756	5	35.7	601	4	US-09-949-016-62477	Sequence 62477, A
C 684	5	35.7	601	4	US-09-949-016-44582	Sequence 44582, A	C 757	5	35.7	601	4	US-09-949-016-62681	Sequence 62681, A
C 685	5	35.7	601	4	US-09-949-016-45160	Sequence 45160, A	C 758	5	35.7	601	4	US-09-949-016-62716	Sequence 62716, A
C 686	5	35.7	601	4	US-09-949-016-45161	Sequence 45161, A	C 759	5	35.7	601	4	US-09-949-016-62716	Sequence 62716, A
C 687	5	35.7	601	4	US-09-949-016-45162	Sequence 45162, A	C 760	5	35.7	601	4	US-09-949-016-62756	Sequence 62756, A
C 688	5	35.7	601	4	US-09-949-016-45869	Sequence 45869, A	C 761	5	35.7	601	4	US-09-949-016-62757	Sequence 62757, A
C 689	5	35.7	601	4	US-09-949-016-45870	Sequence 45870, A	C 762	5	35.7	601	4	US-09-949-016-63529	Sequence 63529, A
C 690	5	35.7	601	4	US-09-949-016-46484	Sequence 46484, A	C 763	5	35.7	601	4	US-09-949-016-63529	Sequence 63529, A
C 691	5	35.7	601	4	US-09-949-016-46485	Sequence 46485, A	C 764	5	35.7	601	4	US-09-949-016-63591	Sequence 63591, A
C 692	5	35.7	601	4	US-09-949-016-47280	Sequence 47280, A	C 765	5	35.7	601	4	US-09-949-016-66306	Sequence 66306, A
C 693	5	35.7	601	4	US-09-949-016-47280	Sequence 47280, A	C 766	5	35.7	601	4	US-09-949-016-66708	Sequence 66708, A
C 694	5	35.7	601	4	US-09-949-016-47789	Sequence 47789, A	C 767	5	35.7	601	4	US-09-949-016-66708	Sequence 66708, A
C 695	5	35.7	601	4	US-09-949-016-48332	Sequence 48332, A	C 768	5	35.7	601	4	US-09-949-016-66776	Sequence 66776, A
C 696	5	35.7	601	4	US-09-949-016-49643	Sequence 49643, A	C 769	5	35.7	601	4	US-09-949-016-66776	Sequence 66776, A
C 697	5	35.7	601	4	US-09-949-016-49644	Sequence 49644, A	C 770	5	35.7	601	4	US-09-949-016-67079	Sequence 67079, A
C 698	5	35.7	601	4	US-09-949-016-49645	Sequence 49645, A	C 771	5	35.7	601	4	US-09-949-016-67080	Sequence 67080, A
C 699	5	35.7	601	4	US-09-949-016-49646	Sequence 49646, A	C 772	5	35.7	601	4	US-09-949-016-67080	Sequence 67080, A
C 700	5	35.7	601	4	US-09-949-016-49647	Sequence 49647, A	C 773	5	35.7	601	4	US-09-949-016-67421	Sequence 67421, A
C 701	5	35.7	601	4	US-09-949-016-50501	Sequence 50501, A	C 774	5	35.7	601	4	US-09-949-016-67421	Sequence 67421, A
C 702	5	35.7	601	4	US-09-949-016-50588	Sequence 50588, A	C 775	5	35.7	601	4	US-09-949-016-67489	Sequence 67489, A
C 703	5	35.7	601	4	US-09-949-016-51521	Sequence 51521, A	C 776	5	35.7	601	4	US-09-949-016-67489	Sequence 67489, A
C 704	5	35.7	601	4	US-09-949-016-51751	Sequence 51751, A	C 777	5	35.7	601	4	US-09-949-016-67489	Sequence 67489, A
C 705	5	35.7	601	4	US-09-949-016-53164	Sequence 53164, A	C 778	5	35.7	601	4	US-09-949-016-67492	Sequence 67492, A
C 706	5	35.7	601	4	US-09-949-016-53165	Sequence 53165, A	C 779	5	35.7	601	4	US-09-949-016-67559	Sequence 67559, A
C 707	5	35.7	601	4	US-09-949-016-53250	Sequence 53250, A	C 780	5	35.7	601	4	US-09-949-016-67559	Sequence 67559, A
C 708	5	35.7	601	4	US-09-949-016-53383	Sequence 53383, A	C 781	5	35.7	601	4	US-09-949-016-67561	Sequence 67561, A
C 709	5	35.7	601	4	US-09-949-016-53384	Sequence 53384, A	C 782	5	35.7	601	4	US-09-949-016-67562	Sequence 67562, A
C 710	5	35.7	601	4	US-09-949-016-54383	Sequence 54383, A	C 783	5	35.7	601	4	US-09-949-016-67562	Sequence 67562, A
C 711	5	35.7	601	4	US-09-949-016-54384	Sequence 54384, A	C 784	5	35.7	601	4	US-09-949-016-67726	Sequence 67726, A
C 712	5	35.7	601	4	US-09-949-016-54891	Sequence 54891, A	C 785	5	35.7	601	4	US-09-949-016-68864	Sequence 68864, A
C 713	5	35.7	601	4	US-09-949-016-54904	Sequence 54904, A	C 786	5	35.7	601	4	US-09-949-016-68865	Sequence 68865, A
C 714	5	35.7	601	4	US-09-949-016-54917	Sequence 54917, A	C 787	5	35.7	601	4	US-09-949-016-68866	Sequence 68866, A
C 715	5	35.7	601	4	US-09-949-016-54930	Sequence 54930, A	C 788	5	35.7	601	4	US-09-949-016-68867	Sequence 68867, A
C 716	5	35.7	601	4	US-09-949-016-54943	Sequence 54943, A	C 789	5	35.7	601	4	US-09-949-016-68953	Sequence 68953, A
C 717	5	35.7	601	4	US-09-949-016-54956	Sequence 54956, A	C 790	5	35.7	601	4	US-09-949-016-69720	Sequence 69720, A
C 718	5	35.7	601	4	US-09-949-016-54967	Sequence 54967, A	C 791	5	35.7	601	4	US-09-949-016-69803	Sequence 69803, A
C 719	5	35.7	601	4	US-09-949-016-54975	Sequence 54975, A	C 792	5	35.7	601	4	US-09-949-016-70168	Sequence 70168, A
C 720	5	35.7	601	4	US-09-949-016-55076	Sequence 55076, A	C 793	5	35.7	601	4	US-09-949-016-70169	Sequence 70169, A
C 721	5	35.7	601	4	US-09-949-016-55077	Sequence 55077, A	C 794	5	35.7	601	4	US-09-949-016-70170	Sequence 70170, A
C 722	5	35.7	601	4	US-09-949-016-55078	Sequence 55078, A	C 795	5	35.7	601	4	US-09-949-016-70853	Sequence 70853, A
C 723	5	35.7	601	4	US-09-949-016-55245	Sequence 55245, A	C 796	5	35.7	601	4	US-09-949-016-70854	Sequence 70854, A
C 724	5	35.7	601	4	US-09-949-016-55553	Sequence 55553, A	C 797	5	35.7	601	4	US-09-949-016-71141	Sequence 71141, A
C 725	5	35.7	601	4	US-09-949-016-55554	Sequence 55554, A	C 798	5	35.7	601	4	US-09-949-016-71142	Sequence 71142, A
C 726	5	35.7	601	4	US-09-949-016-55555	Sequence 55555, A	C 799	5	35.7	601	4	US-09-949-016-71143	Sequence 71143, A
C 727	5	35.7	601	4	US-09-949-016-56057	Sequence 56057, A	C 800	5	35.7	601	4	US-09-949-016-71268	Sequence 71268, A
C 728	5	35.7	601	4	US-09-949-016-56057	Sequence 56057, A	C 801	5	35.7	601	4	US-09-949-016-71269	Sequence 71269, A
C 729	5	35.7	601	4	US-09-949-016-56709	Sequence 56709, A	C 802	5	35.7	601	4	US-09-949-016-71398	Sequence 71398, A
C 730	5	35.7	601	4	US-09-949-016-57362	Sequence 57362, A	C 803	5	35.7	601	4	US-09-949-016-72357	Sequence 72357, A
C 731	5	35.7	601	4	US-09-949-016-57733	Sequence 57733, A	C 804	5	35.7	601	4	US-09-949-016-72357	Sequence 72357, A
C 732	5	35.7	601	4	US-09-949-016-58168	Sequence 58168, A	C 805	5	35.7	601	4	US-09-949-016-73884	Sequence 73884, A
C 733	5	35.7	601	4	US-09-949-016-58169	Sequence 58169, A	C 806	5	35.7	601	4	US-09-949-016-73885	Sequence 73885, A
C 734	5	35.7	601	4	US-09-949-016-58413	Sequence 58413, A	C 807	5	35.7	601	4	US-09-949-016-73886	Sequence 73886, A
C 735	5	35.7	601	4	US-09-949-016-58442	Sequence 58442, A	C 808	5	35.7	601	4	US-09-949-016-74515	Sequence 74515, A
C 736	5	35.7	601	4	US-09-949-016-58668	Sequence 58668, A	C 809	5	35.7	601	4	US-09-949-016-76128	Sequence 76128, A
C 737	5	35.7	601	4	US-09-949-016-59062	Sequence 59062, A	C 810	5	35.7	601	4	US-09-949-016-76232	Sequence 76232, A
C 738	5	35.7	601	4	US-09-949-016-59063	Sequence 59063, A	C 811	5	35.7	601	4	US-09-949-016-76326	Sequence 76326, A
C 739	5	35.7	601	4	US-09-949-016-59064	Sequence 59064, A	C 812	5	35.7	601	4	US-09-949-016-76899	Sequence 76899, A
C 740	5	35.7	601	4	US-09-949-016-59525	Sequence 59525, A	C 813	5	35.7	601	4	US-09-949-016-76899	Sequence 76899, A
C 741	5	35.7	601	4	US-09-949-016-59526	Sequence 59526, A	C 814	5	35.7	601	4	US-09-949-016-76918	Sequence 76918, A
C 742	5	35.7	601	4	US-09-949-016-59612	Sequence 59612, A	C 815	5	35.7	601	4	US-09-949-016-76919	Sequence 76919, A
C 743	5	35.7	601	4	US-09-949-016-59613	Sequence 59613, A	C 816	5	35.7	601	4	US-09-949-016-77628	Sequence 77628, A

C 816	5	35.7	601	4	US-09-949-016-77629	Sequence 77629, A	C 889	5	35.7	601	4	US-09-949-016-98019	Sequence 98019, A
C 817	5	35.7	601	4	US-09-949-016-77630	Sequence 77630, A	C 890	5	35.7	601	4	US-09-949-016-98025	Sequence 98025, A
C 818	5	35.7	601	4	US-09-949-016-77631	Sequence 77631, A	C 891	5	35.7	601	4	US-09-949-016-98051	Sequence 98051, A
C 819	5	35.7	601	4	US-09-949-016-78113	Sequence 78113, A	C 892	5	35.7	601	4	US-09-949-016-98817	Sequence 98817, A
C 820	5	35.7	601	4	US-09-949-016-78117	Sequence 78117, A	C 893	5	35.7	601	4	US-09-949-016-99083	Sequence 99083, A
C 821	5	35.7	601	4	US-09-949-016-78496	Sequence 78496, A	C 894	5	35.7	601	4	US-09-949-016-99349	Sequence 99349, A
C 822	5	35.7	601	4	US-09-949-016-78497	Sequence 78497, A	C 895	5	35.7	601	4	US-09-949-016-99615	Sequence 99615, A
C 823	5	35.7	601	4	US-09-949-016-78819	Sequence 78819, A	C 896	5	35.7	601	4	US-09-949-016-99881	Sequence 99881, A
C 824	5	35.7	601	4	US-09-949-016-78820	Sequence 78820, A	C 897	5	35.7	601	4	US-09-949-016-100147	Sequence 100147, A
C 825	5	35.7	601	4	US-09-949-016-78821	Sequence 78821, A	C 898	5	35.7	601	4	US-09-949-016-100413	Sequence 100413, A
C 826	5	35.7	601	4	US-09-949-016-78822	Sequence 78822, A	C 899	5	35.7	601	4	US-09-949-016-100679	Sequence 100679, A
C 827	5	35.7	601	4	US-09-949-016-79020	Sequence 79020, A	C 900	5	35.7	601	4	US-09-949-016-100983	Sequence 100983, A
C 828	5	35.7	601	4	US-09-949-016-79021	Sequence 79021, A	C 901	5	35.7	601	4	US-09-949-016-101249	Sequence 101249, A
C 829	5	35.7	601	4	US-09-949-016-79626	Sequence 79626, A	C 902	5	35.7	601	4	US-09-949-016-101515	Sequence 101515, A
C 830	5	35.7	601	4	US-09-949-016-79627	Sequence 79627, A	C 903	5	35.7	601	4	US-09-949-016-101781	Sequence 101781, A
C 831	5	35.7	601	4	US-09-949-016-79628	Sequence 79628, A	C 904	5	35.7	601	4	US-09-949-016-102053	Sequence 102053, A
C 832	5	35.7	601	4	US-09-949-016-79948	Sequence 79948, A	C 905	5	35.7	601	4	US-09-949-016-102795	Sequence 102795, A
C 833	5	35.7	601	4	US-09-949-016-79949	Sequence 79949, A	C 906	5	35.7	601	4	US-09-949-016-103229	Sequence 103229, A
C 834	5	35.7	601	4	US-09-949-016-80182	Sequence 80182, A	C 907	5	35.7	601	4	US-09-949-016-103242	Sequence 103242, A
C 835	5	35.7	601	4	US-09-949-016-80183	Sequence 80183, A	C 908	5	35.7	601	4	US-09-949-016-103255	Sequence 103255, A
C 836	5	35.7	601	4	US-09-949-016-80462	Sequence 80462, A	C 909	5	35.7	601	4	US-09-949-016-103268	Sequence 103268, A
C 837	5	35.7	601	4	US-09-949-016-80793	Sequence 80793, A	C 910	5	35.7	601	4	US-09-949-016-103281	Sequence 103281, A
C 838	5	35.7	601	4	US-09-949-016-80940	Sequence 80940, A	C 911	5	35.7	601	4	US-09-949-016-103294	Sequence 103294, A
C 839	5	35.7	601	4	US-09-949-016-81042	Sequence 81042, A	C 912	5	35.7	601	4	US-09-949-016-103422	Sequence 103422, A
C 840	5	35.7	601	4	US-09-949-016-81053	Sequence 81053, A	C 913	5	35.7	601	4	US-09-949-016-103423	Sequence 103423, A
C 841	5	35.7	601	4	US-09-949-016-81054	Sequence 81054, A	C 914	5	35.7	601	4	US-09-949-016-103424	Sequence 103424, A
C 842	5	35.7	601	4	US-09-949-016-81259	Sequence 81259, A	C 915	5	35.7	601	4	US-09-949-016-103776	Sequence 103776, A
C 843	5	35.7	601	4	US-09-949-016-83012	Sequence 83012, A	C 916	5	35.7	601	4	US-09-949-016-104081	Sequence 104081, A
C 844	5	35.7	601	4	US-09-949-016-83528	Sequence 83528, A	C 917	5	35.7	601	4	US-09-949-016-104803	Sequence 104803, A
C 845	5	35.7	601	4	US-09-949-016-83529	Sequence 83529, A	C 918	5	35.7	601	4	US-09-949-016-104804	Sequence 104804, A
C 846	5	35.7	601	4	US-09-949-016-84096	Sequence 84096, A	C 919	5	35.7	601	4	US-09-949-016-104805	Sequence 104805, A
C 847	5	35.7	601	4	US-09-949-016-84147	Sequence 84147, A	C 920	5	35.7	601	4	US-09-949-016-107402	Sequence 107402, A
C 848	5	35.7	601	4	US-09-949-016-86273	Sequence 86273, A	C 921	5	35.7	601	4	US-09-949-016-107411	Sequence 107411, A
C 849	5	35.7	601	4	US-09-949-016-86645	Sequence 86645, A	C 922	5	35.7	601	4	US-09-949-016-107412	Sequence 107412, A
C 850	5	35.7	601	4	US-09-949-016-86647	Sequence 86647, A	C 923	5	35.7	601	4	US-09-949-016-107413	Sequence 107413, A
C 851	5	35.7	601	4	US-09-949-016-87176	Sequence 87176, A	C 924	5	35.7	601	4	US-09-949-016-107463	Sequence 107463, A
C 852	5	35.7	601	4	US-09-949-016-87177	Sequence 87177, A	C 925	5	35.7	601	4	US-09-949-016-107532	Sequence 107532, A
C 853	5	35.7	601	4	US-09-949-016-87178	Sequence 87178, A	C 926	5	35.7	601	4	US-09-949-016-109960	Sequence 109960, A
C 854	5	35.7	601	4	US-09-949-016-87301	Sequence 87301, A	C 927	5	35.7	601	4	US-09-949-016-110041	Sequence 110041, A
C 855	5	35.7	601	4	US-09-949-016-87302	Sequence 87302, A	C 928	5	35.7	601	4	US-09-949-016-110146	Sequence 110146, A
C 856	5	35.7	601	4	US-09-949-016-87903	Sequence 87903, A	C 929	5	35.7	601	4	US-09-949-016-110273	Sequence 110273, A
C 857	5	35.7	601	4	US-09-949-016-88289	Sequence 88289, A	C 930	5	35.7	601	4	US-09-949-016-110288	Sequence 110288, A
C 858	5	35.7	601	4	US-09-949-016-88681	Sequence 88681, A	C 931	5	35.7	601	4	US-09-949-016-110303	Sequence 110303, A
C 859	5	35.7	601	4	US-09-949-016-88727	Sequence 88727, A	C 932	5	35.7	601	4	US-09-949-016-110318	Sequence 110318, A
C 860	5	35.7	601	4	US-09-949-016-88728	Sequence 88728, A	C 933	5	35.7	601	4	US-09-949-016-110333	Sequence 110333, A
C 861	5	35.7	601	4	US-09-949-016-89043	Sequence 89043, A	C 934	5	35.7	601	4	US-09-949-016-110348	Sequence 110348, A
C 862	5	35.7	601	4	US-09-949-016-89244	Sequence 89244, A	C 935	5	35.7	601	4	US-09-949-016-110363	Sequence 110363, A
C 863	5	35.7	601	4	US-09-949-016-90135	Sequence 90135, A	C 936	5	35.7	601	4	US-09-949-016-110378	Sequence 110378, A
C 864	5	35.7	601	4	US-09-949-016-91300	Sequence 91300, A	C 937	5	35.7	601	4	US-09-949-016-110393	Sequence 110393, A
C 865	5	35.7	601	4	US-09-949-016-91404	Sequence 91404, A	C 938	5	35.7	601	4	US-09-949-016-110408	Sequence 110408, A
C 866	5	35.7	601	4	US-09-949-016-93106	Sequence 93106, A	C 939	5	35.7	601	4	US-09-949-016-110423	Sequence 110423, A
C 867	5	35.7	601	4	US-09-949-016-93209	Sequence 93209, A	C 940	5	35.7	601	4	US-09-949-016-110438	Sequence 110438, A
C 868	5	35.7	601	4	US-09-949-016-93210	Sequence 93210, A	C 941	5	35.7	601	4	US-09-949-016-110483	Sequence 110483, A
C 869	5	35.7	601	4	US-09-949-016-93522	Sequence 93522, A	C 942	5	35.7	601	4	US-09-949-016-110528	Sequence 110528, A
C 870	5	35.7	601	4	US-09-949-016-94578	Sequence 94578, A	C 943	5	35.7	601	4	US-09-949-016-110573	Sequence 110573, A
C 871	5	35.7	601	4	US-09-949-016-94579	Sequence 94579, A	C 944	5	35.7	601	4	US-09-949-016-110618	Sequence 110618, A
C 872	5	35.7	601	4	US-09-949-016-94580	Sequence 94580, A	C 945	5	35.7	601	4	US-09-949-016-110663	Sequence 110663, A
C 873	5	35.7	601	4	US-09-949-016-94581	Sequence 94581, A	C 946	5	35.7	601	4	US-09-949-016-110861	Sequence 110861, A
C 874	5	35.7	601	4	US-09-949-016-95315	Sequence 95315, A	C 947	5	35.7	601	4	US-09-949-016-110862	Sequence 110862, A
C 875	5	35.7	601	4	US-09-949-016-95316	Sequence 95316, A	C 948	5	35.7	601	4	US-09-949-016-110862	Sequence 110862, A
C 876	5	35.7	601	4	US-09-949-016-94578	Sequence 94578, A	C 949	5	35.7	601	4	US-09-949-016-110862	Sequence 110862, A
C 877	5	35.7	601	4	US-09-949-016-94579	Sequence 94579, A	C 950	5	35.7	601	4	US-09-949-016-111183	Sequence 111183, A
C 878	5	35.7	601	4	US-09-949-016-95494	Sequence 95494, A	C 951	5	35.7	601	4	US-09-949-016-111184	Sequence 111184, A
C 879	5	35.7	601	4	US-09-949-016-95671	Sequence 95671, A	C 952	5	35.7	601	4	US-09-949-016-111184	Sequence 111184, A
C 880	5	35.7	601	4	US-09-949-016-95672	Sequence 95672, A	C 953	5	35.7	601	4	US-09-949-016-111345	Sequence 111345, A
C 881	5	35.7	601	4	US-09-949-016-95849	Sequence 95849, A	C 954	5	35.7	601	4	US-09-949-016-111345	Sequence 111345, A
C 882	5	35.7	601	4	US-09-949-016-95850	Sequence 95850, A	C 955	5	35.7	601	4	US-09-949-016-112661	Sequence 112661, A
C 883	5	35.7	601	4	US-09-949-016-96268	Sequence 96268, A	C 956	5	35.7	601	4	US-09-949-016-113500	Sequence 113500, A
C 884	5	35.7	601	4	US-09-949-016-96423	Sequence 96423, A	C 957	5	35.7	601	4	US-09-949-016-113501	Sequence 113501, A
C 885	5	35.7	601	4	US-09-949-016-96689	Sequence 96689, A	C 958	5	35.7	601	4	US-09-949-016-115237	Sequence 115237, A
C 886	5	35.7	601	4	US-09-949-016-96955	Sequence 96955, A	C 959	5	35.7	601	4	US-09-949-016-115237	Sequence 115237, A
C 887	5	35.7	601	4	US-09-949-016-97221	Sequence 97221, A	C 960	5	35.7	601	4	US-09-949-016-115239	Sequence 115239, A
C 888	5	35.7	601	4	US-09-949-016-97487	Sequence 97487, A	C 961	5	35.7	601	4	US-09-949-016-115535	Sequence 115535, A
					Sequence 97753, A	Sequence 97753, A						US-09-949-016-115536	Sequence 115536, A

Sequence 115570, 601 4 US-09-949-016-115570
Sequence 115628, 5 35.7 601 4 US-09-949-016-115628
Sequence 115629, 5 35.7 601 4 US-09-949-016-115629
Sequence 115663, 5 35.7 601 4 US-09-949-016-115663
Sequence 115721, 5 35.7 601 4 US-09-949-016-115721
Sequence 115722, 5 35.7 601 4 US-09-949-016-115722
Sequence 115756, 5 35.7 601 4 US-09-949-016-115756
Sequence 115814, 5 35.7 601 4 US-09-949-016-115814
Sequence 115815, 5 35.7 601 4 US-09-949-016-115815
Sequence 115849, 5 35.7 601 4 US-09-949-016-115849
Sequence 115907, 5 35.7 601 4 US-09-949-016-115907
Sequence 115908, 5 35.7 601 4 US-09-949-016-115908
Sequence 115942, 5 35.7 601 4 US-09-949-016-115942
Sequence 116000, 5 35.7 601 4 US-09-949-016-116000
Sequence 116001, 5 35.7 601 4 US-09-949-016-116001
Sequence 116035, 5 35.7 601 4 US-09-949-016-116035
Sequence 116093, 5 35.7 601 4 US-09-949-016-116093
Sequence 116094, 5 35.7 601 4 US-09-949-016-116094
Sequence 116128, 5 35.7 601 4 US-09-949-016-116128
Sequence 116186, 5 35.7 601 4 US-09-949-016-116186
Sequence 116187, 5 35.7 601 4 US-09-949-016-116187
Sequence 116221, 5 35.7 601 4 US-09-949-016-116221
Sequence 116279, 5 35.7 601 4 US-09-949-016-116279
Sequence 116280, 5 35.7 601 4 US-09-949-016-116280
Sequence 116314, 5 35.7 601 4 US-09-949-016-116314
Sequence 116372, 5 35.7 601 4 US-09-949-016-116372
Sequence 116373, 5 35.7 601 4 US-09-949-016-116373
Sequence 116407, 5 35.7 601 4 US-09-949-016-116407
Sequence 116887, 5 35.7 601 4 US-09-949-016-116887
Sequence 117778, 5 35.7 601 4 US-09-949-016-117778
Sequence 118095, 5 35.7 601 4 US-09-949-016-118095
Sequence 119488, 5 35.7 601 4 US-09-949-016-119488
Sequence 120402, 5 35.7 601 4 US-09-949-016-120402
Sequence 120891, 5 35.7 601 4 US-09-949-016-120891
Sequence 122063, 5 35.7 601 4 US-09-949-016-122063
Sequence 122134, 5 35.7 601 4 US-09-949-016-122134
Sequence 122186, 5 35.7 601 4 US-09-949-016-122186
Sequence 122384, 5 35.7 601 4 US-09-949-016-122384
Sequence 122831, 5 35.7 601 4 US-09-949-016-122831

ALIGNMENTS

RESULT 1
US-09-054-492B-2
; Sequence 2, Application US/09054492B
; Patent No. 6218115
; GENERAL INFORMATION:
; APPLICANT: TAKESHI NAKAMURA
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/054,492B
; FILING DATE: APRIL 3, 1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PAUL E. WHITE, JR.
; REGISTRATION NUMBER: 32,011
; REFERENCE/DOCKET NUMBER: 7898/252159
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000

TELEFAX: (202) 822-0944
TELEX: 6714627CUSH
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1133
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-09-054-492B-2
Alignment Scores:
Pred. No.: 5.61e-07 Length: 1133
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0
US-09-736-250-5 (1-14) x US-09-054-492B-2 (1-1133)
Qy 1 GLUAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAATGGGGTTCTGTGTGGCACT 1068
RESULT 2
US-08-969-106-5
; Sequence 5, Application US/08969106
; Patent No. 5986055
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1131
; OTHER INFORMATION:
US-08-969-106-5
Alignment Scores:

Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0

US-09-736-250-5 (1-14) x US-08-969-106-5 (1-1260)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 3

US-09-338-125-5
; Sequence 5, Application US/09338125
; Patent No. 6521412
; GENERAL INFORMATION:
; APPLICANT: Yang, M.
; APPLICANT: Nandabalan, K.
; APPLICANT: Schulz, V.
; TITLE OF INVENTION: CDK2 INTERACTIONS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/338,125
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/969,106
; FILING DATE: 13-NOV-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7934-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1..1131
; OTHER INFORMATION:
US-09-338-125-5

Alignment Scores:
Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-338-125-5 (1-1260)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 4

US-09-023-655-899
; Sequence 899, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 895-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
US-09-023-655-899

Alignment Scores:
Pred. No.: 6.18e-07 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-023-655-899 (1-1260)

Qy 1 GluAspAenValSerGluAenValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 1068

RESULT 5

US-09-513-999C-29894
; Sequence 29894, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REFERENCE: 59.US2.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 29894
LENGTH: 304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 230
OTHER INFORMATION: m-a or c
FEATURE:
NAME/KEY: misc_feature
LOCATION: 231
OTHER INFORMATION: n-a, g, c or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: 268
OTHER INFORMATION: w-a or t
US-09-513-999C-29894

Alignment Scores:
Pred. No.: 2,196-06 Length: 304
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 92.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-513-999C-29894 (1-304)
QY 2 AsnValSerGluAsnValGlySerValCysGlyThr 14
DB 2 GATATGTCAGAAATGGGTTCTGTGTGGCACT 40

RESULT 6
US-09-949-016-187337/c
Sequence 187337, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187337
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187337

Alignment Scores:
Pred. No.: 19 Length: 601
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 0 Gaps: 0

Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-187337 (1-601)
QY 7 AsnValGlySerValCysGly 13
DB 600 AATGTGGGTTCAAGTTTGTGGC 580

RESULT 7
US-09-949-016-187338/c
Sequence 187338, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187338
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187338

Alignment Scores:
Pred. No.: 19 Length: 601
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-187338 (1-601)
QY 7 AsnValGlySerValCysGly 13
DB 339 AATGTGGGTTCAAGTTTGTGGC 319

RESULT 8
US-09-949-016-187339/c
Sequence 187339, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 187339
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-187339

; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12497
; LENGTH: 78269
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12497

Alignment Scores:
Pred. No.: 1.61e+03 Length: 78269
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 50.00% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-949-016-12497 (1-78269)

Qy 7 AsnValGlySerValCysGly 13
Db 16283 AATGTGGGTTCAGTTTGTGGC 16263

RESULT 13
US-09-422-978-6641/c
; Sequence 6641, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilva
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1998-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1998-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6641
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..19
; OTHER INFORMATION: upstream amplification primer 99-14949 for SEQ 2707,
US-09-422-978-6641

Alignment Scores:
Pred. No.: 10.6 Length: 19
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-422-978-6641 (1-19)

Qy 1 GluAspAsnValSerGlu 6
Db 19 GAGGATAATGTGAGTGAA 2

RESULT 14
US-09-489-039A-3894
; Sequence 3894, Application US/09489039A
; Patent No. 6610836

; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 3894
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-3894

Alignment Scores:
Pred. No.: 90.7 Length: 201
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.86% Indels: 0
DB: 4 Gaps: 0

US-09-736-250-5 (1-14) x US-09-489-039A-3894 (1-201)

Qy 8 ValGlySerValCysGly 13
Db 44 GTAGGCTCTGTTTGGGT 61

RESULT 15
US-09-513-999C-27371/c
; Sequence 27371, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 27371
; LENGTH: 256
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 18
; OTHER INFORMATION: k=g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 55
; OTHER INFORMATION: r=a or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 173
; OTHER INFORMATION: h=a or c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 227
; OTHER INFORMATION: y=c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 228
; OTHER INFORMATION: d=a or g or t
US-09-513-999C-27371

Alignment Scores: 113 Length: 256
 Pred. No.: 6.00 Matches: 6
 Score: 100.00% Conservative: 0
 Percent Similarity: 100.00% Mismatches: 0
 Best Local Similarity: 42.86% Indels: 0
 Query Match: 4 Gaps: 0
 DB: 4

US-09-736-250-5 (1-14) x US-09-513-999C-27371 (1-256)

Qy 5 SerGluAsnValGlySer 10
 |||||
 Db 156 TCTGAAACGTGGGCTCT 139

Search completed: February 11, 2005, 14:37:45
 Job time : 34.1356 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: February 11, 2005, 12:22:06 ; Search time 36.665 Seconds
(without alignments)
2253.008 Million cell updates/sec

Title: US-09-736-250-5

Perfect score: 14

Sequence: 1 EDNVSENVGSVCGT 14

Scoring table:

Gapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5378673 seqs, 2950229984 residues

Word size: 1

Total number of hits satisfying chosen parameters: 10734570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09736250/runat_07022005_154944_20748/app_query.fasta_1.718
-DB=Published Applications NA -OEMT=fastap -SUFFIX=oligo.rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=1000 -DOCLIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USAR=US09736250 @CGN_1_1.582 @runat_07022005_154944_20748
-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Published Applications NA:**
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq**
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq**
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq**
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq**
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq**
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq**
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq**
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq**
9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq**
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq**
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq**
12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq**
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq**
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq**
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq**
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq**
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq**
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq**
19: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq**
20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq**
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq**
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	14	100.0	288	17	US-10-242-535A-57578	Sequence 57578, A
2	14	100.0	288	17	US-10-085-783A-57578	Sequence 57578, A
3	14	100.0	350	17	US-10-242-535A-20816	Sequence 20816, A
4	14	100.0	350	17	US-10-085-783A-20816	Sequence 20816, A
5	14	100.0	444	9	US-09-920-300A-1413	Sequence 1413, Ap
6	14	100.0	444	13	US-10-033-528-1413	Sequence 1413, Ap
7	14	100.0	444	16	US-10-099-926-1413	Sequence 1413, Ap
8	14	100.0	447	9	US-09-777-564-1252	Sequence 1252, Ap
9	14	100.0	447	14	US-10-015-219-1252	Sequence 1252, Ap
10	14	100.0	1134	12	US-09-732-250-2	Sequence 2, Appl1
11	14	100.0	1260	17	US-10-172-118-1326	Sequence 1326, Ap
12	14	100.0	1260	17	US-10-342-887-1326	Sequence 1326, Ap
13	14	100.0	1260	17	US-10-641-643-899	Sequence 899, App
14	14	100.0	1889	9	US-09-867-701-10907	Sequence 10907, A
15	14	100.0	2146	10	US-09-814-353-21294	Sequence 21294, A
16	14	100.0	2755	10	US-09-814-353-21586	Sequence 21586, A
17	13	92.9	308	17	US-10-242-535A-41781	Sequence 41781, A
18	13	92.9	308	17	US-10-085-783A-41781	Sequence 41781, A
19	9	64.3	200	17	US-10-242-535A-5568	Sequence 5568, Ap
20	9	64.3	200	17	US-10-085-783A-5568	Sequence 5568, Ap
21	8	57.1	791	18	US-10-363-345A-23639	Sequence 23639, A
22	8	57.1	791	18	US-10-363-345A-23640	Sequence 23640, A
23	8	57.1	796	18	US-10-363-345A-20749	Sequence 20749, A
24	8	57.1	796	18	US-10-363-345A-20750	Sequence 20750, A
25	7	50.0	25	19	US-10-719-900-712383	Sequence 712383, A
26	7	50.0	82	13	US-10-027-632-177870	Sequence 177870, A
27	7	50.0	82	17	US-10-027-632-177870	Sequence 177870, A
28	7	50.0	283	17	US-10-424-599-66605	Sequence 66605, A
29	7	50.0	293	18	US-10-723-860-2410	Sequence 2410, Ap
30	7	50.0	420	9	US-09-960-352-9810	Sequence 9810, Ap
31	7	50.0	578	16	US-10-029-386-12911	Sequence 12911, A
32	7	50.0	622	17	US-10-424-599-54530	Sequence 54530, A
33	7	50.0	642	17	US-10-424-599-114534	Sequence 114534, A
34	7	50.0	1044	18	US-10-437-963-27914	Sequence 27914, A
35	7	50.0	1210	17	US-10-425-114-6115	Sequence 6115, Ap
36	7	50.0	1226	13	US-10-071-766-34	Sequence 25, Appl1
37	7	50.0	1265	13	US-10-027-632-254386	Sequence 254386, A
38	7	50.0	1265	17	US-10-027-632-254386	Sequence 254386, A
39	7	50.0	1338	17	US-10-149-310-279	Sequence 279, App
40	7	50.0	1428	18	US-10-489-425-63	Sequence 63, Appl
41	7	50.0	1682	16	US-10-247-671-11	Sequence 110, App
42	7	50.0	1696	17	US-10-424-599-114535	Sequence 114535, A
43	7	50.0	2321	13	US-10-071-766-34	Sequence 34, Appl1
44	7	50.0	3573	17	US-10-369-493-42233	Sequence 42233, A
45	7	50.0	92563	11	US-09-997-722-70	Sequence 70, Appl1
46	6	42.9	19	17	US-10-349-143-6641	Sequence 6641, Ap
47	6	42.9	25	15	US-10-098-263B-50944	Sequence 50944, A
48	6	42.9	25	18	US-10-717-597-493	Sequence 493, App
49	6	42.9	25	19	US-10-719-900-128648	Sequence 128648, A
50	6	42.9	25	19	US-10-719-900-40668	Sequence 40668, A
51	6	42.9	60	10	US-09-908-975-16123	Sequence 16123, A
52	6	42.9	108	9	US-09-864-761-25183	Sequence 25183, A
53	6	42.9	157	18	US-10-425-115-176491	Sequence 176491, A
54	6	42.9	159	18	US-10-809-824-2	Sequence 2, Appl1
55	6	42.9	164	18	US-10-425-115-135453	Sequence 135453, A
56	6	42.9	174	17	US-10-242-535A-40314	Sequence 40314, A
57	6	42.9	174	17	US-10-085-783A-40314	Sequence 40314, A
58	6	42.9	181	18	US-10-674-124A-28543	Sequence 28543, A
59	6	42.9	193	17	US-10-424-599-92176	Sequence 92176, A
60	6	42.9	201	17	US-10-424-599-9266	Sequence 9266, Ap
61	6	42.9	201	18	US-10-741-601-21451	Sequence 21451, A
62	6	42.9	201	18	US-10-741-601-25686	Sequence 25686, A
63	6	42.9	201	18	US-10-719-993-8393	Sequence 8393, Ap
64	6	42.9	201	18	US-10-719-993-48999	Sequence 48999, A
65	6	42.9	201	19	US-10-741-600-3477	Sequence 3477, Ap
66	6	42.9	201	19	US-10-741-600-20861	Sequence 20861, A
67	6	42.9	201	19	US-10-741-600-60742	Sequence 60742, A
68	6	42.9	201	19	US-10-741-600-70375	Sequence 70375, A
69	6	42.9	216	18	US-10-425-115-184546	Sequence 184546, A

C	70	6	42.9	228	18	US-10-437-963-26997	Sequence 26997, A	C 143	6	42.9	446	9	US-09-967-768A-273	Sequence 273, App
	71	6	42.9	233	17	US-10-424-599-12090	Sequence 12090, A	C 144	6	42.9	450	18	US-10-357-930-9324	Sequence 9324, App
	72	6	42.9	235	14	US-10-062-727-864	Sequence 864, App	C 145	6	42.9	455	18	US-10-425-115-72260	Sequence 72260, A
	73	6	42.9	241	18	US-10-674-124A-3318	Sequence 3318, App	C 146	6	42.9	458	10	US-09-918-995-11290	Sequence 11290, A
	74	6	42.9	263	17	US-10-242-535A-16597	Sequence 16597, A	C 147	6	42.9	465	10	US-09-918-995-11236	Sequence 11236, A
	75	6	42.9	263	17	US-10-085-783A-16597	Sequence 16597, A	C 148	6	42.9	465	10	US-09-918-995-15224	Sequence 15224, A
	76	6	42.9	279	9	US-09-983-965-1356	Sequence 1356, App	C 149	6	42.9	469	9	US-09-770-444-224	Sequence 224, App
	77	6	42.9	279	17	US-10-242-535A-11199	Sequence 12199, A	C 150	6	42.9	471	17	US-10-242-535A-16761	Sequence 16761, A
	78	6	42.9	279	17	US-10-085-783A-11199	Sequence 12199, A	C 151	6	42.9	471	17	US-10-085-783A-16761	Sequence 16761, A
	79	6	42.9	287	18	US-10-425-115-67525	Sequence 67525, A	C 152	6	42.9	472	10	US-09-866-050A-429	Sequence 429, App
	80	6	42.9	287	18	US-10-425-115-67525	Sequence 67525, A	C 153	6	42.9	472	14	US-10-152-661-429	Sequence 429, App
	81	6	42.9	289	17	US-10-437-963-77425	Sequence 77425, A	C 154	6	42.9	476	17	US-10-424-599-141472	Sequence 141472, A
	82	6	42.9	289	17	US-10-242-535A-15501	Sequence 15501, A	C 155	6	42.9	477	17	US-09-864-761-5825	Sequence 5825, App
	83	6	42.9	291	18	US-10-085-783A-15501	Sequence 15501, A	C 156	6	42.9	478	18	US-10-357-930-30527	Sequence 30527, A
	84	6	42.9	293	9	US-10-437-963-83648	Sequence 83648, A	C 157	6	42.9	478	18	US-10-357-930-30527	Sequence 30527, A
	85	6	42.9	293	9	US-09-736-457-538	Sequence 538, App	C 158	6	42.9	480	10	US-09-866-050A-208	Sequence 208, App
	86	6	42.9	293	9	US-09-902-941-538	Sequence 538, App	C 159	6	42.9	480	10	US-09-866-050A-208	Sequence 208, App
	87	6	42.9	293	9	US-09-849-626-538	Sequence 538, App	C 160	6	42.9	480	14	US-10-152-661-39	Sequence 39, Appl
	88	6	42.9	293	14	US-09-476-300-538	Sequence 538, App	C 161	6	42.9	480	14	US-10-152-661-39	Sequence 39, Appl
	89	6	42.9	293	16	US-10-017-754-538	Sequence 538, App	C 162	6	42.9	482	13	US-10-027-632-324416	Sequence 324416, A
	90	6	42.9	293	16	US-10-113-872-538	Sequence 538, App	C 163	6	42.9	482	17	US-10-027-632-324416	Sequence 324416, A
	91	6	42.9	304	9	US-10-283-017-538	Sequence 538, App	C 164	6	42.9	482	18	US-10-425-115-75654	Sequence 75654, A
	92	6	42.9	306	17	US-09-960-352-8963	Sequence 8963, App	C 165	6	42.9	483	9	US-09-728-445-337	Sequence 337, App
	93	6	42.9	309	17	US-10-425-114-25753	Sequence 25753, A	C 166	6	42.9	483	9	US-10-437-963-66930	Sequence 66930, A
	94	6	42.9	309	17	US-10-242-535A-42634	Sequence 42634, A	C 167	6	42.9	498	9	US-09-879-536-252	Sequence 252, App
	95	6	42.9	318	17	US-10-085-783A-42634	Sequence 42634, A	C 168	6	42.9	500	10	US-09-991-936-130	Sequence 130, App
	96	6	42.9	336	18	US-10-424-599-101178	Sequence 101178, A	C 169	6	42.9	505	10	US-09-918-995-20170	Sequence 20170, A
	97	6	42.9	337	18	US-10-425-115-94724	Sequence 94724, A	C 170	6	42.9	508	9	US-09-823-245A-381	Sequence 381, App
	98	6	42.9	343	14	US-10-674-124A-23764	Sequence 23764, A	C 171	6	42.9	510	17	US-10-369-493-41048	Sequence 41048, A
	99	6	42.9	343	15	US-10-267-849-13	Sequence 13, Appl	C 172	6	42.9	519	13	US-10-027-632-26991	Sequence 26991, A
	100	6	42.9	344	17	US-10-069-698-3396	Sequence 3396, App	C 173	6	42.9	519	17	US-10-027-632-26991	Sequence 26991, A
	101	6	42.9	346	17	US-10-062-674-926	Sequence 926, App	C 174	6	42.9	520	9	US-09-864-761-8435	Sequence 8435, App
	102	6	42.9	346	17	US-10-242-535A-34937	Sequence 34937, A	C 175	6	42.9	526	17	US-10-276-774-333	Sequence 333, App
	103	6	42.9	346	17	US-10-242-535A-1042	Sequence 1042, App	C 176	6	42.9	526	17	US-10-276-774-333	Sequence 333, App
	104	6	42.9	346	17	US-10-085-783A-34937	Sequence 34937, A	C 177	6	42.9	532	13	US-10-027-632-43849	Sequence 43849, A
	105	6	42.9	347	17	US-10-242-535A-36276	Sequence 36276, A	C 178	6	42.9	532	13	US-10-027-632-43850	Sequence 43850, A
	106	6	42.9	347	17	US-10-085-783A-36276	Sequence 36276, A	C 179	6	42.9	532	17	US-10-027-632-43849	Sequence 43849, A
	107	6	42.9	348	14	US-10-062-727-705	Sequence 705, App	C 180	6	42.9	532	11	US-10-027-632-43850	Sequence 43850, A
	108	6	42.9	351	14	US-10-062-727-461	Sequence 461, App	C 181	6	42.9	533	17	US-09-801-9448-105	Sequence 105, App
	109	6	42.9	353	10	US-09-918-995-7552	Sequence 7552, App	C 182	6	42.9	534	14	US-10-424-599-7219	Sequence 7219, App
	110	6	42.9	354	17	US-10-369-493-29172	Sequence 29172, A	C 183	6	42.9	534	14	US-10-060-036-4027	Sequence 4027, App
	111	6	42.9	357	17	US-10-398-221-998	Sequence 998, App	C 184	6	42.9	542	13	US-10-027-632-206700	Sequence 206700, A
	112	6	42.9	357	17	US-10-398-221-2790	Sequence 2790, App	C 185	6	42.9	542	17	US-10-027-632-206700	Sequence 206700, A
	113	6	42.9	358	13	US-10-040-739-45	Sequence 45, Appl	C 186	6	42.9	543	14	US-10-066-543-1953	Sequence 1953, App
	114	6	42.9	360	10	US-09-918-995-7574	Sequence 7574, App	C 187	6	42.9	549	17	US-10-424-599-140508	Sequence 140508, A
	115	6	42.9	361	17	US-10-424-599-6767	Sequence 6767, App	C 188	6	42.9	549	18	US-10-425-115-84809	Sequence 84809, A
	116	6	42.9	368	9	US-09-924-401-28	Sequence 28, Appl	C 189	6	42.9	549	18	US-10-363-345A-24469	Sequence 24469, A
	117	6	42.9	386	14	US-10-062-727-405	Sequence 405, App	C 190	6	42.9	549	18	US-10-363-345A-24470	Sequence 24470, A
	118	6	42.9	391	18	US-10-437-963-99409	Sequence 99409, A	C 191	6	42.9	554	9	US-09-878-178-2080	Sequence 2080, App
	119	6	42.9	392	17	US-10-296-115-42	Sequence 42, Appl	C 192	6	42.9	554	13	US-10-046-503-2080	Sequence 2080, App
	120	6	42.9	393	18	US-10-767-795-2576	Sequence 2576, App	C 193	6	42.9	561	9	US-09-998-598-1340	Sequence 1340, App
	121	6	42.9	398	17	US-10-242-535A-20017	Sequence 20017, A	C 194	6	42.9	561	18	US-10-425-115-175172	Sequence 175172, A
	122	6	42.9	398	17	US-10-085-783A-20017	Sequence 20017, A	C 195	6	42.9	561	9	US-09-796-692-352	Sequence 352, App
	123	6	42.9	401	9	US-09-918-995-36734	Sequence 36734, A	C 196	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	124	6	42.9	406	17	US-09-864-761-14172	Sequence 14172, A	C 197	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	125	6	42.9	406	17	US-10-264-049-1711	Sequence 1711, App	C 198	6	42.9	563	9	US-09-796-692-352	Sequence 352, App
	126	6	42.9	410	13	US-10-027-632-13506	Sequence 13506, A	C 199	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	127	6	42.9	410	17	US-10-027-632-13506	Sequence 13506, A	C 200	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	128	6	42.9	411	18	US-10-437-963-56648	Sequence 56648, A	C 201	6	42.9	563	14	US-10-040-862-480	Sequence 480, App
	129	6	42.9	412	17	US-10-424-599-4907	Sequence 24907, A	C 202	6	42.9	563	17	US-10-040-862-481	Sequence 481, App
	130	6	42.9	414	9	US-09-974-300-7520	Sequence 7520, App	C 203	6	42.9	563	17	US-10-057-475B-480	Sequence 480, App
	131	6	42.9	416	18	US-10-425-115-43376	Sequence 43376, A	C 204	6	42.9	563	17	US-10-057-475B-480	Sequence 480, App
	132	6	42.9	427	18	US-10-437-963-17379	Sequence 17379, A	C 205	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	133	6	42.9	429	18	US-10-357-930-155	Sequence 155, App	C 206	6	42.9	563	17	US-10-057-475B-481	Sequence 481, App
	134	6	42.9	433	18	US-10-425-115-72773	Sequence 72773, A	C 207	6	42.9	563	17	US-10-154-884B-480	Sequence 480, App
	135	6	42.9	436	17	US-10-242-535A-15995	Sequence 15995, A	C 208	6	42.9	563	17	US-10-154-884B-480	Sequence 480, App
	136	6	42.9	436	17	US-10-085-783A-15995	Sequence 15995, A	C 209	6	42.9	563	17	US-10-154-884B-480	Sequence 480, App
	137	6	42.9	441	10	US-09-918-995-28803	Sequence 28803, A	C 210	6	42.9	563	17	US-10-154-884B-481	Sequence 481, App
	138	6	42.9	441	17	US-10-424-599-93340	Sequence 93340, A	C 211	6	42.9	563	17	US-10-154-884B-481	Sequence 481, App
	139	6	42.9	445	17	US-10-242-535A-56459	Sequence 56459, A	C 212	6	42.9	563	18	US-10-764-324-480	Sequence 324-480
	140	6	42.9	445	17	US-10-085-783A-56459	Sequence 56459, A	C 213	6	42.9	563	18	US-10-764-324-480	Sequence 324-480
	141	6	42.9	446	9	US-09-954-456-436	Sequence 436, App	C 214	6	42.9	563	18	US-10-764-324-481	Sequence 481, App
	142	6	42.9	446	9	US-09-954-456-2188	Sequence 2188, App	C 215	6	42.9	563	18	US-10-764-324-481	Sequence 481, App

362	6	42.9	1140	11	US-09-938-8428-2000	Sequence 2000, App	435	18	US-10-425-115-65532	Sequence 65532, A
363	6	42.9	1140	11	US-09-764-875-1214	Sequence 1214, App	436	18	US-09-822-846-200	Sequence 200, App
364	6	42.9	1140	14	US-10-073-865-131	Sequence 131, App	437	10	US-10-723-860-8157	Sequence 8157, App
365	6	42.9	1140	14	US-10-103-313-602	Sequence 602, App	438	14	US-10-073-885-15	Sequence 15, Appl
366	6	42.9	1140	17	US-10-227-646-149	Sequence 149, App	439	17	US-10-369-493-26651	Sequence 26651, A
367	6	42.9	1146	17	US-10-282-122A-24149	Sequence 24149, A	440	17	US-10-276-774-881	Sequence 881, App
368	6	42.9	1148	17	US-10-424-599-1403	Sequence 1403, App	441	17	US-10-437-963-94941	Sequence 94941, A
369	6	42.9	1157	17	US-10-425-114-31746	Sequence 31746, A	442	17	US-10-260-238-1860	Sequence 1860, App
370	6	42.9	1160	17	US-10-424-599-26547	Sequence 26547, A	443	18	US-10-437-963-43011	Sequence 43011, A
371	6	42.9	1160	18	US-10-841-796-27	Sequence 27, Appl	444	13	US-10-087-192-1985	Sequence 1985, App
372	6	42.9	1163	17	US-10-398-221-3047	Sequence 3047, App	445	17	US-10-425-114-7566	Sequence 7566, App
373	6	42.9	1175	17	US-10-653-047-5924	Sequence 5924, App	446	17	US-10-104-047-1712	Sequence 1712, App
374	6	42.9	1178	18	US-10-821-273-79	Sequence 79, Appl	447	17	US-10-282-122A-41296	Sequence 41296, A
375	6	42.9	1198	16	US-10-006-285-312	Sequence 312, App	448	15	US-10-282-122A-40201	Sequence 40201, A
376	6	42.9	1202	18	US-10-425-115-13573	Sequence 13573, A	449	9	US-09-906-226-33	Sequence 33, Appl
377	6	42.9	1215	18	US-10-363-345A-28505	Sequence 28505, A	450	13	US-10-027-632-101709	Sequence 101709, A
378	6	42.9	1215	18	US-10-363-345A-28506	Sequence 28506, A	451	13	US-10-027-632-101709	Sequence 101709, A
379	6	42.9	1236	13	US-10-027-632-101099	Sequence 101099, A	452	17	US-09-974-300-1541	Sequence 1541, App
380	6	42.9	1236	17	US-10-027-632-101099	Sequence 101099, A	453	17	US-10-191-997-92	Sequence 92, Appl
381	6	42.9	1236	17	US-10-424-599-108037	Sequence 108037, A	454	13	US-10-027-632-110396	Sequence 110396, A
382	6	42.9	1239	17	US-10-282-122A-14579	Sequence 14579, A	455	13	US-10-027-632-110397	Sequence 110397, A
383	6	42.9	1286	17	US-10-767-701-13663	Sequence 13663, A	456	13	US-10-027-632-110398	Sequence 110398, A
384	6	42.9	1309	17	US-10-374-780A-1873	Sequence 1873, App	457	17	US-10-027-632-110397	Sequence 110397, A
385	6	42.9	1310	18	US-10-739-565-3	Sequence 3, Appl	458	17	US-10-027-632-110397	Sequence 110397, A
386	6	42.9	1336	9	US-09-799-777-114	Sequence 114, App	459	17	US-10-027-632-110398	Sequence 110398, A
387	6	42.9	1341	18	US-10-363-345A-1641	Sequence 1641, App	460	17	US-10-027-632-110398	Sequence 110398, A
388	6	42.9	1341	18	US-10-363-345A-1642	Sequence 1642, App	461	17	US-09-960-706-955	Sequence 955, App
389	6	42.9	1351	18	US-10-494-672-243	Sequence 243, App	462	17	US-09-873-319-624	Sequence 624, App
390	6	42.9	1378	13	US-10-001-843-90	Sequence 90, Appl	463	17	US-10-094-749-1141	Sequence 1141, App
391	6	42.9	1383	18	US-10-437-963-17062	Sequence 17062, A	464	13	US-10-087-192-611	Sequence 611, App
392	6	42.9	1412	18	US-10-437-963-61052	Sequence 61052, A	465	17	US-10-282-122A-16623	Sequence 16623, A
393	6	42.9	1413	9	US-09-764-893-16	Sequence 16, Appl	466	17	US-10-282-122A-17111	Sequence 17111, A
394	6	42.9	1413	9	US-09-764-886-17	Sequence 17, Appl	467	17	US-10-282-122A-17097	Sequence 17097, A
395	6	42.9	1413	9	US-09-764-886-17	Sequence 17, Appl	468	18	US-10-282-122A-32581	Sequence 32581, A
396	6	42.9	1413	9	US-09-860-670-12	Sequence 12, Appl	469	18	US-10-425-115-107095	Sequence 107095, A
397	6	42.9	1413	10	US-09-989-442-25	Sequence 25, Appl	470	17	US-10-104-047-1867	Sequence 1867, App
398	6	42.9	1413	10	US-09-764-886-17	Sequence 17, Appl	471	18	US-10-437-963-81151	Sequence 81151, A
399	6	42.9	1413	11	US-09-764-875-103	Sequence 103, App	472	18	US-10-425-115-73560	Sequence 73560, A
400	6	42.9	1413	14	US-10-073-865-16	Sequence 16, Appl	473	18	US-10-398-221-3473	Sequence 3473, App
401	6	42.9	1413	14	US-10-103-313-53	Sequence 53, Appl	474	17	US-10-302-172-373	Sequence 373, App
402	6	42.9	1413	17	US-10-073-885-43	Sequence 43, Appl	475	17	US-10-094-749-974	Sequence 974, App
403	6	42.9	1413	17	US-10-227-646-12	Sequence 12, Appl	476	10	US-09-781-693A-3	Sequence 3, Appl
404	6	42.9	1420	18	US-10-425-115-63513	Sequence 63513, A	477	14	US-10-205-737-1	Sequence 1, Appl
405	6	42.9	1451	18	US-10-425-115-118516	Sequence 118516, A	478	14	US-10-723-860-5853	Sequence 5853, App
406	6	42.9	1502	17	US-10-424-599-111856	Sequence 111856, A	479	18	US-10-425-115-78456	Sequence 78456, A
407	6	42.9	1536	18	US-10-425-115-12495	Sequence 12495, A	480	18	US-10-739-930-2471	Sequence 2471, App
408	6	42.9	1563	18	US-10-425-115-73567	Sequence 73567, A	481	17	US-10-425-114-34971	Sequence 34971, A
409	6	42.9	1567	18	US-10-425-115-151250	Sequence 151250, A	482	10	US-09-957-763-1	Sequence 1, Appl
410	6	42.9	1572	18	US-10-425-115-150505	Sequence 150505, A	483	10	US-09-957-763-3	Sequence 3, Appl
411	6	42.9	1601	17	US-10-425-114-25599	Sequence 25599, A	484	17	US-10-424-599-81828	Sequence 81828, A
412	6	42.9	1618	9	US-09-925-300-271	Sequence 271, App	485	14	US-10-172-573-1	Sequence 1, Appl
413	6	42.9	1646	9	US-09-815-828-3	Sequence 3, Appl	486	17	US-10-425-115-33058	Sequence 33058, A
414	6	42.9	1718	17	US-10-425-114-3299	Sequence 3299, App	487	18	US-10-425-115-21515	Sequence 21515, A
415	6	42.9	1726	17	US-10-369-493-29967	Sequence 29967, A	488	18	US-10-374-780A-1861	Sequence 1861, App
416	6	42.9	1754	17	US-10-425-114-28227	Sequence 28227, A	489	17	US-10-320-797-262	Sequence 262, App
417	6	42.9	1782	9	US-09-925-298-233	Sequence 233, App	490	17	US-10-320-797-262	Sequence 262, App
418	6	42.9	1801	14	US-10-102-806-233	Sequence 233, App	491	14	US-10-206-566-1	Sequence 1, Appl
419	6	42.9	1802	15	US-10-425-114-28027	Sequence 28027, A	492	14	US-10-172-573-3	Sequence 3, Appl
420	6	42.9	1802	15	US-10-273-517-5	Sequence 5, Appl	493	17	US-10-739-930-1001	Sequence 1001, App
421	6	42.9	1802	17	US-10-311-104-5	Sequence 5, Appl	494	17	US-10-108-260A-419	Sequence 419, App
422	6	42.9	1807	17	US-10-425-114-24720	Sequence 24720, A	495	18	US-09-988-462-27	Sequence 27, Appl
423	6	42.9	1809	17	US-10-282-122A-12055	Sequence 12055, A	496	18	US-10-437-963-9728	Sequence 9728, App
424	6	42.9	1811	18	US-10-425-115-120743	Sequence 120743, A	497	18	US-09-764-891-10076	Sequence 10076, A
425	6	42.9	1816	18	US-10-425-115-147226	Sequence 147226, A	498	15	US-10-205-428-986	Sequence 205, App
426	6	42.9	1842	17	US-10-305-720-46	Sequence 46, Appl	499	15	US-10-283-975A-291	Sequence 291, App
427	6	42.9	1844	18	US-10-425-115-10679	Sequence 10679, A	500	17	US-10-641-643-1066	Sequence 1066, App
428	6	42.9	1850	18	US-10-425-115-94481	Sequence 94481, A	501	19	US-10-741-600-48	Sequence 48, Appl
429	6	42.9	1853	17	US-10-425-114-31477	Sequence 31477, A	502	17	US-10-620-532-1	Sequence 1, Appl
430	6	42.9	1866	18	US-10-437-963-68132	Sequence 68132, A	503	11	US-09-968-007A-377	Sequence 377, App
431	6	42.9	1888	17	US-10-369-493-37743	Sequence 37743, A	504	10	US-09-919-039-358	Sequence 358, App
432	6	42.9	1890	17	US-10-094-749-742	Sequence 742, App	505	13	US-10-044-090-350	Sequence 350, App
433	6	42.9	1902	17	US-10-282-122A-12718	Sequence 12718, A	506	17	US-10-302-172-85	Sequence 85, Appl
434	6	42.9	1933	17	US-10-641-643-739	Sequence 739, App	507	15	US-10-241-220-25	Sequence 25, Appl

508	6	42.9	4709	18	US-10-872-972-25	Sequence 25, Appl	c 581	6	42.9	31946	13	US-10-087-192-1909	Sequence 1909, Ap
509	6	42.9	4709	18	US-10-872-991-25	Sequence 25, Appl	c 582	6	42.9	33486	16	US-10-085-959-143	Sequence 143, App
510	6	42.9	4722	18	US-10-602-494-146	Sequence 146, App	c 583	6	42.9	39003	17	US-10-672-781-21	Sequence 21, Appl
511	6	42.9	4736	17	US-10-398-221-3763	Sequence 3763, Ap	c 584	6	42.9	41322	15	US-10-024-396-13	Sequence 13, Appl
512	6	42.9	4819	17	US-10-120-988-72	Sequence 72, Appl	c 585	6	42.9	41936	9	US-09-967-768A-116	Sequence 116, App
c 513	6	42.9	4974	15	US-10-156-761-2487	Sequence 2487, Ap	c 586	6	42.9	45845	9	US-09-927-091-6	Sequence 6, Appli
514	6	42.9	5047	18	US-10-171-597-11	Sequence 11, Appl	c 587	6	42.9	45862	13	US-10-216-355-3	Sequence 3, Appli
515	6	42.9	5159	17	US-10-334-143-111	Sequence 111, App	c 588	6	42.9	49088	13	US-10-087-192-13	Sequence 13, Appl
c 516	6	42.9	5567	17	US-10-361-522-2	Sequence 2, Appli	c 589	6	42.9	50460	13	US-10-087-192-1633	Sequence 1633, Ap
517	6	42.9	5989	17	US-10-221-714A-257	Sequence 257, App	c 590	6	42.9	55005	18	US-10-719-993-6968	Sequence 6968, Ap
518	6	42.9	6343	18	US-10-473-126-334	Sequence 334, App	c 591	6	42.9	56773	18	US-10-331-053-47	Sequence 47, Appli
519	6	42.9	6436	15	US-10-311-455-1665	Sequence 1665, Ap	c 592	6	42.9	57082	18	US-10-715-066-1	Sequence 1, Appli
c 520	6	42.9	6574	13	US-10-194-163-1097	Sequence 1097, Ap	c 593	6	42.9	65042	9	US-09-784-316-3	Sequence 3, Appli
521	6	42.9	7069	15	US-10-311-455-1325	Sequence 1325, Ap	c 594	6	42.9	65042	14	US-10-229-124-3	Sequence 3, Appli
522	6	42.9	7069	17	US-10-221-613-179	Sequence 179, App	c 595	6	42.9	65042	18	US-10-778-301-3	Sequence 3, Appli
523	6	42.9	7069	17	US-10-221-714A-375	Sequence 375, App	c 596	6	42.9	66765	18	US-10-715-066-4	Sequence 4, Appli
524	6	42.9	7069	18	US-10-433-793-13	Sequence 13, Appl	c 597	6	42.9	66916	18	US-10-741-601-5708	Sequence 5708, Ap
525	6	42.9	7431	15	US-10-311-455-54	Sequence 54, Appl	c 598	6	42.9	66916	19	US-10-741-600-17810	Sequence 17810, A
526	6	42.9	7518	18	US-10-437-963-68129	Sequence 68129, A	c 599	6	42.9	85915	18	US-10-647-196-1	Sequence 1, Appli
c 527	6	42.9	7538	17	US-10-062-674-1996	Sequence 1996, Ap	c 600	6	42.9	86131	18	US-10-741-601-5665	Sequence 5665, Ap
528	6	42.9	7695	18	US-10-437-963-68125	Sequence 68125, A	c 601	6	42.9	86131	19	US-10-741-600-17895	Sequence 17895, A
529	6	42.9	8325	17	US-10-369-493-33563	Sequence 33563, A	c 602	6	42.9	88398	18	US-10-810-788A-5	Sequence 5, Appli
530	6	42.9	8530	17	US-10-311-455-406	Sequence 406, App	c 603	6	42.9	99957	11	US-09-997-722-298	Sequence 298, App
531	6	42.9	8776	17	US-10-257-166-149	Sequence 149, App	c 604	6	42.9	100534	18	US-10-367-094-160	Sequence 160, App
c 532	6	42.9	9393	16	US-10-085-959-22	Sequence 22, Appl	c 605	6	42.9	106938	18	US-10-322-281-566	Sequence 566, App
533	6	42.9	9631	15	US-10-017-161-1569	Sequence 1569, Ap	c 606	6	42.9	109977	18	US-10-719-993-6870	Sequence 6870, Ap
534	6	42.9	9935	18	US-10-489-242-9	Sequence 9, Appli	c 607	6	42.9	114911	18	US-10-723-860-3910	Sequence 3910, Ap
535	6	42.9	10464	9	US-09-957-974-1	Sequence 1, Appli	c 608	6	42.9	115284	13	US-10-087-192-673	Sequence 673, App
536	6	42.9	11473	15	US-10-311-455-1328	Sequence 1328, Ap	c 609	6	42.9	121410	19	US-10-087-192-673	Sequence 17733, A
537	6	42.9	11473	17	US-10-257-166-112	Sequence 112, App	c 610	6	42.9	124884	10	US-09-913-514-1	Sequence 1, Appli
c 538	6	42.9	11809	17	US-10-280-183A-2	Sequence 2, Appli	c 611	6	42.9	124884	16	US-10-288-823-76	Sequence 76, Appl
539	6	42.9	12192	9	US-09-764-860-629	Sequence 629, App	c 612	6	42.9	125157	10	US-09-913-514-2	Sequence 2, Appli
540	6	42.9	12192	14	US-10-074-095-629	Sequence 629, App	c 613	6	42.9	125157	18	US-10-741-601-5738	Sequence 5738, Ap
541	6	42.9	12192	17	US-10-212-872-629	Sequence 629, App	c 614	6	42.9	126872	19	US-10-741-600-17885	Sequence 17885, A
542	6	42.9	13635	17	US-10-464-368-30	Sequence 30, Appl	c 615	6	42.9	127238	13	US-10-087-192-787	Sequence 787, App
543	6	42.9	13635	17	US-10-210-175-13	Sequence 13, Appl	c 616	6	42.9	127917	18	US-10-775-169-82	Sequence 82, Appl
544	6	42.9	13638	17	US-10-464-368-29	Sequence 29, Appl	c 617	6	42.9	133955	13	US-10-087-192-1984	Sequence 1984, Ap
545	6	42.9	13836	13	US-10-087-192-671	Sequence 671, App	c 618	6	42.9	136338	15	US-10-741-600-17574	Sequence 17574, A
546	6	42.9	14538	18	US-10-741-601-49	Sequence 49, Appl	c 619	6	42.9	171936	15	US-10-265-071-24	Sequence 24, Appl
547	6	42.9	14745	18	US-10-741-601-48	Sequence 48, Appl	c 620	6	42.9	171936	15	US-10-025-966A-24	Sequence 24, Appl
548	6	42.9	14849	9	US-09-873-403-1	Sequence 1, Appli	c 621	6	42.9	172569	13	US-10-087-192-1366	Sequence 1366, Ap
549	6	42.9	14849	11	US-09-750-972-1	Sequence 1, Appli	c 622	6	42.9	179997	9	US-09-822-246-3	Sequence 3, Appli
550	6	42.9	14887	17	US-10-276-774-373	Sequence 373, App	c 623	6	42.9	179997	18	US-10-469-028-3	Sequence 3, Appli
551	6	42.9	14889	15	US-10-101-510-356	Sequence 356, App	c 624	6	42.9	203070	13	US-10-087-192-247	Sequence 247, App
552	6	42.9	14896	11	US-09-750-972-6	Sequence 6, Appli	c 625	6	42.9	207433	17	US-10-277-216-5	Sequence 5, Appli
553	6	42.9	14896	17	US-10-159-563-206	Sequence 206, App	c 626	6	42.9	207433	17	US-10-126-022-5	Sequence 5, Appli
554	6	42.9	14896	18	US-10-473-974-243	Sequence 243, App	c 627	6	42.9	210204	18	US-10-723-860-1746	Sequence 1746, Ap
555	6	42.9	15518	15	US-10-311-455-2145	Sequence 2145, Ap	c 628	6	42.9	219715	18	US-10-417-375-63	Sequence 63, Appl
556	6	42.9	15518	15	US-10-240-485-177	Sequence 177, App	c 629	6	42.9	240825	10	US-09-790-289-1	Sequence 1, Appli
c 557	6	42.9	16371	18	US-10-741-601-5618	Sequence 5618, Ap	c 630	6	42.9	240825	18	US-10-468-582-1	Sequence 1, Appli
c 558	6	42.9	16371	19	US-10-741-600-17823	Sequence 17823, A	c 631	6	42.9	254366	10	US-09-822-871-3	Sequence 3, Appli
559	6	42.9	16545	9	US-09-835-996A-32	Sequence 32, Appl	c 632	6	42.9	254366	17	US-10-673-885-3	Sequence 3, Appli
560	6	42.9	16559	14	US-10-198-846-12181	Sequence 12181, A	c 633	6	42.9	256190	18	US-10-322-281-320	Sequence 320, App
561	6	42.9	16842	17	US-10-221-613-298	Sequence 298, App	c 634	6	42.9	304905	17	US-10-271-416-1	Sequence 1, Appli
562	6	42.9	16842	17	US-10-221-714A-134	Sequence 134, App	c 635	6	42.9	318760	18	US-10-719-993-6755	Sequence 6755, Ap
563	6	42.9	17114	18	US-10-741-601-5770	Sequence 5770, Ap	c 636	6	42.9	321019	19	US-10-741-600-17566	Sequence 17566, A
564	6	42.9	17114	19	US-10-741-600-17982	Sequence 17982, A	c 637	6	42.9	326014	9	US-09-731-231A-3	Sequence 3, Appli
565	6	42.9	17200	9	US-09-764-877-3390	Sequence 3390, Ap	c 638	6	42.9	326014	18	US-10-751-985-3	Sequence 3, Appli
566	6	42.9	17200	17	US-10-242-515-3390	Sequence 3390, Ap	c 639	6	42.9	329019	18	US-10-388-838-48	Sequence 48, Appl
c 567	6	42.9	17492	18	US-10-719-993-6914	Sequence 6914, Ap	c 640	6	42.9	339234	18	US-10-322-696-73	Sequence 73, Appl
c 568	6	42.9	18364	15	US-10-243-243A-7	Sequence 7, Appli	c 641	6	42.9	339234	18	US-10-322-696-73	Sequence 73, Appl
c 569	6	42.9	18404	14	US-10-142-515-10	Sequence 10, Appl	c 642	6	42.9	339234	18	US-10-322-696-73	Sequence 73, Appl
570	6	42.9	18966	9	US-09-764-877-3372	Sequence 3372, Ap	c 643	6	42.9	370001	18	US-10-319-908-16	Sequence 16, Appl
571	6	42.9	18966	17	US-10-242-515-3372	Sequence 3372, Ap	c 644	6	42.9	398287	18	US-10-719-993-6805	Sequence 6805, Ap
c 572	6	42.9	21721	17	US-10-650-507-41	Sequence 41, Appl	c 645	6	42.9	398287	19	US-10-741-601-5719	Sequence 5719, Ap
c 573	6	42.9	22976	17	US-10-650-507-19	Sequence 19, Appl	c 646	6	42.9	436331	13	US-10-087-192-205	Sequence 205, App
574	6	42.9	23107	11	US-09-997-722-28	Sequence 28, Appl	c 647	6	42.9	518360	18	US-10-367-094-125	Sequence 125, App
c 575	6	42.9	23187	16	US-10-214-684A-1	Sequence 1, Appli	c 648	6	42.9	561515	18	US-10-741-601-5682	Sequence 5682, Ap
c 576	6	42.9	27689	17	US-10-312-222-1	Sequence 1, Appli	c 649	6	42.9	561515	13	US-10-600-17730	Sequence 17730, A
577	6	42.9	27890	18	US-10-741-601-5686	Sequence 5686, Ap	c 650	6	42.9	653122	19	US-10-087-192-226	Sequence 226, App
578	6	42.9	27890	19	US-10-741-600-17751	Sequence 17751, A	c 651	6	42.9	684707	17	US-10-398-221-9	Sequence 9, Appli
579	6	42.9	30625	9	US-09-927-091-5	Sequence 5, Appli	c 652	6	42.9	713059	13	US-10-027-632-174581	Sequence 174581, A
580	6	42.9	30676	9	US-09-927-091-8	Sequence 8, Appli	c 653	6	42.9	713059	17	US-10-027-632-174581	Sequence 174581, A

654	6	42.9	744802	17	US-10-232-798-1369	Sequence 1369, Ap	c 727	5	35.7	25	19	US-10-719-900-43176	Sequence 43176, A
655	6	42.9	786452	18	US-10-719-993-6822	Sequence 6822, Ap	c 728	5	35.7	25	19	US-10-719-900-47542	Sequence 47542, A
656	6	42.9	1790242	18	US-10-719-993-6940	Sequence 6940, Ap	c 729	5	35.7	25	19	US-10-719-900-62178	Sequence 62178, A
657	6	42.9	2140405	13	US-10-027-632-76212	Sequence 76212, A	c 730	5	35.7	25	19	US-10-719-900-62964	Sequence 62964, A
658	6	42.9	2140405	17	US-10-027-632-76212	Sequence 76212, A	c 731	5	35.7	25	19	US-10-719-900-70403	Sequence 70403, A
659	6	42.9	2940917	13	US-10-027-633-174763	Sequence 174763, A	c 732	5	35.7	25	19	US-10-719-900-71951	Sequence 71951, A
660	6	42.9	3011208	17	US-10-027-633-174763	Sequence 174763, A	c 733	5	35.7	25	19	US-10-719-900-78832	Sequence 78832, A
661	6	42.9	3011208	17	US-10-398-221-2058	Sequence 2058, Ap	c 734	5	35.7	25	19	US-10-719-900-84811	Sequence 84811, A
662	6	42.9	3186778	13	US-10-027-633-174961	Sequence 174961, A	c 735	5	35.7	25	19	US-10-719-900-93092	Sequence 93092, A
663	6	42.9	3186778	17	US-10-027-633-174961	Sequence 174961, A	c 736	5	35.7	25	19	US-10-719-900-128662	Sequence 128662, A
664	6	42.9	3309400	9	US-09-738-626-1	Sequence 1, Appli	c 737	5	35.7	25	19	US-10-719-900-128777	Sequence 128777, A
665	6	42.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	c 738	5	35.7	25	19	US-10-719-900-128778	Sequence 128778, A
666	6	42.9	9025608	15	US-10-156-761-1	Sequence 1, Appli	c 739	5	35.7	25	19	US-10-719-900-130977	Sequence 130977, A
667	5	35.7	17	15	US-10-060-895A-686	Sequence 686, App	c 740	5	35.7	25	19	US-10-719-900-138295	Sequence 138295, A
668	5	35.7	17	15	US-10-060-895A-687	Sequence 687, App	c 741	5	35.7	25	19	US-10-719-900-147378	Sequence 147378, A
669	5	35.7	17	15	US-10-060-895A-688	Sequence 688, App	c 742	5	35.7	25	19	US-10-719-900-154461	Sequence 154461, A
670	5	35.7	17	17	US-10-138-674-2043	Sequence 2043, Ap	c 743	5	35.7	25	19	US-10-719-900-162361	Sequence 162361, A
671	5	35.7	17	17	US-10-138-674-2043	Sequence 2043, Ap	c 744	5	35.7	25	19	US-10-719-900-183494	Sequence 183494, A
672	5	35.7	17	18	US-10-287-949A-2043	Sequence 2043, Ap	c 745	5	35.7	25	19	US-10-719-900-205913	Sequence 205913, A
673	5	35.7	17	18	US-10-287-949A-2043	Sequence 2043, Ap	c 746	5	35.7	25	19	US-10-719-900-205682	Sequence 205682, A
674	5	35.7	17	18	US-10-712-633-4246	Sequence 4246, Ap	c 747	5	35.7	25	19	US-10-719-900-235445	Sequence 235445, A
675	5	35.7	19	16	US-10-235-079B-19	Sequence 19, Appli	c 748	5	35.7	25	19	US-10-719-900-234871	Sequence 234871, A
676	5	35.7	19	18	US-10-654-253-4	Sequence 4, Appli	c 749	5	35.7	25	19	US-10-719-900-250128	Sequence 250128, A
677	5	35.7	20	10	US-09-969-086A-3	Sequence 3, Appli	c 750	5	35.7	25	19	US-10-719-900-252724	Sequence 252724, A
678	5	35.7	20	16	US-10-369-378-50	Sequence 50, Appli	c 751	5	35.7	25	19	US-10-719-900-253673	Sequence 253673, A
679	5	35.7	21	18	US-10-786-720-3029	Sequence 3029, Ap	c 752	5	35.7	25	19	US-10-719-900-253769	Sequence 253769, A
680	5	35.7	21	18	US-10-751-736-49153	Sequence 49153, A	c 753	5	35.7	25	19	US-10-719-900-253770	Sequence 253770, A
681	5	35.7	21	18	US-10-751-736-49154	Sequence 49154, A	c 754	5	35.7	25	19	US-10-719-900-281405	Sequence 281405, A
682	5	35.7	23	9	US-09-520-538-15	Sequence 15, Appli	c 755	5	35.7	25	19	US-10-719-900-296256	Sequence 296256, A
683	5	35.7	25	14	US-10-215-112-6863	Sequence 6863, Ap	c 756	5	35.7	25	19	US-10-719-900-303768	Sequence 303768, A
684	5	35.7	25	14	US-10-215-112-10262	Sequence 10262, A	c 757	5	35.7	25	19	US-10-719-900-303769	Sequence 303769, A
685	5	35.7	25	14	US-10-215-112-10388	Sequence 10388, A	c 758	5	35.7	25	19	US-10-719-900-307034	Sequence 307034, A
686	5	35.7	25	15	US-10-060-895A-1455	Sequence 1455, Ap	c 759	5	35.7	25	19	US-10-719-900-307035	Sequence 307035, A
687	5	35.7	25	15	US-10-060-895A-1456	Sequence 1456, Ap	c 760	5	35.7	25	19	US-10-719-900-321725	Sequence 321725, A
688	5	35.7	25	15	US-10-060-895A-1457	Sequence 1457, Ap	c 761	5	35.7	25	19	US-10-719-900-330959	Sequence 330959, A
689	5	35.7	25	15	US-10-060-895A-1458	Sequence 1458, Ap	c 762	5	35.7	25	19	US-10-719-900-335330	Sequence 335330, A
690	5	35.7	25	15	US-10-060-895A-1459	Sequence 1459, Ap	c 763	5	35.7	25	19	US-10-719-900-343584	Sequence 343584, A
691	5	35.7	25	15	US-10-060-895A-1460	Sequence 1460, Ap	c 764	5	35.7	25	19	US-10-719-900-362511	Sequence 362511, A
692	5	35.7	25	15	US-10-060-895A-1461	Sequence 1461, Ap	c 765	5	35.7	25	19	US-10-719-900-362513	Sequence 362513, A
693	5	35.7	25	15	US-10-060-895A-1462	Sequence 1462, Ap	c 766	5	35.7	25	19	US-10-719-900-373409	Sequence 373409, A
694	5	35.7	25	15	US-10-060-895A-1463	Sequence 1463, Ap	c 767	5	35.7	25	19	US-10-719-900-396244	Sequence 396244, A
695	5	35.7	25	15	US-10-060-895A-1464	Sequence 1464, Ap	c 768	5	35.7	25	19	US-10-719-900-404281	Sequence 404281, A
696	5	35.7	25	15	US-10-060-895A-1465	Sequence 1465, Ap	c 769	5	35.7	25	19	US-10-719-900-406234	Sequence 406234, A
697	5	35.7	25	15	US-10-098-263B-2915	Sequence 2915, Ap	c 770	5	35.7	25	19	US-10-719-900-417601	Sequence 417601, A
698	5	35.7	25	15	US-10-098-263B-3551	Sequence 3551, Ap	c 771	5	35.7	25	19	US-10-719-900-432978	Sequence 432978, A
699	5	35.7	25	15	US-10-098-263B-3733	Sequence 3733, Ap	c 772	5	35.7	25	19	US-10-719-900-433971	Sequence 433971, A
700	5	35.7	25	15	US-10-098-263B-13257	Sequence 13257, A	c 773	5	35.7	25	19	US-10-719-900-454720	Sequence 454720, A
701	5	35.7	25	15	US-10-098-263B-13268	Sequence 13268, A	c 774	5	35.7	25	19	US-10-719-900-455098	Sequence 455098, A
702	5	35.7	25	15	US-10-098-263B-24248	Sequence 24248, A	c 775	5	35.7	25	19	US-10-719-900-455734	Sequence 455734, A
703	5	35.7	25	15	US-10-098-263B-31469	Sequence 31469, A	c 776	5	35.7	25	19	US-10-719-900-467323	Sequence 467323, A
704	5	35.7	25	15	US-10-098-263B-42172	Sequence 42172, A	c 777	5	35.7	25	19	US-10-719-900-479181	Sequence 479181, A
705	5	35.7	25	15	US-10-098-263B-44754	Sequence 44754, A	c 778	5	35.7	25	19	US-10-719-900-507371	Sequence 507371, A
706	5	35.7	25	15	US-10-098-263B-53338	Sequence 53338, A	c 779	5	35.7	25	19	US-10-719-900-507490	Sequence 507490, A
707	5	35.7	25	15	US-10-098-263B-56978	Sequence 56978, A	c 780	5	35.7	25	19	US-10-719-900-507491	Sequence 507491, A
708	5	35.7	25	15	US-10-098-263B-58431	Sequence 58431, A	c 781	5	35.7	25	19	US-10-719-900-509731	Sequence 509731, A
709	5	35.7	25	15	US-10-098-263B-58432	Sequence 58432, A	c 782	5	35.7	25	19	US-10-719-900-529244	Sequence 529244, A
710	5	35.7	25	15	US-10-098-263B-79483	Sequence 79483, A	c 783	5	35.7	25	19	US-10-719-900-529245	Sequence 529245, A
711	5	35.7	25	15	US-10-098-263B-79964	Sequence 79964, A	c 784	5	35.7	25	19	US-10-719-900-530460	Sequence 530460, A
712	5	35.7	25	15	US-10-098-263B-82696	Sequence 82696, A	c 785	5	35.7	25	19	US-10-719-900-530461	Sequence 530461, A
713	5	35.7	25	15	US-10-098-263B-84184	Sequence 84184, A	c 786	5	35.7	25	19	US-10-719-900-537546	Sequence 537546, A
714	5	35.7	25	15	US-10-098-263B-94185	Sequence 94185, A	c 787	5	35.7	25	19	US-10-719-900-545787	Sequence 545787, A
715	5	35.7	25	15	US-10-098-263B-94186	Sequence 94186, A	c 788	5	35.7	25	19	US-10-719-900-568399	Sequence 568399, A
716	5	35.7	25	15	US-10-098-263B-98476	Sequence 98476, A	c 789	5	35.7	25	19	US-10-719-900-576321	Sequence 576321, A
717	5	35.7	25	15	US-10-098-263B-99830	Sequence 99830, A	c 790	5	35.7	25	19	US-10-719-900-607820	Sequence 607820, A
718	5	35.7	25	15	US-10-098-263B-103628	Sequence 103628, A	c 791	5	35.7	25	19	US-10-719-900-634123	Sequence 634123, A
719	5	35.7	25	15	US-10-098-263B-126214	Sequence 126214, A	c 792	5	35.7	25	19	US-10-719-900-635696	Sequence 635696, A
720	5	35.7	25	15	US-10-098-263B-125710	Sequence 125710, A	c 793	5	35.7	25	19	US-10-719-900-678174	Sequence 678174, A
721	5	35.7	25	15	US-10-098-263B-126285	Sequence 126285, A	c 794	5	35.7	25	19	US-10-719-900-693294	Sequence 693294, A
722	5	35.7	25	15	US-10-098-263B-127241	Sequence 127241, A	c 795	5	35.7	25	19	US-10-719-900-694113	Sequence 694113, A
723	5	35.7	25	15	US-10-098-263B-130715	Sequence 130715, A	c 796	5	35.7	25	19	US-10-719-900-709662	Sequence 709662, A
724	5	35.7	25	18	US-10-717-597-492	Sequence 492, App	c 797	5	35.7	25	19	US-10-719-900-712003	Sequence 712003, A
725	5	35.7	25	19	US-10-719-900-6000	Sequence 6000, Ap	c 798	5	35.7	25	19	US-10-719-900-714936	Sequence 714936, A
726	5	35.7	25	19	US-10-719-900-36500	Sequence 36500, A	c 799	5	35.7	25	19	US-10-719-900-717597	Sequence 717597, A

C 800	5	35.7	25	19	US-10-719-900-726334	Sequence 726334,	C 873	5	35.7	60	10	US-09-908-975-17531	Sequence 17531, A
C 801	5	35.7	25	19	US-10-719-900-729972	Sequence 729972,	C 874	5	35.7	60	10	US-09-908-975-13505	Sequence 13505, A
C 802	5	35.7	25	19	US-10-719-900-752750	Sequence 752750,	C 875	5	35.7	65	10	US-09-908-975-13505	Sequence 13505, Ap
C 803	5	35.7	25	19	US-10-719-900-754258	Sequence 754258,	C 876	5	35.7	65	10	US-09-908-975-3640	Sequence 3640, Ap
C 804	5	35.7	25	19	US-10-719-900-758859	Sequence 758859,	C 877	5	35.7	65	10	US-09-908-975-26807	Sequence 26807, A
C 805	5	35.7	25	19	US-10-719-900-763636	Sequence 763636,	C 878	5	35.7	65	10	US-09-908-975-27013	Sequence 27013, A
C 806	5	35.7	25	19	US-10-719-900-772731	Sequence 772731,	C 879	5	35.7	65	10	US-09-908-975-29561	Sequence 29561, A
C 807	5	35.7	25	19	US-10-719-900-777496	Sequence 777496,	C 880	5	35.7	76	17	US-10-388-360-126	Sequence 126, App
C 808	5	35.7	25	19	US-10-719-900-782800	Sequence 782800,	C 881	5	35.7	77	9	US-09-449-204-15	Sequence 15, Appl
C 809	5	35.7	25	19	US-10-719-900-783131	Sequence 783131,	C 882	5	35.7	77	10	US-09-860-474-38	Sequence 38, Appl
C 810	5	35.7	25	19	US-10-719-900-795817	Sequence 795817,	C 883	5	35.7	77	16	US-10-409-565-38	Sequence 38, Appl
C 811	5	35.7	25	19	US-10-719-900-798884	Sequence 798884,	C 884	5	35.7	77	18	US-10-729-581-128	Sequence 128, App
C 812	5	35.7	25	19	US-10-719-900-806667	Sequence 806667,	C 885	5	35.7	79	16	US-10-029-386-21442	Sequence 21442, A
C 813	5	35.7	25	19	US-10-719-900-816908	Sequence 816908,	C 886	5	35.7	80	10	US-09-817-748-2	Sequence 2, Appli
C 814	5	35.7	25	19	US-10-719-900-820675	Sequence 820675,	C 887	5	35.7	84	9	US-09-880-821-7	Sequence 7, Appli
C 815	5	35.7	25	19	US-10-719-900-821711	Sequence 821711,	C 888	5	35.7	85	10	US-09-817-748-1	Sequence 1, Appli
C 816	5	35.7	25	19	US-10-719-900-831369	Sequence 831369,	C 889	5	35.7	87	9	US-09-880-821-6	Sequence 6, Appli
C 817	5	35.7	25	19	US-10-719-900-883895	Sequence 883895,	C 890	5	35.7	89	10	US-09-803-454-17	Sequence 17, Appl
C 818	5	35.7	25	19	US-10-719-900-890027	Sequence 890027,	C 891	5	35.7	90	10	US-09-747-377-381	Sequence 381, App
C 819	5	35.7	25	19	US-10-719-900-890028	Sequence 890028,	C 892	5	35.7	90	14	US-10-105-613-381	Sequence 381, App
C 820	5	35.7	25	19	US-10-719-900-894815	Sequence 894815,	C 893	5	35.7	90	17	US-10-296-734-1363	Sequence 1363, Ap
C 821	5	35.7	25	19	US-10-719-900-927001	Sequence 927001,	C 894	5	35.7	100	8	US-08-781-986A-4860	Sequence 4860, Ap
C 822	5	35.7	25	19	US-10-719-900-927801	Sequence 927801,	C 895	5	35.7	100	17	US-10-329-624-4860	Sequence 4860, Ap
C 823	5	35.7	25	19	US-10-719-900-937486	Sequence 937486,	C 896	5	35.7	101	18	US-10-674-124A-1784	Sequence 1784, Ap
C 824	5	35.7	25	19	US-10-719-900-940515	Sequence 940515,	C 897	5	35.7	101	18	US-10-674-124A-24968	Sequence 24968, A
C 825	5	35.7	25	19	US-10-719-900-952915	Sequence 952915,	C 898	5	35.7	101	18	US-10-425-115-155546	Sequence 155546,
C 826	5	35.7	25	19	US-10-719-900-974891	Sequence 974891,	C 899	5	35.7	102	17	US-08-781-986A-4831	Sequence 4831, Ap
C 827	5	35.7	27	9	US-09-815-656-25	Sequence 25, Appl	C 900	5	35.7	102	17	US-10-329-624-4831	Sequence 4831, Ap
C 828	5	35.7	27	9	US-09-815-656-39	Sequence 39, Appl	C 901	5	35.7	103	9	US-09-867-701-3640	Sequence 3640, Ap
C 829	5	35.7	28	17	US-10-621-758A-49	Sequence 49, Appl	C 902	5	35.7	104	9	US-09-983-965-4695	Sequence 4695, Ap
C 830	5	35.7	28	18	US-10-663-208A-49	Sequence 49, Appl	C 903	5	35.7	104	16	US-10-029-386-21407	Sequence 21407, A
C 831	5	35.7	28	18	US-10-646-308A-49	Sequence 49, Appl	C 904	5	35.7	106	17	US-10-242-535A-13819	Sequence 13819, A
C 832	5	35.7	28	18	US-10-736-769-49	Sequence 49, Appl	C 905	5	35.7	106	17	US-10-085-783A-13819	Sequence 13819, A
C 833	5	35.7	30	17	US-10-394-388A-20	Sequence 20, Appl	C 906	5	35.7	110	18	US-10-674-124A-18460	Sequence 18460, A
C 834	5	35.7	31	14	US-10-062-848-20	Sequence 20, Appl	C 907	5	35.7	110	18	US-10-674-124A-21187	Sequence 21187, A
C 835	5	35.7	31	18	US-10-776-104-20	Sequence 20, Appl	C 908	5	35.7	114	17	US-10-373-802-3	Sequence 3, Appli
C 836	5	35.7	32	10	US-09-530-169-6	Sequence 6, Appli	C 909	5	35.7	114	18	US-10-674-124A-16304	Sequence 16304, A
C 837	5	35.7	32	18	US-10-676-248B-132	Sequence 132, Appl	C 910	5	35.7	115	18	US-10-425-115-47986	Sequence 47986, A
C 838	5	35.7	32	18	US-10-823-730-6	Sequence 6, Appli	C 911	5	35.7	116	17	US-10-424-599-29703	Sequence 29703, A
C 839	5	35.7	33	9	US-09-834-109-1	Sequence 1, Appli	C 912	5	35.7	117	18	US-10-437-963-75653	Sequence 75653, A
C 840	5	35.7	34	9	US-09-829-381A-6	Sequence 6, Appli	C 913	5	35.7	118	9	US-09-864-761-29408	Sequence 29408, A
C 841	5	35.7	34	17	US-10-681-972-6	Sequence 6, Appli	C 914	5	35.7	119	15	US-10-189-916A-3	Sequence 3, Appli
C 842	5	35.7	35	10	US-09-860-474-56	Sequence 56, Appl	C 915	5	35.7	124	9	US-09-923-876-1731	Sequence 1731, Ap
C 843	5	35.7	35	16	US-10-409-565-56	Sequence 56, Appl	C 916	5	35.7	124	9	US-09-864-761-22846	Sequence 22846, A
C 844	5	35.7	35	18	US-10-363-552-45	Sequence 45, Appl	C 917	5	35.7	124	10	US-09-923-876-1731	Sequence 1731, Ap
C 845	5	35.7	37	9	US-09-834-109-3	Sequence 3, Appli	C 918	5	35.7	124	18	US-10-437-963-38624	Sequence 38624, A
C 846	5	35.7	38	10	US-09-997-623-17	Sequence 17, Appl	C 919	5	35.7	127	18	US-10-674-124A-4142	Sequence 4142, Ap
C 847	5	35.7	38	10	US-09-997-623-18	Sequence 18, Appl	C 920	5	35.7	128	9	US-09-864-761-26927	Sequence 26927, A
C 848	5	35.7	38	10	US-09-978-917A-17	Sequence 17, Appl	C 921	5	35.7	129	17	US-10-296-115-308	Sequence 308, App
C 849	5	35.7	38	10	US-09-978-917A-18	Sequence 18, Appl	C 922	5	35.7	129	18	US-10-852-973-2	Sequence 2, Appli
C 850	5	35.7	39	17	US-10-423-688A-21	Sequence 21, Appl	C 923	5	35.7	130	9	US-09-864-761-19929	Sequence 19929, A
C 851	5	35.7	40	15	US-10-008-960-33	Sequence 33, Appl	C 924	5	35.7	130	9	US-09-864-761-24378	Sequence 24378, A
C 852	5	35.7	41	10	US-09-969-086A-6	Sequence 6, Appli	C 925	5	35.7	130	9	US-09-864-761-24703	Sequence 24703, A
C 853	5	35.7	41	10	US-09-969-086A-6	Sequence 6, Appli	C 926	5	35.7	132	16	US-10-029-386-21062	Sequence 21062, A
C 854	5	35.7	41	17	US-10-035-833A-2469	Sequence 2469, Ap	C 927	5	35.7	132	18	US-10-674-124A-20958	Sequence 20958, A
C 855	5	35.7	41	17	US-10-035-833A-4804	Sequence 4804, Ap	C 928	5	35.7	135	9	US-09-998-598-2385	Sequence 2385, Ap
C 856	5	35.7	41	17	US-10-035-833A-4843	Sequence 4843, Ap	C 929	5	35.7	137	17	US-10-424-599-114909	Sequence 114909, A
C 857	5	35.7	47	17	US-10-349-143-733	Sequence 733, App	C 930	5	35.7	138	17	US-09-815-242-3667	Sequence 3667, Ap
C 858	5	35.7	47	17	US-10-333-829-118	Sequence 118, App	C 931	5	35.7	138	16	US-10-029-386-17105	Sequence 17105, A
C 859	5	35.7	50	17	US-10-131-827-2775	Sequence 2775, Ap	C 932	5	35.7	138	17	US-10-282-122A-4910	Sequence 4910, Ap
C 860	5	35.7	50	17	US-10-131-827-3611	Sequence 3611, Ap	C 933	5	35.7	141	9	US-09-864-761-21454	Sequence 21454, A
C 861	5	35.7	54	15	US-10-008-960-35	Sequence 35, Appl	C 934	5	35.7	141	18	US-10-425-115-177538	Sequence 177538, A
C 862	5	35.7	59	8	US-08-781-986A-4956	Sequence 4956, Ap	C 935	5	35.7	144	18	US-10-437-963-39237	Sequence 39237, A
C 863	5	35.7	59	9	US-09-797-410-11	Sequence 11, Appl	C 936	5	35.7	145	18	US-10-767-701-16206	Sequence 16206, A
C 864	5	35.7	59	17	US-10-329-624-4956	Sequence 4956, Ap	C 937	5	35.7	146	9	US-09-783-590-4109	Sequence 4109, Ap
C 865	5	35.7	59	17	US-10-362-263-11	Sequence 11, Appl	C 938	5	35.7	147	9	US-09-880-821-8	Sequence 8, Appli
C 866	5	35.7	60	10	US-09-908-975-5414	Sequence 5414, Ap	C 939	5	35.7	148	17	US-10-242-535A-37555	Sequence 37555, A
C 867	5	35.7	60	10	US-09-908-975-5778	Sequence 5778, Ap	C 940	5	35.7	148	17	US-10-085-783A-37555	Sequence 37555, A
C 868	5	35.7	60	10	US-09-908-975-8123	Sequence 8123, Ap	C 941	5	35.7	148	18	US-10-425-115-104591	Sequence 104591, A
C 869	5	35.7	60	10	US-09-908-975-12229	Sequence 12229, A	C 942	5	35.7	149	18	US-10-425-115-126133	Sequence 126133, A
C 870	5	35.7	60	10	US-09-908-975-12446	Sequence 12446, A	C 943	5	35.7	150	13	US-10-027-632-175656	Sequence 175656, A
C 871	5	35.7	60	10	US-09-908-975-14060	Sequence 14060, A	C 944	5	35.7	150	14	US-10-198-846-10346	Sequence 10346, A
C 872	5	35.7	60	10	US-09-908-975-14372	Sequence 14372, A	C 945	5	35.7	150	16	US-10-029-386-22305	Sequence 22305, A

Sequence 175656,
Sequence 50954, A
Sequence 27689, A
Sequence 23032, A
Sequence 31975, A
Sequence 24, Appl
Sequence 61849, A
Sequence 12342,
Sequence 50540, A
Sequence 3163, Ap
Sequence 29591, A
Sequence 21179, A
Sequence 6070, Ap
Sequence 6667, Ap
Sequence 22134, A
Sequence 9649, Ap
Sequence 24593, A
Sequence 11939, A
Sequence 11939, A
Sequence 34971, A
Sequence 123487,
Sequence 44679, A
Sequence 109841,
Sequence 4666, Ap
Sequence 102364,
Sequence 3927, Ap
Sequence 21665, A
Sequence 6274, Ap
Sequence 23529, A
Sequence 4953, Ap
Sequence 8521, Ap
Sequence 42184, A
Sequence 2134, Ap
Sequence 14, Appl
Sequence 43522, A
Sequence 17338, A
Sequence 131630,
Sequence 1898, Ap
Sequence 37128, A
Sequence 37128, A
Sequence 1122, Ap
Sequence 80578, A
Sequence 3076, Ap
Sequence 39739, A
Sequence 27156, A
Sequence 156610,
Sequence 31, Appl
Sequence 11787, A
Sequence 26615, A
Sequence 173424,
Sequence 180260,
Sequence 17043, A
Sequence 132, App
Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-242-535A-57578
; Sequence 57578, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340

US-10-242-535A-57578
; Sequence 57578, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57578
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Human

US-10-085-783A-57578
Alignment Scores:
Pred. No.: 3,15e-06 Length: 288
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-57578 (1-288)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 63 GAAGATAATGCTCTCAGAAAATGTGGGTCTCTGTGTGGCACT 104

RESULT 3
US-10-242-535A-20816
; Sequence 20816, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.

; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PATENT NO. US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-20816

Alignment Scores:
Pred. No.: 3.69e-06 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-242-535A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 170

RESULT 4

US-10-085-783A-20816
; Sequence 20816, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20816
; LENGTH: 350
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-20816

Alignment Scores:
Pred. No.: 3.69e-06 Length: 350
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-085-783A-20816 (1-350)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 129 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 170

RESULT 5

US-09-920-300A-1413/c
; Sequence 1413, Application US/09920300A
; Patent No. US20020136728A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547
; CURRENT APPLICATION NUMBER: US/09/920,300A
; CURRENT FILING DATE: 2001-07-31
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-920-300A-1413

Alignment Scores:
Pred. No.: 4.47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-920-300A-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 395

RESULT 6

US-10-033-528-1413/c
; Sequence 1413, Application US/10033528
; Publication No. US20020131971A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.547C1
; CURRENT APPLICATION NUMBER: US/10/033,528
; CURRENT FILING DATE: 2001-12-26
; NUMBER OF SEQ ID NOS: 1896
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-528-1413

Alignment Scores:
Pred. No.: 4.47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-736-250-5 (1-14) x US-10-033-528-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAATGCGGTCTCTGTGTGGCACT 395

RESULT 7

US-10-099-926-1413/c
; Sequence 1413, Application US/10099926
; Publication No. US20030166064A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; APPLICANT: Jiang, Yugu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C2
; CURRENT APPLICATION NUMBER: US/10/099,926
; CURRENT FILING DATE: 2002-03-17
; NUMBER OF SEQ ID NOS: 1982
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1413
; LENGTH: 444
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-099-926-1413

Alignment Scores:
Pred. No.: 4,47e-06 Length: 444
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-09-736-250-5 (1-14) x US-10-099-926-1413 (1-444)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 436 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 395

RESULT 8
US-09-777-564-1252
; Sequence 1252, Application US/09777564
; Patent No. US20020022591A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493
; CURRENT APPLICATION NUMBER: US/09/777,564
; CURRENT FILING DATE: 2001-02-05
; NUMBER OF SEQ ID NOS: 1730
; SOFTWARE: FastSeq for Window Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: misc.feature
; LOCATION: (1)...(447)
; OTHER INFORMATION: n = A,T,C or G
US-09-777-564-1252

Alignment Scores:
Pred. No.: 4,49e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-736-250-5 (1-14) x US-09-777-564-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 134

RESULT 9
US-10-015-219-1252
; Sequence 1252, Application US/10015219
; Publication No. US20030008299A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.493C1
; CURRENT APPLICATION NUMBER: US/10/015,219
; CURRENT FILING DATE: 2002-03-02
; NUMBER OF SEQ ID NOS: 1739
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1252
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: NAME/KEY: misc.feature
; LOCATION: 424, 428, 437, 440
; OTHER INFORMATION: n = A,T,C or G
US-10-015-219-1252

Alignment Scores:
Pred. No.: 4,49e-06 Length: 447
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-736-250-5 (1-14) x US-10-015-219-1252 (1-447)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 93 GAAGATAATGCTCAGAAAATGGGTTCTGTGTGGCACT 134

RESULT 10
US-09-736-250-2
; Sequence 2, Application US/09736250
; Publication No. US20050014139A1
; GENERAL INFORMATION:
; APPLICANT: SUMITOMO ELECTRIC INDUSTRIES, LTD.
; APPLICANT: NAKAMURA, Takeshi
; TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING THE SAME
; FILE REFERENCE: 050212-0278
; CURRENT APPLICATION NUMBER: US/09/736,250
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/054,492
; PRIOR FILING DATE: 1998-04-03
; PRIOR APPLICATION NUMBER: PCT/JP96/02905
; PRIOR FILING DATE: 1996-10-07
; PRIOR APPLICATION NUMBER: 284663/1995
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 1134
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-250-2

Alignment Scores:
Pred. No.: 9,5e-06 Length: 1134
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-736-250-5 (1-14) x US-09-736-250-2 (1-1134)

Qy 1 GluAspAsnValSerGluAsnValCysValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 11

US-10-172-118-1326
; Sequence 1326, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_006835
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1326

Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-172-118-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValCysValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 12

US-10-342-887-1326
; Sequence 1326, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Van de Vijver, Marc J.
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1326
; LENGTH: 1260

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1326
Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-09-736-250-5 (1-14) x US-10-342-887-1326 (1-1260)

Qy 1 GluAspAsnValSerGluAsnValCysValCysGlyThr 14
Db 1027 GAAGATAATGTCAGAAAATGTGGTTCTGTGTGGCACT 1068

RESULT 13

US-10-641-643-899
; Sequence 899, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 899:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1260 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g1183161
; SEQUENCE DESCRIPTION: SEQ ID NO: 899 :

US-10-641-643-899
Alignment Scores:
Pred. No.: 1.03e-05 Length: 1260
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0

```
DB: 17 Gaps: 0
US-09-736-250-5 (1-14) x US-10-641-643-899 (1-1260)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1027 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 1068
RESULT 14
US-09-867-701-10907
; Sequence 10907, Application US/09867701
; Patent No. US20020132237A1
; GENERAL INFORMATION:
; APPLICANT: Aglate, Paul A.
; APPLICANT: Jones, Robert
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.497
; CURRENT APPLICATION NUMBER: US/09/867,701
; CURRENT FILING DATE: 2001-05-29
; NUMBER OF SEQ ID NOS: 10912
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10907
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-867-701-10907
Alignment Scores:
Pred. No.: 1.43e-05 Length: 1889
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-736-250-5 (1-14) x US-09-867-701-10907 (1-1889)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1570 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 1611
RESULT 15
US-09-814-353-21294
; Sequence 21294, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; APPLICANT: Lee, John
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF OVARIAN CANCER
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21294
; LENGTH: 2146
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-814-353-21294
Alignment Scores:
Pred. No.: 1.59e-05 Length: 2146
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0
US-09-736-250-5 (1-14) x US-09-814-353-21294 (1-2146)
Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14
Db 1213 GAAGATAATGCTCAGAAAATGTGGTTCTGTGTGGCACT 1254
Search completed: February 11, 2005, 17:09:44
Job time : 75.665 secs
```

Result No.	Score	Query		DB	ID	Description	
		Match	Length				
1	14	100.0	136	7	Z20123	Z20123 HSAABLIIE P	
C	2	14	100.0	139	1	AA678060	AA678060 z125f08.8
	3	14	100.0	139	1	AA094874	AA094874 cp2090.se
C	4	14	100.0	197	1	AA659220	AA659220 nt92c11.8
	5	14	100.0	234	1	AA058781	AA058781 zf58f03.r
C	6	14	100.0	246	4	BG180306	BG180306 602331150
	7	14	100.0	251	5	BQ327548	BQ327548 CM0-RT001
C	8	14	100.0	251	5	BQ327560	BQ327560 CM0-RT001
	9	14	100.0	265	7	R85184	R85184 y043f02.r1

C 83	14	100.0	408	1	AA057087	AA057087 zfs9d06.r	C 156	14	100.0	449	1	AA864947	AA864947 oh36b04.s
C 84	14	100.0	408	4	BI063454	BI063454 IL3-UT011	C 157	14	100.0	450	1	AI795935	AI795935 wh40c11.x
C 85	14	100.0	409	1	AA021333	AA021333 z68D08.r	C 158	14	100.0	450	1	AI158006	AI158006 zo53h03.s
C 86	14	100.0	409	2	AW387725	AW387725 MR4-ST011	C 159	14	100.0	451	1	AI301708	AI301708 gn36h05.x
C 87	14	100.0	409	2	AW401698	AW401698 UI-HF-BK0	C 160	14	100.0	451	7	H86415	H86415 y83e05.r1
C 88	14	100.0	409	2	AW438598	AW438598 xu37a07.x	C 161	14	100.0	452	1	AA411127	AA411127 zc29g02.r
C 89	14	100.0	411	6	CA868145	CA868145 i-78e02.y	C 162	14	100.0	452	1	AA101887	AA101887 zk85b06.r
C 90	14	100.0	411	7	TI5517	TI5517 IB1478 Infa	C 163	14	100.0	453	2	AA406913	AA406913 UI-HF-BK0
C 91	14	100.0	413	7	N24351	N24351 yx14a05.r1	C 164	14	100.0	454	2	AW135630	AW135630 UI-H-B11-
C 92	14	100.0	414	1	AI370280	AI370280 qv76a01.x	C 165	14	100.0	454	2	BI063988	BI063988 IL3-UT011-
C 93	14	100.0	414	2	BE168324	BE168324 QV3-HT051	C 166	14	100.0	455	7	CN403769	CN403769 170006001
C 94	14	100.0	414	2	BI063807	BI063807 IL3-UT011	C 167	14	100.0	456	7	N91218	N91218 zal3f01.r1
C 95	14	100.0	415	1	AA018940	AA018940 ze56a07.r	C 168	14	100.0	457	7	N32671	N32671 yx77e10.r1
C 96	14	100.0	415	2	BP22344	BP22344 7p51f01.x	C 169	14	100.0	459	1	AA001081	AA001081 ze47a01.r
C 97	14	100.0	417	1	AI085425	AI085425 oW82h01.s	C 170	14	100.0	459	1	AI032951	AI032951 ox06h03.s
C 98	14	100.0	417	7	HO1313	HO1313 y199c04.s1	C 171	14	100.0	459	1	AI347777	AI347777 qO96c05.x
C 99	14	100.0	417	7	R89574	R89574 yp97b03.s1	C 172	14	100.0	459	2	AW403463	AW403463 UI-HF-BK0
C 100	14	100.0	418	1	AA857209	AA857209 of63d04.s	C 173	14	100.0	459	7	N29011	N29011 yx40b06.r1
C 101	14	100.0	418	1	AA226929	AA226929 zr21b11.s	C 174	14	100.0	460	1	AA021650	AA021650 zee9d06.r
C 102	14	100.0	418	1	BI063848	BI063848 IL3-UT011	C 175	14	100.0	461	1	AA054388	AA054388 zf54f01.r
C 103	14	100.0	419	1	AA158818	AA158818 z647c01.r	C 176	14	100.0	461	1	AA057851	AA057851 z195f08.s
C 104	14	100.0	420	1	AA704015	AA704015 ag80b04.r	C 177	14	100.0	461	7	N25815	N25815 yx22b02.r1
C 105	14	100.0	420	4	BI063843	BI063843 IL3-UT011	C 178	14	100.0	461	7	R87382	R87382 ym88f06.r1
C 106	14	100.0	420	7	H84867	H84867 ys90h07.r1	C 179	14	100.0	462	1	AI499883	AI499883 tn97c04.x
C 107	14	100.0	421	1	AI952335	AI952335 wx72c10.x	C 180	14	100.0	462	1	AJ708106	AJ708106 AJ708106
C 108	14	100.0	421	1	AA157562	AA157562 zo68g05.s	C 181	14	100.0	463	1	AA773958	AA773958 ab67d05.r
C 109	14	100.0	422	4	BI063835	BI063835 IL3-UT011	C 182	14	100.0	463	2	BE326321	BE326321 hw01f10.x
C 110	14	100.0	423	1	AA058780	AA058780 zfs8f02.r	C 183	14	100.0	463	4	BI850226	BI850226 ima9gqc.1
C 111	14	100.0	423	1	AI002297	AI002297 qO86f06.s	C 184	14	100.0	463	5	BU059467	BU059467 im22f05.x
C 112	14	100.0	424	1	AA223161	AA223161 zr06b10.s	C 185	14	100.0	466	1	AI274874	AI274874 qk61e11.x
C 113	14	100.0	424	2	BF197808	BF197808 7p29g06.x	C 186	14	100.0	466	1	AI306635	AI306635 qn45h11.x
C 114	14	100.0	426	1	AA043972	AA043972 zk58e02.s	C 187	14	100.0	466	7	W21065	W21065 z5b5a09.r1
C 115	14	100.0	426	1	AA146787	AA146787 zo35g12.s	C 188	14	100.0	467	5	BQ302769	BQ302769 CN1-BT059
C 116	14	100.0	426	2	BF852263	BF852263 MR3-EN009	C 189	14	100.0	468	1	AA134108	AA134108 z129c01.s
C 117	14	100.0	427	1	AA767578	AA767578 oa31b12.s	C 190	14	100.0	468	1	AI879492	AI879492 au53b06.x
C 118	14	100.0	427	1	AA961959	AA961959 oq92c10.s	C 191	14	100.0	468	2	BF927593	BF927593 CM2-NT019
C 119	14	100.0	427	7	N68425	N68425 zal3e08.s1	C 192	14	100.0	468	4	BI063827	BI063827 IL3-UT011
C 120	14	100.0	428	1	AA525244	AA525244 ni52f05.s	C 193	14	100.0	468	7	N43869	N43869 yy43c12.r1
C 121	14	100.0	431	7	H82548	H82548 yv77a05.r1	C 194	14	100.0	470	1	AA837513	AA837513 o831b11.s
C 122	14	100.0	432	7	CN645730	CN645730 ILLUMIGEN	C 195	14	100.0	470	2	AA213687	AA213687 zq92h06.r
C 123	14	100.0	433	1	AA150672	AA150672 z146b02.s	C 196	14	100.0	470	2	AW062552	AW062552 ILO-CT007
C 124	14	100.0	433	2	BF431566	BF431566 na45f09.s	C 197	14	100.0	472	1	AA861414	AA861414 ak34b06.s
C 125	14	100.0	433	4	BI063839	BI063839 IL3-UT011	C 198	14	100.0	472	2	BE675931	BE675931 7f18f07.x
C 126	14	100.0	434	1	AA503477	AA503477 nh59e05.s	C 199	14	100.0	475	1	AI046124	AI046124 T8NU1210
C 127	14	100.0	435	1	AA021376	AA021376 ze68c10.r	C 200	14	100.0	475	1	AI801762	AI801762 zc95b05.x
C 128	14	100.0	435	1	AA121968	AA121968 zm25c09.s	C 201	14	100.0	475	1	AA459535	AA459535 z8x8g08.r
C 129	14	100.0	435	7	W96274	W96274 ze42e02.r1	C 202	14	100.0	475	5	BQ548661	BQ548661 ik93h12.x
C 130	14	100.0	436	1	AA021071	AA021071 ze85e08.r	C 203	14	100.0	476	1	AA954106	AA954106 oq65d12.s
C 131	14	100.0	436	5	BQ379929	BQ379929 IL3-UT011	C 204	14	100.0	476	4	BI063844	BI063844 IL3-UT011
C 132	14	100.0	437	1	AA758948	AA758948 ah77e07.s	C 205	14	100.0	477	6	CA445832	CA445832 UI-H-E10-
C 133	14	100.0	437	1	AA121443	AA121443 zm23g08.s	C 206	14	100.0	478	1	AA456153	AA456153 zc20f06.r
C 134	14	100.0	437	1	AA159531	AA159531 zo72g08.s	C 207	14	100.0	478	1	AA456153	AA456153 zc20f06.r
C 135	14	100.0	437	4	BI063825	BI063825 IL3-UT011	C 208	14	100.0	478	4	BI063991	BI063991 IL3-UT011
C 136	14	100.0	438	1	AA128673	AA128673 zo4b02.s	C 209	14	100.0	478	4	BI491939	BI491939 df17c01.w
C 137	14	100.0	440	1	AA128673	AA128673 zo4b02.s	C 210	14	100.0	478	4	BI906154	BI906154 603062603
C 138	14	100.0	440	1	AI635372	AI635372 t694c11.x	C 211	14	100.0	479	2	BF942472	BF942472 n8e9a03
C 139	14	100.0	441	2	AW299224	AW299224 xs48a02.x	C 212	14	100.0	479	2	AW020980	AW020980 df17c01.y
C 140	14	100.0	441	2	BF109033	BF109033 7l49d03.x	C 213	14	100.0	480	2	BE205841	BE205841 db46h01.x
C 141	14	100.0	441	7	H30847	H30847 yO78e09.r1	C 214	14	100.0	482	4	BI063983	BI063983 IL3-UT011
C 142	14	100.0	441	7	W46581	W46581 zc32e09.s1	C 215	14	100.0	482	5	BX280952	BX280952 BX280952
C 143	14	100.0	442	1	AA157272	AA157272 z052d07.s	C 216	14	100.0	482	7	R90752	R90752 yno2a05.r1
C 144	14	100.0	442	2	BE295596	BE295596 601176557	C 217	14	100.0	483	1	AA586757	AA586757 nm71c04.s
C 145	14	100.0	443	2	BI063807	BI063807 QV3-HT051	C 218	14	100.0	484	1	AJ707455	AJ707455 AJ707455
C 146	14	100.0	444	1	AI342973	AI342973 qo27c04.x	C 219	14	100.0	484	2	AW403704	AW403704 UI-HF-BK0
C 147	14	100.0	444	1	AA130255	AA130255 z129c01.r	C 220	14	100.0	485	1	AA157999	AA157999 z057D09.s
C 148	14	100.0	445	1	AA102742	AA102742 zn75c10.s	C 221	14	100.0	485	1	AA417175	AA417175 zu13b07.r
C 149	14	100.0	445	5	BU740183	BU740183 t40b07.x	C 222	14	100.0	485	2	AW264664	AW264664 xg33d03.x
C 150	14	100.0	446	1	AI680686	AI680686 tx40b07.x	C 223	14	100.0	485	2	BE206087	BE206087 ba97c12.x
C 151	14	100.0	446	1	BI063833	BI063833 IL3-UT011	C 224	14	100.0	486	2	BF842750	BF842750 QV2-HT101
C 152	14	100.0	446	5	BU785406	BU785406 in45c04.x	C 225	14	100.0	486	4	BI063468	BI063468 IL3-UT011
C 153	14	100.0	447	1	AI636109	AI636109 tz92h04.x	C 226	14	100.0	487	1	AI813543	AI813543 wj03d01.x
C 154	14	100.0	447	6	CA943599	CA943599 lr82d01.x	C 227	14	100.0	487	1	AA291445	AA291445 zt44d09.r
C 155	14	100.0	448	1	AA027118	AA027118 zk04h06.s	C 228	14	100.0	487	4	BI063801	BI063801 IL3-UT011

C 229	14	100.0	488	1	A1149667	A1149667	qf37d07.x	302	14	100.0	541	4	BM312319	BM312319	ig4th09.y
C 230	14	100.0	488	1	A712254	A712254	QV73-H101	C 303	14	100.0	544	2	AW236763	AW236763	xm4f08.x
C 231	14	100.0	488	2	BF836252	BF836252	QV3-H101	C 304	14	100.0	549	1	AU160225	AU160225	AI160225
C 232	14	100.0	489	1	AA937188	AA937188	ok13c10.s	C 305	14	100.0	549	1	AA599293	AA599293	ag35c03.s
C 233	14	100.0	489	1	A1580775	A1580775	ta04f05.x	C 306	14	100.0	550	5	BP306529	BP306529	BP306529
C 234	14	100.0	489	2	AW473016	AW473016	x827e05.x	C 307	14	100.0	552	2	AW176627	AW176627	IL4-CT007
C 235	14	100.0	492	4	B1063842	B1063842	IL3-UT011	C 308	14	100.0	554	2	AW515055	AW515055	xu83b04.x
C 236	14	100.0	492	4	BM509658	BM509658	ig92e01.y	C 309	14	100.0	555	1	AA211288	AA211288	zp44g11.s
C 237	14	100.0	493	2	AW873472	AW873472	hm01h04.x	C 310	14	100.0	556	4	AA523356	AA523356	ni67b10.s
C 238	14	100.0	494	1	A1268435	A1268435	qm03h09.x	C 311	14	100.0	556	4	BG656173	BG656173	ib37h12.y
C 239	14	100.0	495	4	BM707945	BM707945	UI-E-C11-	C 312	14	100.0	557	2	BF318192	BF318192	6018g16189
C 240	14	100.0	497	1	AA088548	AA088548	z189c07.r	C 313	14	100.0	558	1	A1419541	A1419541	tf23d08.x
C 241	14	100.0	498	1	AW714067	AW714067	nw18g11.s	C 314	14	100.0	558	1	AU159472	AU159472	AU159472
C 242	14	100.0	498	2	AW302456	AW302456	xw04c02.x	C 315	14	100.0	559	1	AA521260	AA521260	aa75e06.s
C 243	14	100.0	499	1	AA827740	AA827740	ob54h11.s	C 316	14	100.0	559	4	BG684675	BG684675	603635957
C 244	14	100.0	499	1	AA612651	AA612651	no42f02.s	C 317	14	100.0	561	4	BF975395	BF975395	602245924
C 245	14	100.0	500	2	BF093118	BF093118	PM1-TN012	C 318	14	100.0	562	1	AA664175	AA664175	ac04h04.s
C 246	14	100.0	500	5	BUT31805	BUT31805	UI-E-C11-	C 319	14	100.0	562	2	BF437208	BF437208	7p67h12.x
C 247	14	100.0	501	1	A1340077	A1340077	qQ44b07.x	C 320	14	100.0	562	4	BG686057	BG686057	602638626
C 248	14	100.0	501	1	AA533127	AA533127	nj46902.s	C 321	14	100.0	563	2	AW612687	AW612687	hh30e12.x
C 249	14	100.0	501	5	BU430243	BU430243	UI-HF-BN0	C 322	14	100.0	564	1	AA088443	AA088443	z189c07.s
C 250	14	100.0	502	1	A1126969	A1126969	qB96d02.x	C 323	14	100.0	564	1	A1755086	A1755086	cr35c06.x
C 251	14	100.0	502	2	AW772789	AW772789	h196h02.x	C 324	14	100.0	567	5	BP259087	BP259087	BP259087
C 252	14	100.0	502	4	BM687893	BM687893	UI-E-CK1-	C 325	14	100.0	568	1	A1144511	A1144511	qB73h04.x
C 253	14	100.0	504	1	A156184	A156184	z047c01.s	C 326	14	100.0	568	2	AW409690	AW409690	fh01d06.y
C 254	14	100.0	504	4	B1063658	B1063658	IL3-UT011	C 327	14	100.0	569	1	AA595249	AA595249	no33b07.s
C 255	14	100.0	504	4	B1063676	B1063676	IL3-UT011	C 328	14	100.0	570	1	AA525154	AA525154	ni51a08.s
C 256	14	100.0	504	4	B1063677	B1063677	IL3-UT011	C 329	14	100.0	572	1	AU146040	AU146040	AU146040
C 257	14	100.0	504	4	B1063980	B1063980	IL3-UT011	C 330	14	100.0	576	5	BM996837	BM996837	UI-H-DH0-
C 258	14	100.0	505	4	B1063987	B1063987	IL3-UT011	C 331	14	100.0	577	4	B1869952	B1869952	603394102
C 259	14	100.0	505	4	B1063693	B1063693	IL3-UT011	C 332	14	100.0	578	5	BP258271	BP258271	BP258271
C 260	14	100.0	505	4	B1063815	B1063815	IL3-UT011	C 333	14	100.0	580	1	A1598247	A1598247	cn15d02.x
C 261	14	100.0	505	4	B1063845	B1063845	IL3-UT011	C 334	14	100.0	580	2	AW009156	AW009156	ws78b05.x
C 262	14	100.0	505	4	B1063973	B1063973	IL3-UT011	C 335	14	100.0	581	1	AA056104	AA056104	zf55c03.r
C 263	14	100.0	505	4	B1063998	B1063998	IL3-UT011	C 336	14	100.0	581	2	AW162274	AW162274	au75h05.x
C 264	14	100.0	506	1	AA456187	AA456187	zx74d06.r	C 337	14	100.0	581	5	BP258977	BP258977	BP258977
C 265	14	100.0	506	4	B1063678	B1063678	IL3-UT011	C 338	14	100.0	582	1	AU147052	AU147052	AU147052
C 266	14	100.0	506	4	B1063687	B1063687	IL3-UT011	C 339	14	100.0	582	2	AW411227	AW411227	fh11b01.y
C 267	14	100.0	506	6	CA868199	CA868199	ir79e01.y	C 340	14	100.0	587	1	AA496420	AA496420	zv37c03.r
C 268	14	100.0	507	2	BF837876	BF837876	QV3-H101	C 341	14	100.0	587	5	BP205055	BP205055	BP205055
C 269	14	100.0	507	4	B1063663	B1063663	IL3-UT011	C 342	14	100.0	588	5	BU078719	BU078719	im69c04.x
C 270	14	100.0	507	4	B1063665	B1063665	IL3-UT011	C 343	14	100.0	589	5	BU620209	BU620209	UI-H-PH1-
C 271	14	100.0	508	4	B1063990	B1063990	IL3-UT011	C 344	14	100.0	589	5	AU145099	AU145099	AU145099
C 272	14	100.0	509	4	B1063979	B1063979	IL3-UT011	C 345	14	100.0	596	1	AA434521	AA434521	zw31d12.r
C 273	14	100.0	511	1	BG656485	BG656485	ib37h12.x	C 346	14	100.0	596	6	CA868387	CA868387	ir78e02.x
C 274	14	100.0	513	1	AA443651	AA443651	zw35b10.r	C 347	14	100.0	597	6	N58511	N58511	yy72f08.s1
C 275	14	100.0	514	4	B1063978	B1063978	df01h03.y	C 348	14	100.0	597	7	AA053834	AA053834	zf53b06.r
C 276	14	100.0	515	2	AW019937	AW019937	iq19c12.y	C 349	14	100.0	598	1	AA593432	AA593432	no34a11.s
C 277	14	100.0	515	6	CA948213	CA948213	qf76d05.s	C 350	14	100.0	601	1	AA846727	AA846727	aj99a10.s
C 278	14	100.0	516	1	AA968669	AA968669	EST181758	C 351	14	100.0	601	1	AA593789	AA593789	nm65d01.s
C 279	14	100.0	516	1	A1288797	A1288797	qm06g10.x	C 352	14	100.0	601	2	BE891426	BE891426	601434883
C 280	14	100.0	517	2	BE207846	BE207846	bb06a09.x	C 353	14	100.0	603	5	BQ272152	BQ272152	ij90a09.x
C 281	14	100.0	517	2	BF110854	BF110854	7n41b06.x	C 354	14	100.0	603	7	CN805010	CN805010	IL4UMIGEN
C 282	14	100.0	520	2	BF110854	BF110854	7n41b06.x	C 355	14	100.0	603	1	AA664102	AA664102	ac06a03.s
C 283	14	100.0	521	1	AA417071	AA417071	zu13b07.s	C 356	14	100.0	605	1	AA664102	AA664102	ac06a03.s
C 284	14	100.0	524	4	B1063679	B1063679	IL3-UT011	C 357	14	100.0	606	5	BU579739	BU579739	im90a11.x
C 285	14	100.0	524	4	BF1912257	BF1912257	603068487	C 358	14	100.0	607	1	AA044648	AA044648	DKE2p434p
C 286	14	100.0	526	1	AA758596	AA758596	ah58a08.s	C 359	14	100.0	607	1	AA629751	AA629751	ae63c01.s
C 287	14	100.0	526	1	AA604363	AA604363	no79g10.s	C 360	14	100.0	608	4	BM015005	BM015005	603640960
C 288	14	100.0	526	2	BE549514	BE549514	7b39e01.x	C 361	14	100.0	610	2	BF243478	BF243478	601879503
C 289	14	100.0	527	2	BF843136	BF843136	MR2-H104	C 362	14	100.0	610	2	AW151319	AW151319	xg47h08.x
C 290	14	100.0	531	1	A1601273	A1601273	ar99b01.x	C 363	14	100.0	611	1	AA188001	AA188001	zp67h10.s
C 291	14	100.0	531	5	BQ653339	BQ653339	AGENCOURT	C 364	14	100.0	611	2	BE223082	BE223082	hu47a07.x
C 292	14	100.0	532	1	AA018843	AA018843	ze57h10.r	C 365	14	100.0	611	4	BM690806	BM690806	UI-E-CK0-
C 293	14	100.0	532	1	AA707260	AA707260	ag84d03.r	C 366	14	100.0	617	7	N30602	N30602	yy72b06.s1
C 294	14	100.0	534	2	AW051330	AW051330	wy89d03.x	C 367	14	100.0	612	1	A1420758	A1420758	tf02h11.x
C 295	14	100.0	534	6	CA867868	CA867868	ir82d01.y	C 368	14	100.0	613	2	AW612458	AW612458	hh02e09.x
C 296	14	100.0	535	1	AA215707	AA215707	zr97h07.r	C 369	14	100.0	614	1	AA053911	AA053911	zf52f06.r
C 297	14	100.0	537	2	AW290919	AW290919	UI-H-B12-	C 370	14	100.0	614	1	A1436613	A1436613	t103h01.x
C 298	14	100.0	538	1	AA487524	AA487524	ab20e06.s	C 371	14	100.0	617	2	AW249490	AW249490	2821433.3
C 299	14	100.0	538	4	BM505258	BM505258	ig92e01.x	C 372	14	100.0	619	4	B1063996	B1063996	IL3-UT011
C 300	14	100.0	540	1	AA225516	AA225516	nc25b10.r	C 373	14	100.0	619	4	BM857651	BM857651	ij69c03.x
C 301	14	100.0	541	2	AW265239	AW265239	xq54a01.x	C 374	14	100.0	624	4	BG482778	BG482778	60502564

C 375	14	100.0	626	1	AA057586	AA057586 zfc2909.1	448	14	100.0	750	4	BQ428886	602494673
C 376	14	100.0	628	2	BE220798	BE220798 hu18h03.x	449	14	100.0	751	5	EX422046	EX422046
C 377	14	100.0	629	6	CB381894	CB381894 TgESTzyh2	450	14	100.0	754	4	AW079270	AW079270
C 378	14	100.0	632	6	CA947959	CA947959 iql19c12.x	C 451	14	100.0	756	2	AM073133	AM073133 wy94b02.x
C 379	14	100.0	633	5	BM991335	BM991335 UI-H-D10-	C 452	14	100.0	757	4	BG211683	BG211683 RST31252
C 380	14	100.0	634	1	AA053839	AA053839 zfc53c08.1	C 453	14	100.0	757	4	BG777885	BG777885 603665623
C 381	14	100.0	635	2	BF594792	BF594792 zfc55d03.x	C 454	14	100.0	760	4	BI906096	BI906096 603062484
C 382	14	100.0	636	1	AA205570	AA205570 zq6b08.s	C 455	14	100.0	764	6	CB962746	CB962746
C 383	14	100.0	636	7	CN483826	CN483826 hw38g08.y	C 456	14	100.0	765	7	CF135787	CF135787 UI-HF-BN0
C 384	14	100.0	640	5	BQ429097	BQ429097 AGENCOURT	C 457	14	100.0	766	4	BG767215	BG767215 602740208
C 385	14	100.0	642	1	AA573290	AA573290 nk98c09.s	C 458	14	100.0	767	6	CD520815	CD520815 AGENCOURT
C 386	14	100.0	642	5	BU784337	BU784337 tn13g08.x	C 459	14	100.0	770	2	BF036200	BF036200 601483271
C 387	14	100.0	643	1	AI679428	AI679428 tu63f12.x	C 460	14	100.0	775	4	BG219146	BG219146 RST38899
C 388	14	100.0	644	2	BF794011	BF794011 602254657	C 461	14	100.0	778	4	BG213882	BG213882 RST33504
C 389	14	100.0	644	5	BU689348	BU689348 UI-CF-ECL	C 462	14	100.0	782	1	AI018633	AI018633 ou47h04.x
C 390	14	100.0	645	2	AW152399	AW152399 xg64a01.x	C 463	14	100.0	784	5	BU176897	BU176897 AGENCOURT
C 391	14	100.0	645	4	BM312236	BM312236 i941h09.x	C 464	14	100.0	801	2	BE620803	BE620803 601483387
C 392	14	100.0	647	2	BF435610	BF435610 nac33h11.	C 465	14	100.0	801	5	BQ645542	BQ645542 AGENCOURT
C 393	14	100.0	648	7	CN403762	CN403762 170004245	C 466	14	100.0	803	5	BQ071740	BQ071740 AGENCOURT
C 394	14	100.0	653	4	BG759588	BG759588 602712170	C 467	14	100.0	806	2	BF669925	BF669925 602118429
C 395	14	100.0	654	1	AI765328	AI765328 at73f10.x	C 468	14	100.0	810	5	EX461980	EX461980
C 396	14	100.0	654	1	AI832925	AI832925 at73e05.x	C 469	14	100.0	828	5	BU566387	BU566387 AGENCOURT
C 397	14	100.0	654	2	BF792283	BF792283 602252801	C 470	14	100.0	829	1	AI523625	AI523625 t995c02.x
C 398	14	100.0	655	2	AW467341	AW467341 he09e10.x	C 471	14	100.0	833	5	BU532129	BU532129 AGENCOURT
C 399	14	100.0	657	5	BQ773620	BQ773620 UI-H-EZ1-	C 472	14	100.0	834	2	BF698561	BF698561 602130766
C 400	14	100.0	658	1	AI719868	AI719868 as47a04.x	C 473	14	100.0	849	2	BF577160	BF577160 602135454
C 401	14	100.0	661	2	BF925989	BF925989 MR2-NT013	C 474	14	100.0	852	7	CF243019	CF243019 AGENCOURT
C 402	14	100.0	662	1	AI928836	AI928836 au65b11.x	C 475	14	100.0	853	2	BF666533	BF666533 602123987
C 403	14	100.0	663	4	BE613480	BE613480 603504247	C 476	14	100.0	854	4	BG182134	BG182134 RST998 At
C 404	14	100.0	663	4	BI917454	BI917454 603185118	C 477	14	100.0	856	2	BF130818	BF130818 601818484
C 405	14	100.0	664	5	BU603028	BU603028 AGENCOURT	C 478	14	100.0	872	5	BU542568	BU542568 AGENCOURT
C 406	14	100.0	666	1	AA218918	AA218918 UI-CF-DU1	C 479	14	100.0	873	4	BG531994	BG531994 602561020
C 407	14	100.0	666	1	AA218918	AA218918 zt02c03.s	C 480	14	100.0	889	6	CD517935	CD517935 AGENCOURT
C 408	14	100.0	667	6	CA441829	CA441829 UI-H-ED0-	C 481	14	100.0	893	4	BI257270	BI257270 602967201
C 409	14	100.0	668	5	BQ002431	BQ002431 UI-H-E11-	C 482	14	100.0	899	6	CD358716	CD358716 AGENCOURT
C 410	14	100.0	670	5	BM997732	BM997732 UI-H-D10-	C 483	14	100.0	899	6	CD522597	CD522597 AGENCOURT
C 411	14	100.0	671	5	BM980581	BM980581 UI-CF-E01	C 484	14	100.0	911	2	BE747713	BE747713 601578166
C 412	14	100.0	671	5	BQ016234	BQ016234 UI-H-D10-	C 485	14	100.0	913	5	BQ221930	BQ221930 AGENCOURT
C 413	14	100.0	671	5	BQ773013	BQ773013 UI-H-PE0-	C 486	14	100.0	920	2	BE300217	BE300217 600944220
C 414	14	100.0	672	5	BM970544	BM970544 UI-H-PE0-	C 487	14	100.0	921	5	BQ230170	BQ230170 AGENCOURT
C 415	14	100.0	672	5	BU615980	BU615980 UI-CF-ECL	C 488	14	100.0	921	7	CF264864	CF264864 AGENCOURT
C 416	14	100.0	672	6	CD640858	CD640858 AGENCOURT	C 489	14	100.0	927	2	BF575348	BF575348 602134082
C 417	14	100.0	673	1	AI928349	AI928349 w96c03.x	C 490	14	100.0	938	5	BQ710910	BQ710910 AGENCOURT
C 418	14	100.0	673	5	BQ182277	BQ182277 UI-H-EU0-	C 491	14	100.0	946	4	BG031336	BG031336 602299031
C 419	14	100.0	673	5	BU738049	BU738049 UI-E-DW1-	C 492	14	100.0	959	5	BQ230627	BQ230627 AGENCOURT
C 420	14	100.0	674	5	BM994615	BM994615 UI-H-DH0-	C 493	14	100.0	960	5	BQ30674	BQ30674 AGENCOURT
C 421	14	100.0	674	6	CA448476	CA448476 UI-H-E10-	C 494	14	100.0	967	7	CN647834	CN647834 ILLUMGEN
C 422	14	100.0	674	6	CD366863	CD366863 UI-H-F12-	C 495	14	100.0	968	2	BE789168	BE789168 601476292
C 423	14	100.0	676	4	BG762543	BG762543 602734406	C 496	14	100.0	973	5	BQ650937	BQ650937 AGENCOURT
C 424	14	100.0	679	4	BG188438	BG188438 RST7456.A	C 497	14	100.0	975	2	BF570206	BF570206 602185591
C 425	14	100.0	680	4	BG661032	BG661032 N335 SSH-	C 498	14	100.0	976	4	BG392121	BG392121 602410213
C 426	14	100.0	681	6	CD642085	CD642085 AGENCOURT	C 499	14	100.0	978	4	BM463752	BM463752 AGENCOURT
C 427	14	100.0	682	2	BF220183	BF220183 601296732	C 500	14	100.0	979	2	BF344340	BF344340 602014715
C 428	14	100.0	690	7	CF135924	CF135924 UI-HF-BN0	C 501	14	100.0	982	5	BQ708698	BQ708698 AGENCOURT
C 429	14	100.0	691	2	BF337048	BF337048 602034442	C 502	14	100.0	983	2	BF795121	BF795121 602256456
C 430	14	100.0	692	2	BE887738	BE887738 601486303	C 503	14	100.0	986	4	BG32783	BG32783 602410158
C 431	14	100.0	694	1	AA703243	AA703243 z170e05.s	C 504	14	100.0	1024	2	BE613274	BE613274 601452513
C 432	14	100.0	694	6	CA441689	CA441689 UI-H-ED0-	C 505	14	100.0	1029	4	BM454583	BM454583 AGENCOURT
C 433	14	100.0	695	1	AA910671	AA910671 ok84a04.s	C 506	14	100.0	1041	4	BM555910	BM555910 AGENCOURT
C 434	14	100.0	700	2	BF055443	BF055443 7j0b08.x	C 507	14	100.0	1059	4	BG254346	BG254346 602368913
C 435	14	100.0	701	1	AI568713	AI568713 th14g08.x	C 508	14	100.0	1068	5	BM923007	BM923007 AGENCOURT
C 436	14	100.0	716	2	BE888060	BE888060 601511562	C 509	14	100.0	1078	4	BM454194	BM454194 AGENCOURT
C 437	14	100.0	723	1	AI740926	AI740926 wgl18d08.x	C 510	14	100.0	1091	2	BE894125	BE894125 601438253
C 438	14	100.0	724	2	BF667981	BF667981 602122225	C 511	14	100.0	1109	4	BF980373	BF980373 602288255
C 439	14	100.0	724	7	CF135985	CF135985 UI-HF-BN0	C 512	14	100.0	1109	4	BM462171	BM462171 AGENCOURT
C 440	14	100.0	728	2	BE620268	BE620268 601483387	C 513	14	100.0	1126	4	BG119682	BG119682 602349304
C 441	14	100.0	731	2	BF241617	BF241617 601878943	C 514	14	100.0	1134	9	AY412158	AY412158 Homo sap1
C 442	14	100.0	731	5	BU632784	BU632784 UI-H-FE1-	C 515	14	100.0	1142	4	BM466858	BM466858 AGENCOURT
C 443	14	100.0	743	2	BF797400	BF797400 602257046	C 516	14	100.0	1241	4	BG746028	BG746028 60273467
C 444	14	100.0	744	6	CD522104	CD522104 AGENCOURT	C 517	14	100.0	1458	4	BM473295	BM473295 AGENCOURT
C 445	14	100.0	745	5	BQ000493	BQ000493 UI-H-DP0-	C 518	13	92.9	277	2	AW299229	AW299229 x848b02.x
C 446	14	100.0	746	4	BG912921	BG912921 602807320	C 519	13	92.9	298	2	BF902812	BF902812 CN2-MT019
C 447	14	100.0	748	6	CB963441	CB963441 AGENCOURT	C 520	13	92.9	298	2	AW409656	AW409656 FN01B09.Y

C 521	13	92.9	315	2	AW410809	AW410809	Fh08e04.y	C 594	10	71.4	552	7	C0587851	C0587851	DG2-17j6
C 522	13	92.9	383	4	B1063819	B1063819	IL3-UT011	C 595	10	71.4	556	7	C0690076	C0690076	DG11-269p
C 523	13	92.9	408	1	AA578724	AA578724	nh23h11.s	C 596	10	71.4	557	7	C0711347	C0711347	DG14-1671
C 524	13	92.9	418	1	A1329205	A1329205	tg10f04.x	C 597	10	71.4	558	7	C0688565	C0688565	DG11-2470
C 525	13	92.9	437	7	H30719	H30719	yo78h08.r1	C 598	10	71.4	561	7	C0689123	C0689123	DG11-2540
C 526	13	92.9	525	1	A1742970	A1742970	wg76e06.x	C 599	10	71.4	565	7	C0694756	C0694756	DG11-75k2
C 527	13	92.9	643	4	B1197962	B1197962	602761927	C 600	10	71.4	571	7	C0686546	C0686546	DG11-218d
C 528	13	92.9	703	4	BG616164	BG616164	602642744	C 601	10	71.4	574	7	C0701431	C0701431	DG32-2030
C 529	13	92.9	753	4	B1859488	B1859488	603385338	C 602	10	71.4	575	7	C0701622	C0701622	DG32-209a
C 530	13	92.9	839	4	BG397722	BG397722	602438783	C 603	10	71.4	576	7	C0700099	C0700099	DG32-1700
C 531	13	92.9	889	4	BF979086	BF979086	602147596	C 604	10	71.4	577	7	C0690551	C0690551	DG11-2761
C 532	13	92.9	915	4	BG682664	BG682664	602626956	C 605	10	71.4	578	7	BG664994	BG664994	DRABWFO3
C 533	12	85.7	145	1	AA701610	AA701610	zi41e11.s	C 606	10	71.4	582	7	C0693161	C0693161	DG11-59a1
C 534	12	85.7	348	5	BQ334196	BQ334196	PM4-MT010	C 607	10	71.4	585	7	C0683945	C0683945	DG11-176p
C 535	12	85.7	388	1	AA099355	AA099355	zk85b06.s	C 608	10	71.4	585	7	C0686061	C0686061	DG11-210b
C 536	12	85.7	474	1	AA053977	AA053977	zf47c02.r	C 609	10	71.4	586	7	C0589769	C0589769	DG32-30f10
C 537	12	85.7	714	2	BR294585	BR294585	601176160	C 610	10	71.4	586	7	C0689003	C0689003	DG11-253d
C 538	11	78.6	295	6	CB107619	CB107619	K-EST0146	C 611	10	71.4	591	7	C0695929	C0695929	DG11-91h7
C 539	11	78.6	364	4	B1063837	B1063837	IL3-UT011	C 612	10	71.4	592	7	C0681686	C0681686	DG11-132c
C 540	11	78.6	395	2	AW780047	AW780047	hm96g06.x	C 613	10	71.4	593	7	C0684897	C0684897	DG11-192m
C 541	11	78.6	431	1	AA054181	AA054181	zf51b08.r	C 614	10	71.4	595	7	C0691112	C0691112	DG11-286d
C 542	11	78.6	455	2	BF837869	BF837869	QV3-HT101	C 615	10	71.4	599	7	C0687411	C0687411	DG11-231b
C 543	11	78.6	465	4	B1063666	B1063666	IL3-UT011	C 616	10	71.4	599	7	C0716739	C0716739	DG14-2619
C 544	11	78.6	504	2	AA042651	AA042651	UI-RF-BKO	C 617	10	71.4	603	7	C0697636	C0697636	DG32-115n
C 545	11	78.6	550	6	CB554966	CB554966	MMSP0031	C 618	10	71.4	607	7	C0693827	C0693827	DG11-68e2
C 546	11	78.6	627	1	AA044936	AA044936	zf51h09.r	C 619	10	71.4	609	7	C0693559	C0693559	DG11-64f1
C 547	11	78.6	857	2	BB962804	BB962804	601656513	C 620	10	71.4	610	7	C0687549	C0687549	DG11-233f
C 548	11	78.6	1425	4	BG429088	BG429088	602494124	C 621	10	71.4	616	7	C0683741	C0683741	DG11-174e
C 549	10	71.4	212	7	C0582535	C0582535	ILLUMIGEN	C 622	10	71.4	616	7	C0669306	C0669306	DG33-4912
C 550	10	71.4	253	4	B1036115	B1036115	RC5-NT026	C 623	10	71.4	619	7	C0686845	C0686845	DG11-222d
C 551	10	71.4	253	4	B1036116	B1036116	RC5-NT026	C 624	10	71.4	624	7	C0710722	C0710722	DG14-1551
C 552	10	71.4	283	7	CR474271	CR474271	CR474271	C 625	10	71.4	627	7	C0696053	C0696053	DG11-93d4
C 553	10	71.4	291	6	CB710245	CB710245	AMGNNUC:N	C 626	10	71.4	628	7	C0656534	C0656534	DG33-2c12
C 554	10	71.4	294	2	BF800842	BF800842	CMA-CI006	C 627	10	71.4	628	7	C0680061	C0680061	DG11-110a
C 555	10	71.4	296	6	C75090	C75090	C75090 Huma	C 628	10	71.4	628	7	C0693506	C0693506	DG11-63b8
C 556	10	71.4	319	7	C0692628	C0692628	DG11-50i1	C 629	10	71.4	628	7	C0717778	C0717778	DG14-56k1
C 557	10	71.4	331	1	A1508600	A1508600	UI-R-C2-n	C 630	10	71.4	629	4	B1295794	B1295794	UI-R-DK0-
C 558	10	71.4	336	7	Z28780	Z28780	HSB94D042 S	C 631	10	71.4	629	7	C0684311	C0684311	DG11-181d
C 559	10	71.4	350	4	BM422610	BM422610	RSA08_29	C 632	10	71.4	635	7	CF109609	CF109609	Shultzomi
C 560	10	71.4	350	7	C0692475	C0692475	DG11-48n6	C 633	10	71.4	644	2	AW972885	AW972885	EST384980
C 561	10	71.4	354	6	CB779646	CB779646	AMGNNUC:C	C 634	10	71.4	645	7	C0681575	C0681575	DG11-131a
C 562	10	71.4	363	4	B1063847	B1063847	IL3-UT011	C 635	10	71.4	649	7	C0712475	C0712475	DG14-18g1
C 563	10	71.4	373	1	AA483892	AA483892	ne76d08.s	C 636	10	71.4	653	7	C0690561	C0690561	DG11-276n
C 564	10	71.4	377	7	C0711948	C0711948	DG14-179p	C 637	10	71.4	655	7	C0686288	C0686288	DG11-213m
C 565	10	71.4	378	7	C0690584	C0690584	DG11-277d	C 638	10	71.4	665	7	CN004557	CN004557	ip20b09.g
C 566	10	71.4	382	7	H25558	H25558	y148c05.s1	C 639	10	71.4	667	7	CN003894	CN003894	ip40b06.g
C 567	10	71.4	384	7	R76787	R76787	y162b02.s1	C 640	10	71.4	668	7	C0671525	C0671525	DG33-7k4
C 568	10	71.4	389	7	C0681704	C0681704	DG11-132g	C 641	10	71.4	668	7	C0712839	C0712839	DG14-197a
C 569	10	71.4	391	4	B1064004	B1064004	IL3-UT011	C 642	10	71.4	670	7	C0688812	C0688812	DG11-250m
C 570	10	71.4	398	1	AA013295	AA013295	ze28c04.r	C 643	10	71.4	671	7	C0693103	C0693103	DG11-58f1
C 571	10	71.4	403	7	CN542715	CN542715	UI-R-DQ1-	C 644	10	71.4	676	7	C0689890	C0689890	DG11-266p
C 572	10	71.4	404	7	H43440	H43440	YP09h09.s1	C 645	10	71.4	677	7	C0711476	C0711476	DG14-1690
C 573	10	71.4	409	1	AA657275	AA657275	vr27e03.r	C 646	10	71.4	679	7	C0685962	C0685962	DG11-208p
C 574	10	71.4	416	1	AA879848	AA879848	vr99f05.r	C 647	10	71.4	679	7	C0686619	C0686619	DG11-219f
C 575	10	71.4	417	7	H81583	H81583	YU73d02.s1	C 648	10	71.4	681	7	C0714386	C0714386	DG11-219f
C 576	10	71.4	420	1	AA012968	AA012968	ze35a07.r	C 649	10	71.4	686	7	C0687190	C0687190	DG11-2380
C 577	10	71.4	421	4	B1063824	B1063824	IL3-UT011	C 650	10	71.4	691	7	C0570359	C0570359	AGENCOURT
C 578	10	71.4	426	7	C0656112	C0656112	DG32-1g1	C 651	10	71.4	692	7	C0718367	C0718367	DG14-63j8
C 579	10	71.4	427	7	C0684251	C0684251	DG11-180g	C 652	10	71.4	693	7	C0711358	C0711358	DG14-167m
C 580	10	71.4	438	7	C0679953	C0679953	DG11-108p	C 653	10	71.4	695	7	C0692001	C0692001	DG11-40d2
C 581	10	71.4	440	7	RS4642	RS4642	Y778f06.s1	C 654	10	71.4	698	7	C0683294	C0683294	DG11-167g
C 582	10	71.4	442	7	H65038	H65038	Yr69a12.s1	C 655	10	71.4	699	7	C0682968	C0682968	DG11-162a
C 583	10	71.4	454	7	C0712346	C0712346	DG14-187j	C 656	10	71.4	704	7	C0714359	C0714359	DG14-225a
C 584	10	71.4	459	2	BF525036	BF525036	UI-R-ABO-	C 657	10	71.4	707	7	C0696501	C0696501	DG11-99m2
C 585	10	71.4	463	7	C0689602	C0689602	DG11-261i	C 658	10	71.4	707	7	C0610170	C0610170	DG8-90b24
C 586	10	71.4	493	7	C0691805	C0691805	DG11-37p2	C 659	10	71.4	713	7	C0693213	C0693213	DG11-59k5
C 587	10	71.4	512	7	A1154993	A1154993	ud82e01.r	C 660	10	71.4	720	7	C0715438	C0715438	DG14-2511
C 588	10	71.4	513	1	C0692089	C0692089	DG11-41o1	C 661	10	71.4	741	7	CK477989	CK477989	AGENCOURT
C 589	10	71.4	521	7	C0711872	C0711872	DG14-178j	C 662	10	71.4	748	7	CV077745	CV077745	AGENCOURT
C 590	10	71.4	523	7	BF082717	BF082717	PM2-BT072	C 663	10	71.4	759	7	C0654666	C0654666	DG15-1c6
C 591	10	71.4	524	2	C0680564	C0680564	DG11-117k	C 664	10	71.4	796	7	C0558058	C0558058	AGENCOURT
C 592	10	71.4	528	7	C0684316	C0684316	DG11-181e	C 665	10	71.4	803	2	BF794848	BF794848	602256720
C 593	10	71.4	549	7				C 666	10	71.4	826	7	C0571802	C0571802	AGENCOURT

667	10	71.4	852	7	C0569279	COS69279	AGENCOURT	740	9	64.3	646	5	BQ264702	BO264702	NISC	ff01	
668	10	71.4	936	5	BU501311	BUS01311	AGENCOURT	C 741	9	64.3	659	2	BE675818	BE675818	7f16f08.x		
669	10	71.4	1048	7	CR755552	CR755552	AGENCOURT	742	9	64.3	663	2	BF536616	BF536616	602048784		
670	10	71.4	1194	2	BF381715	BF381715	601815930	743	9	64.3	666	1	AA869420	AA869420	vu07ho1.r		
671	10	71.4	1247	7	CF111004	CF111004	Shultzoni	744	9	64.3	669	2	BE370288	BE370288	601222543		
672	9	64.3	67	1	AA085041	AA085041	zn14d06.s	745	9	64.3	669	6	CD769922	CD769922	AGENCOURT		
673	9	64.3	100	5	AA237743	AA237743	mx77a06.r	746	9	64.3	681	2	BE381020	BE381020	601271560		
674	9	64.3	205	5	BQ566775	BQ566775	gi69b06.y	747	9	64.3	681	4	BQ088190	BQ088190	H3149805-		
675	9	64.3	219	1	AA270786	AA270786	va67h05.x	748	9	64.3	682	5	BM950543	BM950543	UI-M-EHOP		
676	9	64.3	229	1	AI242510	AI242510	qu35g12.x	749	9	64.3	693	1	AU134091	AU134091	AU134091		
677	9	64.3	258	7	TI16055	TI16055	IB3060	Infra	750	9	64.3	702	4	BI664158	BI664158	603289276	
678	9	64.3	283	1	AA060810	AA060810	ub44b08.r	751	9	64.3	713	6	CA318826	CA318826	UI-M-EW0-		
679	9	64.3	306	1	AA636862	AA636862	vr20g02.r	752	9	64.3	715	6	BA433441	BA433441	BB433441		
680	9	64.3	312	4	BI491309	BI491309	df16g08.w	753	9	64.3	716	4	BI109437	BI109437	602897241		
681	9	64.3	313	7	T36303	T36303	EST99874	Hu	754	9	64.3	725	4	BI693243	BI693243	603343544	
682	9	64.3	321	7	W11646	W11646	me42d07.r1	755	9	64.3	730	5	BQ444485	BQ444485	UI-M-ERO-		
683	9	64.3	334	7	W62085	W62085	mx84g06.r1	756	9	64.3	731	6	CD578866	CD578866	UI-M-GMO-		
684	9	64.3	338	7	D58262	D58262	HUM359G08B	757	9	64.3	742	4	BG918577	BG918577	602818361		
685	9	64.3	363	1	AA032813	AA032813	mi36g09.r	758	9	64.3	744	7	CO425473	CO425473	UI-M-HU0-		
686	9	64.3	368	2	AW227828	AW227828	up14g06.y	759	9	64.3	750	4	BI109427	BI109427	602897329		
687	9	64.3	388	2	BE285868	BE285868	601096037	760	9	64.3	756	4	BI159253	BI159253	602922778		
688	9	64.3	391	2	BE651680	BE651680	UI-M-AJO-	C 761	9	64.3	758	2	AW212698	AW212698	u010f05.x		
689	9	64.3	396	1	AI286726	AI286726	ub84e02.r	C 762	9	64.3	774	6	CB573199	CB573199	AGENCOURT		
690	9	64.3	406	7	W11289	W11289	mc44d07.r1	763	9	64.3	775	7	CO386590	CO386590	AGENCOURT		
691	9	64.3	408	6	CD565437	CD565437	B0494H08-	764	9	64.3	776	7	CO425463	CO425463	UI-M-HU0-		
692	9	64.3	410	7	BE284815	BE284815	601091130	765	9	64.3	798	7	CF950351	CF950351	UI-M-HU0-		
693	9	64.3	418	7	N41846	N41846	yw72b06.r1	C 766	9	64.3	810	9	CL634334	CL634334	CH243-8F3		
694	9	64.3	420	7	W83977	W83977	me35e06.r1	767	9	64.3	812	4	BI684148	BI684148	603306554		
695	9	64.3	423	6	CD561781	CD561781	B0436C12-	768	9	64.3	817	4	BG919010	BG919010	602819195		
696	9	64.3	425	1	AA260499	AA260499	mz81g11.r	769	9	64.3	836	4	BG862364	BG862364	602962555		
697	9	64.3	427	2	BE624952	BE624952	uu28e08.y	770	9	64.3	836	4	BG1155031	BG1155031	602902555		
698	9	64.3	453	4	BG095222	BG095222	uu85a03.x	771	9	64.3	858	4	BG112293	BG112293	602282442		
699	9	64.3	456	1	AA794632	AA794632	vu66h11.r	772	9	64.3	866	4	BI646132	BI646132	603276342		
700	9	64.3	464	1	AA933799	AA933799	ol84a01.s	773	9	64.3	869	4	BI247958	BI247958	602988745		
701	9	64.3	466	1	AA682145	AA682145	vu13d01.r	774	9	64.3	890	4	BI858571	BI858571	603389030		
702	9	64.3	469	2	AW913458	AW913458	uf53c01.y	775	9	64.3	898	2	BF124028	BF124028	601760121		
703	9	64.3	470	1	AA833452	AA833452	uu58f08.r	776	9	64.3	917	5	BQ934917	BQ934917	AGENCOURT		
704	9	64.3	474	7	CF982140	CF982140	maj78c11.	777	9	64.3	924	5	BQ876232	BQ876232	AGENCOURT		
705	9	64.3	477	2	BE305396	BE305396	601099989	778	9	64.3	933	2	BF099265	BF099265	601752439		
706	9	64.3	478	5	BP753934	BP753934	BP753934	779	9	64.3	933	4	BI695196	BI695196	603346642		
707	9	64.3	478	7	CK382069	CK382069	laq31e11.	780	9	64.3	937	2	BF580447	BF580447	602097215		
708	9	64.3	479	1	AI152814	AI152814	ud31d10.x	781	9	64.3	994	1	AV254915	AV254915	602965992		
709	9	64.3	479	4	BM069425	BM069425	id73g09.y	782	9	64.3	1008	4	BI649944	BI649944	603296592		
710	9	64.3	479	5	BU756426	BU756426	ui31-cf0-	783	9	64.3	1064	4	BG495262	BG495262	602542926		
711	9	64.3	490	4	BG148619	BG148619	uu85a03.y	784	9	64.3	1110	9	AY412160	AY412160	Mus muscu		
712	9	64.3	503	1	AI060433	AI060433	ub40c01.r	785	9	64.3	2045	3	AK050465	AK050465	Mus muscu		
713	9	64.3	507	7	R88891	R88891	yp97b03.r1	-786	9	64.3	2348	3	BC029328	BC029328	Mus muscu		
714	9	64.3	513	1	AI851548	AI851548	UI-M-EH0-	787	9	64.3	2739	3	AK079476	AK079476	Mus muscu		
715	9	64.3	522	5	BX516226	BX516226	BX516226	C 788	8	57.1	208	2	AW901060	AW901060	CM0-NN101		
716	9	64.3	530	2	BE381296	BE381296	601271173	C 789	8	57.1	221	7	CO685194	CO685194	602965992		
717	9	64.3	532	2	CO690581	CO690581	DG11-277b	C 790	8	57.1	232	1	AA091845	AA091845	mm0329.se		
718	9	64.3	543	2	BB821460	BB821460	BB821460	791	8	57.1	247	7	N55813	N55813	J2985F Huma		
719	9	64.3	547	1	AI050464	AI050464	uc86e08.y	792	8	57.1	280	2	BF433379	BF433379	7q69f12.x		
720	9	64.3	569	7	CR757452	CR757452	uu26b02.x	C 793	8	57.1	284	1	AI681819	AI681819	tx39a03.x		
721	9	64.3	571	2	BE852627	BE852627	CR757452	C 794	8	57.1	284	2	BE856106	BE856106	7f88a08.x		
722	9	64.3	571	5	BQ566670	BQ566670	gi66a09.y	C 795	8	57.1	286	7	T64661	T64661	YC25g10.s1		
723	9	64.3	587	2	BE198998	BE198998	ur99c08.x	C 796	8	57.1	315	7	H38381	H38381	VP50f06.r1		
724	9	64.3	593	4	AI082686	AI082686	602877713	C 797	8	57.1	328	4	BI493343	BI493343	df100a06		
725	9	64.3	596	1	AA827353	AA827353	vc15a05.r	798	8	57.1	330	5	BP432781	BP432781	60332781		
726	9	64.3	600	7	BG801714	BG801714	0113-80 M	799	8	57.1	390	7	F33267	F33267	HS2D26583 H		
727	9	64.3	601	4	CR757454	CR757454	CR757454	800	8	57.1	412	1	AA661682	AA661682	AJ661682		
728	9	64.3	604	1	AA869591	AA869591	602441485	C 801	8	57.1	414	1	AA076644	AA076644	zm20c04.s		
729	9	64.3	605	1	AA870443	AA870443	vq09h10.r	C 802	8	57.1	421	7	H56074	H56074	Yq97e04.s1		
730	9	64.3	605	1	AA870528	AA870528	vq22g09.r	C 803	8	57.1	433	4	BI063826	BI063826	IL3-UT011		
731	9	64.3	605	2	AW763774	AW763774	ur65e01.x	C 804	8	57.1	437	7	HO6722	HO6722	Yl83e01.s1		
732	9	64.3	608	7	CR757421	CR757421	CR757421	C 805	8	57.1	469	8	BE286652	BE286652	CH230-39N		
733	9	64.3	611	2	BE285099	BE285099	601097741	C 806	8	57.1	475	1	AA213581	AA213581	zq93b06.r		
734	9	64.3	616	5	BN877227	BN877227	if95g09.x	C 807	8	57.1	506	4	BI063982	BI063982	IL3-UT011		
735	9	64.3	624	6	CD771754	CD771754	AGENCOURT	C 808	8	57.1	520	7	N23823	N23823	YX36h11.r1		
736	9	64.3	626	7	BP428443	BP428443											

813	8	57.1	601	5	BP464377	BP464377 BP464377	C 886	7	50.0	416	1	AA018089
814	8	57.1	640	1	AJ658836	AJ658836 AJ658836	C 887	7	50.0	420	6	CD743630
815	8	57.1	650	8	AZ991285	AZ991285 2M0275H21	C 888	7	50.0	419	7	R87366
816	8	57.1	695	9	CE139522	CE139522 tigr-g88-	C 889	7	50.0	424	3	CNS03809
817	8	57.1	711	9	CE684361	CE684361 tigr-g88-	C 890	7	50.0	430	3	CNS08BWA
818	8	57.1	737	7	CNI166334	CNI166334 997597 MA	C 891	7	50.0	431	4	BI022886
819	8	57.1	759	7	CNI160762	CNI160762 949971 MA	C 892	7	50.0	431	6	CB758501
820	8	57.1	796	7	CNI158846	CNI158846 947667 MA	C 893	7	50.0	440	1	AA150796
821	8	57.1	841	7	CF552849	CF552849 AGENCOURT	C 894	7	50.0	445	1	AA670695
822	8	57.1	866	4	BG339396	BG339396 602416893	C 895	7	50.0	446	4	BM584288
823	8	57.1	913	5	BO674754	BO674754 AGENCOURT	C 896	7	50.0	449	8	AO667591
824	8	57.1	932	5	BO669046	BO669046 AGENCOURT	C 897	7	50.0	450	1	AA074469
825	8	57.1	1083	4	BM460353	BM460353 AGENCOURT	C 898	7	50.0	450	4	BG316274
826	7	50.0	76	1	AA085836	AA085836 zn13g01.s	C 899	7	50.0	454	7	CO969884
827	7	50.0	107	3	CNS08RG6	CNS08RG6 Single re	C 900	7	50.0	455	2	BF424999
828	7	50.0	115	2	BF942477	BF942477 nae95b04.	C 901	7	50.0	455	8	BM031082
829	7	50.0	135	7	CV398108	CV398108 QV4-BN009	C 902	7	50.0	456	8	BM033718
830	7	50.0	135	7	Z20407	Z20407 H8AACEBK P	C 903	7	50.0	459	4	BM656418
831	7	50.0	174	5	BM956062	BM956062 ESTO999 H	C 904	7	50.0	461	1	AI966777
832	7	50.0	179	4	BG315593	BG315593 sab82b10.	C 905	7	50.0	461	4	BM650863
833	7	50.0	183	7	Z20260	Z20260 HGAAABTFM P	C 906	7	50.0	463	4	BM631318
834	7	50.0	194	4	BG315856	BG315856 sab86c03.	C 907	7	50.0	464	4	BM597973
835	7	50.0	221	5	CV192584	CV192584 SNESTbab1	C 908	7	50.0	465	6	CD745135
836	7	50.0	241	5	BU666756	BU666756 NaL3_42B	C 909	7	50.0	467	4	BM68125
837	7	50.0	250	6	CD743633	CD743633 IRB21_C03	C 910	7	50.0	470	4	BM610572
838	7	50.0	267	7	CK927310	CK927310 p3fmgc_01	C 911	7	50.0	472	4	BM619172
839	7	50.0	261	3	CNS09QB7	CK927310 Single re	C 912	7	50.0	472	8	AZ762430
840	7	50.0	267	3	CNS08QX	CK927310 Single re	C 913	7	50.0	475	6	CD743632
841	7	50.0	279	6	CD746492	CD746492 S21_E05_S	C 914	7	50.0	476	3	CNS08EU7
842	7	50.0	281	2	BZ219458	BZ219458 hv58d03_x	C 915	7	50.0	476	6	CD745137
843	7	50.0	293	1	AA321649	AA321649 EST24157	C 916	7	50.0	477	4	BM639794
844	7	50.0	298	3	CNS08LBZ	AX017067 Single re	C 917	7	50.0	479	4	BM597967
845	7	50.0	306	4	BI494153	BI494153 df108a12.	C 918	7	50.0	479	6	CD743628
846	7	50.0	306	4	BI496000	BI496000 df122b08.	C 919	7	50.0	480	4	BM592404
847	7	50.0	307	4	BI494152	BI494152 df108a12.	C 920	7	50.0	480	6	CD745136
848	7	50.0	309	5	BU693912	BU693912 SYD0997 S	C 921	7	50.0	480	6	CF543445
849	7	50.0	310	8	AQ515925	AQ515925 HS_5235 A	C 922	7	50.0	481	2	AW271202
850	7	50.0	313	6	CD743627	CD743627 IRB1Q1_C0	C 923	7	50.0	481	4	BM593285
851	7	50.0	320	1	AA281791	AA281791 zt09b11.s	C 924	7	50.0	481	9	CE355174
852	7	50.0	320	4	BI495999	BI495999 df122b08.	C 925	7	50.0	482	4	BM590863
853	7	50.0	320	6	CD743626	CD743626 IRB15_B10	C 926	7	50.0	482	7	CF541875
854	7	50.0	323	9	CE113499	CE113499 tigr-g88-	C 927	7	50.0	483	6	CD746490
855	7	50.0	329	6	CD743638	CD743638 IRB3_R02	C 928	7	50.0	484	3	CNS08MLD
856	7	50.0	330	3	CNS09145	AX059553 Single re	C 929	7	50.0	485	4	BM584425
857	7	50.0	332	8	AO675313	AO675313 HS_2145 A	C 930	7	50.0	485	6	CD745133
858	7	50.0	333	6	CD743636	CD743636 IRB11_F02	C 931	7	50.0	485	7	CF929901
859	7	50.0	333	7	CR383299	CR383299 CR383299	C 932	7	50.0	485	9	CE748006
860	7	50.0	336	1	A1887000	A1887000 w195c04.x	C 933	7	50.0	487	4	BG042891
861	7	50.0	336	4	BI015424	BI015424 PM0-ET020	C 934	7	50.0	488	4	BM605729
862	7	50.0	338	1	AU189657	AU189657 AU189657	C 935	7	50.0	488	5	BQ133279
863	7	50.0	341	7	CR467553	CR467553 CR467553	C 936	7	50.0	489	7	CN637172
864	7	50.0	346	6	CB405932	CB405932 QSTF059G2	C 937	7	50.0	492	4	BM610012
865	7	50.0	361	6	CD743634	CD743634 IRB2Q1_D1	C 938	7	50.0	493	7	CR527973
866	7	50.0	366	2	BB677894	BB677894 BB677894	C 939	7	50.0	493	7	CR527974
867	7	50.0	370	6	CD743637	CD743637 IRB4Q4_D0	C 940	7	50.0	494	4	BM578604
868	7	50.0	382	2	BE005517	BE005517 CM1-BN011	C 941	7	50.0	495	4	BI892857
869	7	50.0	385	7	CR575838	CR575838 CR575838	C 942	7	50.0	495	4	BM616017
870	7	50.0	387	3	CNS08UVK	AX029436 Single re	C 943	7	50.0	495	4	BM627059
871	7	50.0	390	3	CNS08LBY	AX017066 Single re	C 944	7	50.0	495	6	CD743629
872	7	50.0	391	3	CNS08X94	AX032516 Single re	C 945	7	50.0	497	2	BE080822
873	7	50.0	394	7	CO381419	CO381419 FRA1039 S	C 946	7	50.0	497	4	BM610736
874	7	50.0	396	2	AW804253	AW804253 PM3-UM008	C 947	7	50.0	497	4	BM618338
875	7	50.0	398	4	BI702291	BI702291 sag44g01.	C 948	7	50.0	497	4	BM625709
876	7	50.0	405	2	AW572759	AW572759 hd31a10.x	C 949	7	50.0	498	4	BM631386
877	7	50.0	408	4	CD743635	CD743635 IRB4Q4_B0	C 950	7	50.0	499	4	BM624554
878	7	50.0	409	4	BM643095	BM643095 170006873	C 951	7	50.0	499	6	CD746488
879	7	50.0	410	1	AA689586	AA689586 nv66a05.s	C 952	7	50.0	500	3	CNS09ATC
880	7	50.0	411	2	BF323814	BF323814 sngEST4a20	C 953	7	50.0	500	6	CD746491
881	7	50.0	411	4	BI063688	BI063688 IL3-UT011	C 954	7	50.0	501	6	CD743624
882	7	50.0	411	5	BQ327547	BQ327547 CM0-RT001	C 955	7	50.0	501	6	CD743625
883	7	50.0	411	5	BQ327559	BQ327559 PM1-HT060	C 956	7	50.0	501	8	AQ185130
884	7	50.0	413	2	BE178859	BE178859 PM1-HT060	C 957	7	50.0	502	4	BM606472
885	7	50.0	415	8	B80366	CIT-HSP-204	C 958	7	50.0	503	4	BM600909

```
C 959 7 50.0 505 1 AU240406
C 960 7 50.0 505 4 BM617315
C 961 7 50.0 506 3 CNS087B9
C 962 7 50.0 506 4 BM593189
C 963 7 50.0 506 4 BM601862
C 964 7 50.0 506 4 BM629418
C 965 7 50.0 506 4 BM637119
C 966 7 50.0 506 6 CD745134
C 967 7 50.0 507 4 BM576728
C 968 7 50.0 507 4 BM642509
C 969 7 50.0 507 4 BM655807
C 970 7 50.0 508 3 CNS08BW9
C 971 7 50.0 508 4 BM606937
C 972 7 50.0 508 7 CO687010
C 973 7 50.0 509 5 BP132926
C 974 7 50.0 510 5 BP112779
C 975 7 50.0 510 6 CD743623
C 976 7 50.0 511 5 BU763570
C 977 7 50.0 514 3 CNS09ATB
C 978 7 50.0 515 3 CNS08DSV
C 979 7 50.0 515 4 BI064007
C 980 7 50.0 516 3 CNS0918N
C 981 7 50.0 516 4 BM604463
C 982 7 50.0 516 4 BM646452
C 983 7 50.0 517 3 CNS08ODU
C 984 7 50.0 517 8 AQ556413
C 985 7 50.0 520 1 AJ665628
C 986 7 50.0 520 4 BM610442
C 987 7 50.0 521 3 CNS08UVJ
C 988 7 50.0 521 5 BP180275
C 989 7 50.0 522 3 CNS08RMA
C 990 7 50.0 523 3 CNS08KSN
C 991 7 50.0 526 3 CNS09144
C 992 7 50.0 526 8 AZ970711
C 993 7 50.0 527 3 CNS08KXK
C 994 7 50.0 530 3 CNS08MLE
C 995 7 50.0 531 3 CNS08HX4
C 996 7 50.0 532 6 CA850720
C 997 7 50.0 536 4 BI427629
C 998 7 50.0 538 3 CNS08EU6
C 999 7 50.0 539 1 AL925224
C1000 7 50.0 540 3 CNS08NDK

ALIGNMENTS

Z20123 136 bp mRNA linear EST 07-FEB-1995
DEFINITION HSAABALIE P, Human foetal Brain Whole tissue Homo sapiens cDNA,
mRNA sequence.
ACCESSION Z20123.1 GI:26868
VERSION EST.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 136)
AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE MRC Human Genome Mapping Project Resource Centre.
JOURNAL The UK-HGMP cDNA program
COMMENT Contact: MRC Human Genome Mapping Project Resource Centre
Clinical Research Centre
Watford Road, Harrow, Middlesex HA1 3UJ, U.K.
Email: biolhelp@hgmpr.mrc.ac.uk
single read.
FEATURES
source
Location/Qualifiers
1..136
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="P, Human foetal Brain Whole tissue"

/notes="Vector: Bluescript; clone library=P, Human foetal
Brain Whole tissue; cloning vector is Bluescript."

ORIGIN
Alignment Scores: 9.24e-06 Length: 136
Pred. No.: 14.00 Matches: 14
Score: 100.00% Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 7

US-09-736-250-5 (1-14) x Z20123 (1-136)
Oy 1 GLUApAsnValSerGluAenValGlySerValCysGlyThr 14
Db 24 GAAGATAATGCTCAGAAATGCGGTCTGTGTGGCACT 65

RESULT 2
LOCUS AA678060 139 bp mRNA linear EST 19-DEC-1997
DEFINITION z125f08.s1 Soares fetal liver_spleen_INFLS S1 Homo sapiens cDNA
clone IMAGE:431847 3' similar to TR:G1183162 G1183162 CYCLIN I. ;
mRNA sequence.
ACCESSION AA678060.1 GI:2658582
VERSION EST.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 139)
AUTHORS Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Kritzman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marr, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)
TITLE Unpublished (1997)
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 1.
FEATURES
source
Location/Qualifiers
1..139
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:431847"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal liver_spleen_INFLS S1"
/notes="Organ: Liver and Spleen; Vector: p7T3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco RI;
This is a subcloned version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AATGGAAGAATTAATTAAGACTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified p7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
Alignment Scores:
```

Pred. No.: 9,41e-06 Length: 139
 Score: 14.00 Matches: 14
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA678060 (1-139)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14
 Db 103 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 62

RESULT 3

AA094874

LOCUS

DEFINITION

cp2090.seq.F Human fetal heart, Lambda ZAP Express Homo sapiens

CDNA 5', mRNA sequence.

ACCESSION

AA094874

VERSION

AA094874.1 GI:1640491

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 139)

REFERENCE

AUTHORS

Liew, C.C.

CDNAs from fetal heart (1996)

TITLE

Unpublished (1996)

JOURNAL

Contact: Liew CC

COMMENT

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 617/7328915

Fax: 617/9750995

Email: cliw@rics.bwh.harvard.edu

PCR Primers

FORWARD: 5' GCCAGCTCGAATTAACCTCACTAAAGG 3'

BACKWARD: 5' CCAGTGAATTAACGACTATAGGCG 3'

Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.

FEATURES

Location/Qualifiers

1..139

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/lab_host="E. coli XL1-Blue"

/clone_lib="Human fetal heart, Lambda ZAP Express"

/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). CDNA was synthesized using a XhoI-Oligo dr

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI, for directional cloning into

predigested lambda ZAP Express."

ORIGIN

Alignment Scores:

Pred. No.: 9,41e-06 Length: 139

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA094874 (1-139)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14

Db 50 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 91

RESULT 4

AA659220

LOCUS

DEFINITION

nt92c11.s1 NCI_CGAP_Pri2 Homo sapiens CDNA clone IMAGE:1205972

EST 18-FEB-1998

linear

mRNA

197 bp

Homo sapiens

CDNA clone

IMAGE:1205972

ACCESSION

VERSION

AA659220.1 GI:2595374

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 197)

REFERENCE

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgaps-remail.nih.gov

Tissue Procurement: W. Douglas Figg, Ph.D., Paul H. Duray, M.D.,

Rodrigo F. Chuai, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Length: 288 Std Error: 0.00

Seq primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 161.

FEATURES

Location/Qualifiers

1..197

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="IMAGE:1205972"

/sex="male"

/tissue_type="metastatic prostate bone lesion"

/lab_host="DH10B"

/clone_lib="NCI CGAP Pri2"

/note="Vector: pAMP10; mRNA made from metastatic prostate

lesion of the bone, CDNA made by oligo-dr priming.

Non-directionally cloned. Size-selected on agarose gel,

average insert size 600 bp. Library made by D. Krizman,

NIH."

ORIGIN

Alignment Scores:

Pred. No.: 1.26e-05 Length: 197

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA659220 (1-197)

Qy 1 GluAspAenValSerGluAsnValGlySerValCysGlyThr 14

Db 93 GAAGATAATGCTCAGAAATGTGGTTCTGTGTGGCACT 134

RESULT 5

AA058781/c

LOCUS

DEFINITION

zf58f03.r1 Soares retina NZB4HR Homo sapiens CDNA clone

IMAGE:381149 5', similar to TR:G1183162 G1183162 CYCLIN I. ; mRNA

sequence.

ACCESSION

AA058781

VERSION

AA058781.1 GI:1551591

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 234)

REFERENCE

AUTHORS

Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiappelli, B.,

Chisoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W.,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL

(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-RT0017-211100-702-e07&t3=2000-11-21&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 25.

FEATURES

source

Location/Qualifiers

1..251

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="RT0017"

/note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Alignment Scores:

Pred. No.:	1.53e-05	Length:	251
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-736-250-5 (1-14) x BQ327548 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 163 GAAGATAATGCTCAGAAATGCGGTCTGTGTGGCACT 204

RESULT 8

BQ327560

LOCUS CM0-RT0017-221100-705-e07 RT0017 Homo sapiens cDNA, linear EST 17-MAY-2002

DEFINITION BQ327560 251 bp mRNA

ACCESSION BQ327560.1 GI:20944806

VERSION BQ327560.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 251)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,

Negai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,

Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,

Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V.,

O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and

Simpson, A.J.

Shotgun sequencing of the human transcriptome with ORF expressed

sequence tags

Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL MEDLINE 2020663

PUBMED 10737800

COMMENT Contact: Simpson A.J.G.

Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research

Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil

Tel: +55-11-2704922

Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome

Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-RT0017-221100-705-e07&t3=2000-11-22&t4=1)

Seq primer: puc 18 forward

High quality sequence start: 7

High quality sequence stop: 25.

FEATURES

source

Location/Qualifiers

1..251

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_lib="RT0017"

/note="Organ: kidney tumor; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Pred. No.:	1.53e-05	Length:	251
Score:	14.00	Matches:	14
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	5	Gaps:	0

US-09-736-250-5 (1-14) x BQ327560 (1-251)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 163 GAAGATAATGCTCAGAAATGCGGTCTGTGTGGCACT 204

RESULT 9

R85184/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

R85184 265 bp mRNA linear EST 14-AUG-1995
Y043F02.r1 Soares adult brain N2b4HB55Y Homo sapiens cDNA clone
IMAGE:180699 5', mRNA sequence.

R85184

R85184.1 GI:943590

EST.

Homo sapiens (human)

Homo sapiens

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 265)

Hallier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,

Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,

Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,

Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and

Wilson, R.

The WashU-Merck EST Project

Unpublished (1995)

Contact: Wilson RK

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: est@watson.wustl.edu

Insert Size: 1058

High quality sequence stops: 220

Source: IMAGE Consortium, LLNL

This clone is available royalty-free through LLNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Insert Length: 1058 Std Error: 0.00

Seq primer: M13RP1

High quality sequence stop: 220.

Location/Qualifiers

1..265

/organism="Homo sapiens"

```

sequence revealed clones similarity on wrong strand
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 215.
/dev_stage=35 year old"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares retina N3b4HR"

```

/note="Organ: eye; Vector: pTT3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAAGTGGAGCGCGCTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)⁺ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Alignment Scores:

Pred. No.: 1.65e-05 Length: 275
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA011113 (1-275)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 234 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 193

RESULT 12

LOCUS

AA778982 278 bp mRNA linear EST 05-FEB-1998
ac37f07.s1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:858661 3' similar to TR:Q14094 Q14094 CYCLIN I.; mRNA
sequence.

ACCESSION

AA778982

VERSION

AA778982.1 GI:2838313

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.,
Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M.,
Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F.,
Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R.
WashU-NCI human EST Project
Unpublished (1997)

TITLE

JOURNAL

COMMENT

Contact: Wilson RK
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: es@watson.wustl.edu

FEATURES

source

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 177.
Location/Qualifiers
1..278
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:858661"
/dev_stages="hnt neurons"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene hNT neuron (#937233)"
/note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hNT neurons. Average insert
size: 1.5 Kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5'

GAATTCGGCAGAG 3' ~3' adaptor sequence: 5'
CTCAGATTTTTTTTTTTTTTTT 3"

ORIGIN

Alignment Scores:

Pred. No.: 1.67e-05 Length: 278
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 1 Gaps: 0

US-09-736-250-5 (1-14) x AA778982 (1-278)

Qy 1 GluAspAsnValSerGluAsnValGlySerValCysGlyThr 14

Db 188 GAAGATAATGCTCAGAAATGTGGTCTCTGTGTGGCACT 147

RESULT 13

LOCUS

F32546 296 bp mRNA linear EST 13-MAY-1999
HSPD25369 HM3 Homo sapiens cDNA clone s3000040A06, mRNA sequence.

ACCESSION

F32546

VERSION

F32546.1 GI:4818172

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

1 (bases 1 to 296)

TITLE

Identification of 4370 expressed sequence tags from a
3'-end-specific cDNA library of human skeletal muscle by DNA
sequencing and filter hybridization

JOURNAL

Genome Res. 6 (1), 35-42 (1996)

MEDLINE

98276048

COMMENT

8681137

CONTACT

Contact: Valle G.

CRIBI Biotechnology Centre

University of Padua

Via Trieste 75, 35121 Padua, Italy

ABI Chromatograms and other information are available on WWW at
http://grup.bio.unipd.it.

FEATURES

source

1..296

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clones="s3000040A06"

/sex="female"

/tissue_type="pectoral muscle (after mastectomy)"

/clone_lib="HM3"

/note="Vector: pcDNAII (Invitrogen); Site 1: BstXI;

Site 2: NotI; The library is not subtracted by G.

Lanfranchi. This library is not subtracted nor normalized.

The first strand cDNA was primed with a biotinylated

oligo-dT-NotI primer

(5'-biotin-AACCGGCTCGAGCGCGCTTTTTTTTTTTT-3'). The

ds cDNA was sonicated and size-selected in the range

350-550 bp. The 3' specific fragments were selected by

streptavidin coated magnetic beads, ligated to

non-palindromic BstXI adapters, NotI digested and

directionally cloned into BstXI-NotI cut pcDNAII vector."

ORIGIN

Alignment Scores:

Pred. No.: 1.76e-05 Length: 296

Score: 14.00 Matches: 14

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 7 Gaps: 0

US-09-736-250-5 (1-14) x F32546 (1-296)

Qy 1 GluAspAsnValSerGluAsnValCysGlyThr 14
Db 82 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 123

RESULT 14

BI493342/c

LOCUS BI493342 302 bp mRNA linear EST 28-AUG-2001
DEFINITION df100406.w1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2540459 3', mRNA sequence.

ACCESSION BI493342
VERSION BI493342.1 GI:15332686

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 302)

Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, P.R.

and Morton, C.C.

Isolation of novel and known genes from a human fetal cochlear cDNA

library using subtractive hybridization and differential screening

Genomics 23, 42-50 (1994)

95130111

7829101

Contact: Morton, C. C.

Departments of Pathology and Obstetrics, Gynecology and

Reproductive Biology

Brigham and Women's Hospital

75 Francis Street, Harvard Medical School, Boston, MA 02115, USA

Tel: 617 732 7980

Fax: 617 738 6996

Email: cmorton@rics.bwh.harvard.edu

DNA sequencing and analyses were performed by National Institutes

of Health Intramural Sequencing Center (NISC; see

http://www.nisc.nih.gov).

This clone is available royalty-free through LML; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

Plate: L1AM6328 row: B column: 12

Seq primer: T7 primer.

Location/Qualifiers

1..302

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2540459"

/tissue_type="cochlea"

/dev_stage="16-22 week fetus"

/lab_host="SOLR cells (kanamycin resistant)"

/clone_lib="Morton Fetal Cochlea"

/note="Organ: ear; Vector: pBluescript SK-; Site 1: EcoRI;

Site 2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned

unidirectionally. Primer: Oligo dt. Fetal cochlea, normal.

37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP

XR vector. Library constructed by N. Robertson, C. Morton.

-5' adaptor sequence: 5' GAATTCGGCAGG 3' -3' adaptor

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'

Db 259 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 218

RESULT 15

N84129

LOCUS

N84129

DEFINITION

KK6088F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA

clone KK6088 5' similar to EST(YP97B03.S1), mRNA sequence.

ACCESSION

N84129

VERSION

N84129.1 GI:1259754

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 302)

Liew, C.C.

CDNAs from fetal heart (1996)

Unpublished (1996)

Contact: Liew CC

Brigham and Women's Hospital

Harvard Medical School

75 Francis St. Boston, MA 02115, USA

Tel: 6177328915

Fax: 6179750995

Email: cliew@rics.bwh.harvard.edu

Seq primer: GAAATTAACCTCACTAAAGGG.

FEATURES

source

1..302

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="KK6088"

/lab_host="E. coli XL1-Blue"

/note="Vector: Lambda ZAP Express; Site 1: EcoRI; Site 2:

XhoI; mRNA was purified from human fetal hearts (8-10

weeks). cDNA was synthesized using a XhoI-Oligo dT

adaptor-primer. EcoRI adaptors were ligated, followed by

digestion with XhoI, for directional cloning into

predigested lambda ZAP Express."

ORIGIN

Alignment Scores:

Pred. No.: 1.79e-05

Score: 14.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 100.00%

DB: 7

Length: 302

Matches: 14

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-736-250-5 (1-14) x N84129 (1-302)

Qy 1 GluAspAsnValSerGluAsnValCysGlyThr 14

Db 50 GAAGATAATGCTCAGAAAATGGGTCTGTGTGTGGCACT 91

Search completed: February 11, 2005, 12:22:00

Job time : 274.164 secs